

Tue Dec 11 16:09:58 2003

us-09-601-667c-41.fai

Page 8

LENGTH: 267 amino acids  
TYPE: amino acid  
STANDARDNESS: Single  
TOPOLOGY: Linear  
US-08-338-793D-61

Query Match  
Best Local Similarity 39.1%; Score 376; DB 2; Length 267;  
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 TQGTGKXEPFPIILADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOGXKX 66  
DB 13 TQGTGKXEPFPIILADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOGXKX 66  
QY 67 TQGTGKXEPFPIILADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOGXKX 123  
DB 71 TQGTGKXEPFPIILADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOGXKX 129  
QY 124 AGH-RDQIPGLXOLIOGVYAL--RPGSGSTXKXARSLILQMSISARFPIILMKR 179  
DB 130 AGH-RDQIPGLXOLIOGVYAL--RPGSGSTXKXARSLILQMSISARFPIILMKR 189  
QY 180 OXINSKSFPLDXVMELETSWQSGTQVQSHSTGVNNEKRLAIXGNFTLXNRYVI 239  
DB 190 OXINSKSFPLDXVMELETSWQSGTQVQSHSTGVNNEKRLAIXGNFTLXNRYVI 249  
QY 240 ASIALMLFVCGERPS 255  
DB 250 ASIALMLFVCGERPS 265

RESULT 15  
US-08-839-765-1  
Sequence 1, Application US/08839765  
Patent No. 614631  
GENERAL INFORMATION:  
APPLICANT: Betei, Marc D.  
APPLICANT: Carroll, Stephen F.  
INVENTOR: Betei, Marc D.; Carroll, Stephen F.;  
TITLE OF INVENTION: Early Ribosomes Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: US  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CHECKSUM: 15-APR-1997  
APPLICATION NUMBER: US/08/839,765  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA: US 07/901,707  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708/8869  
FAX: 708/8869  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
NO SIGNAL: 1792: protein

US-08-839-765-1  
Query Match  
Best Local Similarity 39.1%; Score 376; DB 3; Length 267;  
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 TQGTGKXEPFPIILADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOGXKX 66  
DB 13 TQGTGKXEPFPIILADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOGXKX 66  
QY 67 TQGTGKXEPFPIILADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOGXKX 123  
DB 71 TQGTGKXEPFPIILADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOGXKX 129  
QY 124 AGH-RDQIPGLXOLIOGVYAL--RPGSGSTXKXARSLILQMSISARFPIILMKR 179  
DB 130 AGH-RDQIPGLXOLIOGVYAL--RPGSGSTXKXARSLILQMSISARFPIILMKR 189  
QY 180 OXINSKSFPLDXVMELETSWQSGTQVQSHSTGVNNEKRLAIXGNFTLXNRYVI 239  
DB 190 OXINSKSFPLDXVMELETSWQSGTQVQSHSTGVNNEKRLAIXGNFTLXNRYVI 249  
QY 240 ASIALMLFVCGERPS 255  
DB 250 ASIALMLFVCGERPS 265

Search completed: December 11, 2003, 14:11:38  
Job time: 8.86328 secs

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Page 7

Db 13 TGAHTVOSTYFIRAVRGLITGADVRAHEILVLEPVRGVEFLR--QFPLVLESNHAEV 70  
Qy 67 TGAIDVNNVYVAYQKQDQSYFLR-DAPRGAE--THLPTGTTRDSSLPFYSGYXDLERY 123  
Db 71 TLADVTNAYVGVYRAGNSAVFFHPDQCEDAEITHEFT-DVQRYTFARFGYVDRLEQ 129  
Qy 124 AGH-RDQIFLQIXQLQSYVAL--RFGQSTKXKASILLIOMTSKAPFPIIMXR 179  
Db 130 AGNLENIENGLEALISALVYSTGDTLPASFTICIDMISEKAFQYIEBMR 189  
Qy 189 QXINSKSFLEPYXMLELFTSQCQSYQVQSTIDVPRMEXLAIXGNFTLXNEXYI 239  
Db 190 TRFYNRGAPDPSVITLENGRLSTALQSNQAFASPIQLQRMGSKSYVDSIIL 249  
Qy 240 ASLAIMLFCVQSRPS 255  
Db 250 PIALMRYCAPPS 265

RESULT 13  
US-09-601-360-1  
Sequence 1, Application US/08646360

GENERAL INFORMATION:

APPLICANT: Bettey, Marc D.

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

PROTEINS

CORRESPONDENCE ADDRESS:

ADDRESSER: McAndrews, Held & Mallow, Ltd.

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05348

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 26-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McAndrews, Held & Mallow, Ltd.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70, P4

TELEPHONE: 312/670-8889

TELEFAX: 312/670-8889

TELEPHONE: 650 366-1248

TELEFAX: 650 366-1248

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear  
US-08-646-360-1  
Query Match 30.7%, Score 376, DB 2, Length 267;  
Best Local Similarity 39.1%, Pred. No. 3, 7e-37;  
Matches 100; Mismatches 101; Indels 12; Gaps 8;  
Qy 9 TQOTKGEYFRTLLRDVSSGS-TSNHPL-RQSTTPVSDAQFVVELTNGQXDK 66  
Db 13 TGAHTVOSTYFIRAVRGLITGADVRAHEILVLEPVRGVEFLR--QFPLVLESNHAEV 70  
Qy 67 TGAIDVNNVYVAYQKQDQSYFLR-DAPRGAE--THLPTGTTRDSSLPFYSGYXDLERY 123  
Db 71 TLADVTNAYVGVYRAGNSAVFFHPDQCEDAEITHEFT-DVQRYTFARFGYVDRLEQ 129  
Qy 124 AGH-RDQIFLQIXQLQSYVAL--RFGQSTKXKASILLIOMTSKAPFPIIMXR 179  
Db 130 AGNLENIENGLEALISALVYSTGDTLPASFTICIDMISEKAFQYIEBMR 189  
Qy 189 QXINSKSFLEPYXMLELFTSQCQSYQVQSTIDVPRMEXLAIXGNFTLXNEXYI 239  
Db 190 TRFYNRGAPDPSVITLENGRLSTALQSNQAFASPIQLQRMGSKSYVDSIIL 249  
Qy 240 ASLAIMLFCVQSRPS 255  
Db 250 PIALMRYCAPPS 265

RESULT 14  
US-08-338-733D-61  
Sequence 61, Application US/08338793D

GENERAL INFORMATION:

APPLICANT: Barth, Peter Thomas

TITLE OF INVENTION: VECTOR

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS: CISHMAN

ADDRESSER: INTELLECTUAL PROPERTY GROUP OF

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3918

COMPUTER READABLE FORM:

COMPUTER: 3.50 inch 1.44 MB storage

OPERATING SYSTEM: MS-DOS

SOFTWARE: Microsoft Word or ASCII editors

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,793D

FILING DATE: 08-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/842,081

FILING DATE: 26-JUN-92

APPLICATION NUMBER: 9104017.0

FILING DATE: 26-Feb-91

APPLICATION NUMBER: 9109188.4

FILING DATE: 29-Apr-91

ATTORNEY/AGENT INFORMATION:

NAME: Kokulis, Paul N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: US/08/338,793D/215431/TCM

TELEPHONE: 202-861-3900

TELEFAX: 202-861-3900

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 61;



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Page 6

US-08-488-113B-1  
Sequence 1, Application US/08488113B  
Patent No. 5744580

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

INVENTOR: Carroll, Stephen F.

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,113B

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McAndrews, Janet M.

REGISTRATION NUMBER: 32,918

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

REFERENCE/DOCKET NUMBER: 110220507/200-70-P3-C2A

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-113B-1

Query Match

Best Local Similarity 39.1%; Prod. No. 3.7e-37;

Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

DB

9 THGOTGKXEPFPTLNDVSSGS-FSNEIPL-ROSTPVSQAQFVAVLWNGXDX 66

DB

13 TGAATVOSTTTFIRVGRATTTGADVGRPTPLRVGLPTN-QEFLVLSMHELSV 70

QY

67 TLAIDTLYVAVNGROSYR-DARQAE-THTATGDSLSRPSXMYR 123

DB

71 TLAIDVAVVGVGAGNSATFFPHDQDRAITHFT-DVONRYTFAFGNTDRLQL 129

QY

124 AGH-RDOIPIGIXIOLSVKL--RXPQSTKQASILLQWISLARPNTLMRX 179

DB

130 AGNLRNRIELNGPLEALISALVYSTGQTPLLASFTICQISLAPFQYIGEM 189

QY 180 QKNSKSTPDVMTLETSGGOSTGNGTGNPNPRLAIKXGZVLNPKYI 239  
DB 190 TRINRRAADPSVITLNSWRLSTLQSNQCAPAFIOLGRNRSFVSYSILI 249  
QY 240 ASLAIMEPCGERFS 255  
DB 250 PTLNMTKCAPPS 265

US-08-477-484B-1  
Sequence 1, Application US/08477484B  
Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

INVENTOR: Carroll, Stephen F.

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McAndrews, Janet M.

REGISTRATION NUMBER: 32,918

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

REFERENCE/DOCKET NUMBER: 110220507/200-70-P3-C2A

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-1

Query Match

Best Local Similarity 39.1%; Prod. No. 3.7e-37;

Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

DB

9 THGOTGKXEPFPTLNDVSSGS-FSNEIPL-ROSTPVSQAQFVAVLWNGXDX 66

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US-08-218-303-16
/ Sequence 16, Application US/08218303
/ Patent No. 5547867
/ GENERAL INFORMATION:
/ APPLICANT: Kara, Bhupendra V.
/ APPLICANT: Hockney, Robert C.
/ APPLICANT: Filton, John B.
/ TITLE OF INVENTION: ASSEMBLY PROCESS
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cushman, Darby & Cushman
/ STREET: 1615 L Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20036-5601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/218,303
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/841,533
/ FILING DATE: 26-FEB-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Koriulis, Paul N.
/ REGISTRATION NUMBER: 6,773
/ REFERENCE/DOCKET NUMBER: PAK/3893/94908/MJM
/ TELEPHONE: 202-861-3000
/ TELEFAX: 202-822-0944
/ TELEX: 6714627 CUSH
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-218-303-16

Query Match 30.7%; Score 376; DB 1; Length 267;
Best Local Similarity 39.1%; Pred. No. 3.7e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 THGTGKYEYFETILADYVSSGS--FSENIPL--ROSTIPVSDAQRFVIVELINQGXSK 66
DB 13 TAGATVOSYTNFIDVRGSLITGADVHEIVLPRVGLPTN--QRFIVELSHAEISV 70
QY 67 TTAIDVNNXYVAVQNGQSYFLR-DAPRGAE--THLFTGTRRSSLPFGXSYXDLERY 123
DB 71 TTAIDVNNXYVAVQNGQSYFLR-DAPRGAE--THLFTGTRRSSLPFGXSYXDLERY 123
QY 124 AGH-RDQIFLQXLOISVXAL--KXPGSTKXQASILLQWISPAARFPIIMEXR 179
DB 130 AGH-RDQIFLQXLOISVXAL--KXPGSTKXQASILLQWISPAARFPIIMEXR 179
QY 136 AGH-RDQIFLQXLOISVXAL--KXPGSTKXQASILLQWISPAARFPIIMEXR 189
DB 180 QXINSGKSLPDXVLELETSWQSQSYVQSHSTGVFNNPXLAIKXGNFVLNXPXYI 239
QY 190 TRIRYNRSAAPPDYITLSEWGRSLTAIOSSNQAFASPIQLQRWGSKFSYDVSTILI 249
DB 240 ASLAIKMFVCGEPSS 255
QY 250 PIIAMVYRCAPPSS 265
DB 250 PIIAMVYRCAPPSS 265

RESULT 10
US-08-425-336-1
/ Sequence 1, Application US/08425336
/ Patent No. 5521083
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US-08-425-336-1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Gerstl, Stephen F.
/ APPLICANT: Gerstl, Stephen F.
/ TITLE OF INVENTION: Immotocoxins Comprising Ribosome-Inactivating
/ NUMBER OF SEQUENCES: 140
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/425,336
/ FILING DATE: 18-APR-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/054,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: 08/054,691
/ FILING DATE: 12-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meyers, Thomas C.
/ REGISTRATION NUMBER: P-36,989
/ REFERENCE/DOCKET NUMBER: 31394
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/474-6300
/ TELEFAX: 312/474-0448
/ TELEX: 3126474-0448
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-425-336-1

Query Match 30.7%; Score 376; DB 1; Length 267;
Best Local Similarity 39.1%; Pred. No. 3.7e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 THGTGKYEYFETILADYVSSGS--FSENIPL--ROSTIPVSDAQRFVIVELINQGXSK 66
DB 13 TAGATVOSYTNFIDVRGSLITGADVHEIVLPRVGLPTN--QRFIVELSHAEISV 70
QY 67 TTAIDVNNXYVAVQNGQSYFLR-DAPRGAE--THLFTGTRRSSLPFGXSYXDLERY 123
DB 71 TTAIDVNNXYVAVQNGQSYFLR-DAPRGAE--THLFTGTRRSSLPFGXSYXDLERY 123
QY 124 AGH-RDQIFLQXLOISVXAL--KXPGSTKXQASILLQWISPAARFPIIMEXR 179
DB 130 AGH-RDQIFLQXLOISVXAL--KXPGSTKXQASILLQWISPAARFPIIMEXR 179
QY 136 AGH-RDQIFLQXLOISVXAL--KXPGSTKXQASILLQWISPAARFPIIMEXR 189
DB 180 QXINSGKSLPDXVLELETSWQSQSYVQSHSTGVFNNPXLAIKXGNFVLNXPXYI 239
QY 190 TRIRYNRSAAPPDYITLSEWGRSLTAIOSSNQAFASPIQLQRWGSKFSYDVSTILI 249
DB 240 ASLAIKMFVCGEPSS 255
QY 250 PIIAMVYRCAPPSS 265
DB 250 PIIAMVYRCAPPSS 265

RESULT 11
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Page 4

APPLICANT: Cartoll, Steve F.  
APPLICANT: Lane, Julie A.  
TITLE OF INVENTION: Materials Comprising and Methods of  
TITLE OF INVENTION: Materials Comprising and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SERIALS: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 19920619  
FILING DATE: 09/07/90, 707  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 546202and, Greca E.  
REFERENCE/DOCKET NUMBER: 27129/30910  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-5750  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-901-707-1

Query Match 30.7%; Score 376; DB 1; Length 267;  
Best Local Similarity 39.1%; Pred. No. 3.7e-37;  
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;  
QY 9 THQTCXKFRFTLLADYSSGS-FSNEIPL-RSGTIPVSDAQREVLVLELNGGXSK 66  
DB 13 TPAIVGSYTNFIRAVRGSLTADVHHEIPLNKGVEEPLN-GRFLVLSNHELSV 70  
QY 67 TPAIDVTKYVAVQAGDSYFIR-DAPRGAE--TLFTGTTRDSLSLPGSGYDLKRX 123  
DB 71 TLADVTNAYVVRGNSNAIFPHDQEDBAITLFT-DVGNKTFPAFGSDYDLKRX 129  
QY 124 AGH-EQQLPGIXLQISYKAL--KPGGSTRKQARSILILQITSEARPNFLMKRX 179  
DB 130 AKNKNRNIHLNGFLEHLSLSLIIYISYTGQPLFARSPICICNISEARNOYIGEMR 189  
QY 180 GXINSGKSLPDXVLELETNGQSTQVQSHDGVFNKPRALIXGAFVTLNVRKY 239  
DB 190 TRIRNRSAPDSVITLNSWNRSLTAIOESNGAFSPICLOGRNRSNVSIVDSILI 249  
QY 240 ASLAIMLVGCGRRSS 255  
DB 250 PRLIMVTRCAPEPSS 265

RESULT 8  
US-07-988-430-1  
Sequence 1, Application us/07988430  
Patent No. 5416202  
GENERAL INFORMATION:  
APPLICANT: Bernhard, Susan L.

APPLICANT: Betteer, Marc D.  
APPLICANT: Cartoll, Steve F.  
APPLICANT: Lane, Julie A.  
TITLE OF INVENTION: Materials Comprising and Methods of  
TITLE OF INVENTION: Materials Comprising and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SERIALS: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 19921209  
FILING DATE: 09/07/98, 430  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 546202and, Greca E.  
REFERENCE/DOCKET NUMBER: 31133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-988-430-1

Query Match 30.7%; Score 376; DB 1; Length 267;  
Best Local Similarity 39.1%; Pred. No. 3.7e-37;  
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;  
QY 9 THQTCXKFRFTLLADYSSGS-FSNEIPL-RSGTIPVSDAQREVLVLELNGGXSK 66  
DB 13 TPAIVGSYTNFIRAVRGSLTADVHHEIPLNKGVEEPLN-GRFLVLSNHELSV 70  
QY 67 TPAIDVTKYVAVQAGDSYFIR-DAPRGAE--TLFTGTTRDSLSLPGSGYDLKRX 123  
DB 71 TLADVTNAYVVRGNSNAIFPHDQEDBAITLFT-DVGNKTFPAFGSDYDLKRX 129  
QY 124 AGH-EQQLPGIXLQISYKAL--KPGGSTRKQARSILILQITSEARPNFLMKRX 179  
DB 130 AKNKNRNIHLNGFLEHLSLSLIIYISYTGQPLFARSPICICNISEARNOYIGEMR 189  
QY 180 GXINSGKSLPDXVLELETNGQSTQVQSHDGVFNKPRALIXGAFVTLNVRKY 239  
DB 190 TRIRNRSAPDSVITLNSWNRSLTAIOESNGAFSPICLOGRNRSNVSIVDSILI 249  
QY 240 ASLAIMLVGCGRRSS 255  
DB 250 PRLIMVTRCAPEPSS 265

RESULT 9

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Page 3

US-08-378-761A-71  
Sequence 71, Application US/08378761A  
Patent No. 5635384  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
INVENTOR: HEY, TIMOTHY D  
ASSIGNMENT: BERNHARD, SUSAN L  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
PRECUSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
TITLE OF INVENTION: USING  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER: IBM PC COMPATIBLE  
MEDIUM TYPE: FLOPPY DISK  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-761A-71

Query Match 37.1%; Score 453.5; DB 1; Length 250;  
Best Local Similarity 41.9%; Pred No. 1.5e-46;  
Matches 106; Conservative 34; Mismatches 86; Indels 27; Gaps 7;  
QY 9 THQTCKEYFFETLLRDVSSGSFSNEIPLROSTIPVSDAQRFLVETLNOQXDSXTA 68  
DB 9 TEGATSOYKOFIEBALRRL-RGLIHIDIVLPDPT-TLOERNRYIVELNSSTSEIV 66  
QY 69 AIDVTNXYVVAQAGDSYFLDAPRGAETHTLFTGTTRDSSSLPEKXSYDLERYAGR-R 127  
DB 67 GIVTNVAVVAQAGDSYFLDAPRGAETHTLFTGTTRDSSSLPEKXSYDLERYAGR-R 124  
QY 128 DQPIGLXQLOSYVAXLXFGGSRFXQASILLIOMISAAFPNPLMRKXKINSXKS 187  
DB 67 GIVTNVAVVAQAGDSYFLDAPRGAETHTLFTGTTRDSSSLPEKXSYDLERYAGR-R 124  
QY 125 QGPIGLXQLOSYVAXLXFGGSRFXQASILLIOMISAAFPNPLMRKXKINSXKS 184  
DB 125 QGPIGLXQLOSYVAXLXFGGSRFXQASILLIOMISAAFPNPLMRKXKINSXKS 184  
QY 188 FLPDYVMELETSVQGSSTGVGHSTGVNNEPKRLAIXXGNFYTLKXNEX----- 237  
DB 185 FQPDAAVLSLENNV-DNLRGVQESVQDTFPRQ-----VTLNINREPVYDLSH 233  
QY 238 -VIASTALMLFVC 249  
DB 234 PTVAVTALMLFVC 246

RESULT 6  
US-08-485-286-71  
Sequence 71, Application US/08485286  
Patent No. 5646026  
Patent No. 5646026 5646119  
GENERAL INFORMATION:  
APPLICANT: BERNHARD, SUSAN L  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-286-71

US-08-485-286-71  
Sequence 71, Application US/08485286  
Patent No. 5646026  
Patent No. 5646026 5646119  
GENERAL INFORMATION:  
APPLICANT: BERNHARD, SUSAN L  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-286-71

Query Match 37.1%; Score 453.5; DB 1; Length 250;  
Best Local Similarity 41.9%; Pred No. 1.5e-46;  
Matches 106; Conservative 34; Mismatches 86; Indels 27; Gaps 7;  
QY 9 THQTCKEYFFETLLRDVSSGSFSNEIPLROSTIPVSDAQRFLVETLNOQXDSXTA 68  
DB 9 TEGATSOYKOFIEBALRRL-RGLIHIDIVLPDPT-TLOERNRYIVELNSSTSEIV 66  
QY 69 AIDVTNXYVVAQAGDSYFLDAPRGAETHTLFTGTTRDSSSLPEKXSYDLERYAGR-R 127  
DB 67 GIVTNVAVVAQAGDSYFLDAPRGAETHTLFTGTTRDSSSLPEKXSYDLERYAGR-R 124  
QY 128 DQPIGLXQLOSYVAXLXFGGSRFXQASILLIOMISAAFPNPLMRKXKINSXKS 187  
DB 67 GIVTNVAVVAQAGDSYFLDAPRGAETHTLFTGTTRDSSSLPEKXSYDLERYAGR-R 124  
QY 125 QGPIGLXQLOSYVAXLXFGGSRFXQASILLIOMISAAFPNPLMRKXKINSXKS 184  
DB 125 QGPIGLXQLOSYVAXLXFGGSRFXQASILLIOMISAAFPNPLMRKXKINSXKS 184  
QY 188 FLPDYVMELETSVQGSSTGVGHSTGVNNEPKRLAIXXGNFYTLKXNEX----- 237  
DB 185 FQPDAAVLSLENNV-DNLRGVQESVQDTFPRQ-----VTLNINREPVYDLSH 233  
QY 238 -VIASTALMLFVC 249  
DB 234 PTVAVTALMLFVC 246

RESULT 7  
US-07-901-707-1  
Sequence 1, Application US/07901707  
Patent No. 5376546  
GENERAL INFORMATION:  
APPLICANT: BERNHARD, SUSAN L  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-901-707-1

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us-09-601-667c-41.ra1

Page 2

RESULT 2  
US-09-776-059-31  
Query Match  
Best Local Similarity 91.3%; Pred. No. 4.3e-131;  
Matches 212; Conservative 1; Mismatches 19; Indels 2; Gaps 1;  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: ECK, Jurgen  
APPLICANT: BAUR, Axel  
APPLICANT: ZINKE, Holger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 6/4503-2003  
CURRENT FILING DATE: 1996-06-19  
EARLIER FILING DATE: 1996-06-25  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 31  
LENGTH: 253  
ORGANISM: Viscum album  
US-09-776-059-31

Query Match  
Best Local Similarity 94.4%; Score 115; DB 3; Length 253;  
Matches 212; Conservative 1; Mismatches 19; Indels 2; Gaps 1;  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: ECK, Jurgen  
APPLICANT: BAUR, Axel  
APPLICANT: ZINKE, Holger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 6/4503-2003  
CURRENT FILING DATE: 1996-06-19  
EARLIER FILING DATE: 1996-06-25  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 39  
LENGTH: 235  
ORGANISM: Viscum album  
US-09-776-059-39

RESULT 3  
US-09-776-059-39  
Query Match  
Best Local Similarity 91.3%; Pred. No. 4.3e-131;  
Matches 212; Conservative 1; Mismatches 19; Indels 2; Gaps 1;  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: ECK, Jurgen  
APPLICANT: BAUR, Axel  
APPLICANT: ZINKE, Holger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 6/4503-2003  
CURRENT FILING DATE: 1996-06-19  
EARLIER FILING DATE: 1996-06-25  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 39  
LENGTH: 235  
ORGANISM: Viscum album  
US-09-776-059-39

US-09-776-059-39  
Query Match  
Best Local Similarity 97.7%; Score 1073; DB 3; Length 235;  
Matches 217; Conservative 0; Mismatches 18; Indels 2; Gaps 1;  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: ECK, Jurgen  
APPLICANT: BAUR, Axel  
APPLICANT: ZINKE, Holger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 6/4503-2003  
CURRENT FILING DATE: 1996-06-19  
EARLIER FILING DATE: 1996-06-25  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 39  
LENGTH: 235  
ORGANISM: Viscum album  
US-09-776-059-39

US-09-538-873-3  
Query Match  
Best Local Similarity 41.9%; Pred. No. 1.9e-47;  
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;  
GENERAL INFORMATION:  
APPLICANT: VITEVA, ELLEN S.  
APPLICANT: SHETLE, VICTOR F.  
APPLICANT: SKALISNIK, JOAN F.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK  
FILE REFERENCE: US2003-03-90  
CURRENT FILING DATE: 2000-03-30  
EARLIER FILING DATE: 1999-03-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 3  
LENGTH: 251  
TYPE: PRT  
ORGANISM: Abrys precatorius  
US-09-538-873-3

US-09-538-873-3  
Query Match  
Best Local Similarity 41.9%; Pred. No. 1.9e-47;  
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;  
GENERAL INFORMATION:  
APPLICANT: VITEVA, ELLEN S.  
APPLICANT: SHETLE, VICTOR F.  
APPLICANT: SKALISNIK, JOAN F.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK  
FILE REFERENCE: US2003-03-90  
CURRENT FILING DATE: 2000-03-30  
EARLIER FILING DATE: 1999-03-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 3  
LENGTH: 251  
TYPE: PRT  
ORGANISM: Abrys precatorius  
US-09-538-873-3

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: December 11, 2003, 11:53:18 ; Search time 8.8628 seconds  
(without alignments)  
1222.073 Million cell updates/sec

Title: US-09-601-667C-41  
Perfect score: 1223  
Sequence: 1 YERLRLRYHTQTKGKBYRNF.....XYIASIAIMLFCVGRPS88 256  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310850 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, RA.\*  
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2: /cgm2\_5/prodate/1/1aa/45\_COMB.pep.\*  
3: /cgm2\_5/prodate/1/1aa/6X\_COMB.pep.\*  
4: /cgm2\_5/prodate/1/1aa/69\_COMB.pep.\*  
5: /cgm2\_5/prodate/1/1aa/PCOMB\_COMB.pep.\*  
6: /cgm2\_5/prodate/1/1aa/backlist.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1165	95.3	564	3	US-08-776-059-35 Sequence 35, Appl
2	1165	94.4	253	3	US-08-776-059-31 Sequence 31, Appl
3	1073	87.7	235	3	US-08-776-059-39 Sequence 39, Appl
4	461	37.7	251	4	US-09-538-873-3 Sequence 3, Appl
5	453.5	37.1	250	1	US-08-378-761A-71 Sequence 71, Appl
6	453.5	37.1	250	1	US-08-485-286-71 Sequence 71, Appl
7	376	30.7	267	1	US-07-808-790-1 Sequence 1, Appl
8	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
9	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
10	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
11	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
12	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
13	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
14	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
15	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
16	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
17	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
18	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
19	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
20	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
21	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
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23	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
24	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
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26	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl
27	376	30.7	267	1	US-08-428-335-1 Sequence 1, Appl

28	301	24.6	267	1	US-08-378-761A-74 Sequence 74, Appl
29	301	24.6	267	1	US-08-485-286-74 Sequence 74, Appl
30	299	24.4	247	1	US-08-488-113B-6 Sequence 6, Appl
31	299	24.4	247	1	US-08-477-484B-6 Sequence 6, Appl
32	299	24.4	247	1	US-08-446-380-6 Sequence 6, Appl
33	299	24.4	247	1	US-08-432-380-6 Sequence 6, Appl
34	299	24.4	247	1	US-08-432-380-6 Sequence 6, Appl
35	299	24.4	247	1	US-08-432-380-6 Sequence 6, Appl
36	294	24.0	289	1	US-07-923-692C-4 Sequence 4, Appl
37	294	24.0	289	1	US-08-184-237-4 Sequence 4, Appl
38	294	24.0	289	1	US-08-482-920-4 Sequence 4, Appl
39	294	24.0	289	1	US-08-483-341-4 Sequence 4, Appl
40	294	24.0	289	1	US-08-483-341-4 Sequence 4, Appl
41	294	24.0	289	1	US-08-425-336-111 Sequence 11, App
42	284.5	23.3	251	1	US-08-488-113B-111 Sequence 11, App
43	284.5	23.3	251	1	US-08-477-484B-111 Sequence 11, App
44	284.5	23.3	251	1	US-08-477-484B-111 Sequence 11, App
45	284.5	23.3	251	1	US-08-477-484B-111 Sequence 11, App

# ALIGNMENTS

US-08-776-059-35	95.3%	Score 1165, DB 3, Length 564;
Query Match	91.8%	Pred. No. 8,4e+132;
Best Local Similarity	0; Mismatch	2; Gaps 1;
Matches 233; Conservative		
1 YERLRLRYHTQTKGKBYRNF.....XYIASIAIMLFCVGRPS88 256		
34 YERLRLRYHTQTKGKBYRNF.....XYIASIAIMLFCVGRPS88 256		
121 ERYAGHDDIPLDIQLQLOSYALRKGSTEXQANSLITLQMSAARNPIMLRKQ 180		
152 ERYAGHDDIPLDIQLQLOSYALRKGSTEXQANSLITLQMSAARNPIMLRKQ 211		
161 XINSGSEPIPXVMELETFMGOSCTGHSCTGPNPVRALVGNVTLXMYXITA 240		
212 YINSGSEPIPXVMELETFMGOSCTGHSCTGPNPVRALVGNVTLXMYXITA 271		
241 SLAINLFCVGRPS88 256		
272 SLAINLFCVGRPS88 287		



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us-09-601-67c-41.rapb

Db 63 LAEIAIDVTGYVGVNNSRFPDAPDAVEGLFRNTIKR--LHFGSYSLSEGR 120  
Qy 125 GHRDQIPGIXOP--IOSYALRXPGSTKXASRILILIQISEARF---NPIWR 177  
Db 121 AYRETDGIEPRLGIGIKLIDNMIUNYFTEIASLIVLIQWISARFTEIQIRN 180  
Qy 178 XROXINSKSPFDXYMLEETSGQOSTQVQS--TGVFNPKALIXGNFTILANR 236  
Db 181 FQKIR-----PANNITSLKNGGDSQTNSANGHSEAVLELRANRKYTVYND 234  
Qy 237 XYLASLIMLEVC 249  
Db 235 QYKRIALIKFVC 247

RESULT 12

US-10-127-890-4  
Sequence 4, Application US/10127890  
Publication No. US20030165196A1  
GENERAL INFORMATION:  
Applicant: Better, Marc D.  
Cartoll, Stephen F.  
Studdick, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-May-1993  
APPLICATION NUMBER: PC/US94/05348  
FILING DATE: 12-May-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-May-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-Dec-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-Jun-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-Nov-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McAndrews, Held & Malloy, Ltd.  
REGISTRATION NUMBER: 12,918  
REFERENCE/DOCKET NUMBER: 200-70-P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-127-890-4

Query Match 23.0%; Score 281; DB 12; Length 263;

Best Local Similarity 33.9%; Pred. No. 4.5e-26;  
Matches 78; Conservative 44; Mismatches 88; Indels 20; Gaps 9;  
Qy 13 TGKREPTPLRLADYVSGSPN--EIPILKOSTIPNSDQSPULVETLNGQSDKXTA 69  
Db 10 TACTIKR--EDPKALPFAHNYDPLKST--ISDRFILLDLSYAVETISVA 63  
Qy 70 IDVTKXVAVAYKADQSYFLDAPGAEETLPTGTRDPSSEFPGSYXDLRVAQH--R 127  
Db 64 IDVTVVAVAYVTRDVSYPFSPSPPEAVNLPKSTR--KITLPTGNYEQLT-AAKIR 120  
Qy 128 DOIPIGIXOILQSYALRXPGSTKXASRILILIQISEARFPIIMKXKXINSXS 187  
Db 121 ENIDGLALSLSATTLFYNQASAPSA--LVLITQTEAAKRIKIRHVAVY--ATN 176  
Qy 188 FLDKXMLEETSGQOSTQV--QSTDTGVFNPKALIXGNFTILANR 235  
Db 177 FKNALISLKNQMSALSQGLFLAQKQGFKNVVDLIPFGSRQVYVYND 226

RESULT 13

US-10-127-890-102  
Sequence 102, Application US/10127890  
Publication No. US20030165196A1  
GENERAL INFORMATION:  
Applicant: Better, Marc D.  
Cartoll, Stephen F.  
Studdick, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-May-1993  
APPLICATION NUMBER: PC/US94/05348  
FILING DATE: 12-May-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-May-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-Dec-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-Jun-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-Nov-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McAndrews, Held & Malloy, Ltd.  
REGISTRATION NUMBER: 12,918  
REFERENCE/DOCKET NUMBER: 200-70-P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TOPOLOGY: linear



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us-09-601-667c-41.rapb

Page 5

Matches 82; Conservative 50; Mismatches 94; Indels 14; Gaps 9;  
QY 13 TCKKRPFTTIDYSSGSFNSHPIKOSTIPVSDQRFVVELTNGSKDXKALIDV 72  
DB 10 TSSGYVPSNLRKALPKRKKYDPLR-SSLPSS-QYXALHINVADETISVALID 66  
QY 73 TXXVYVYAGDQSYFLBDA-PRGKETHLFTGTRDRSSLPFKSGYXDLERYAGH-RDOI 130  
DB 67 TXXVYVYAGDQSYFLBDA-PRGKETHLFTGTRDRSSLPFKSGYXDLERYAGH-RDOI 125  
QY 131 PLGIXQILOSYYALRXPSSSTKXASILLIQMSEAPFPIIMKXKXINSKXSTP 190  
DB 126 PLGIXQILOSYYALRXPSSSTKXASILLIQMSEAPFPIIMKXKXINSKXSTP 181  
QY 191 DXXMLEFTSMGQSGTQVQ--HSTGVNPNKRLAIXKXNFTLXNPK--VIASLALML 246  
DB 182 SLATISLNSMNSLKQXQJASTNNGCFSSPYVLINAGQVATINVDAGVTSNALID 241  
RESULT 10  
US-10-280-679B-4  
; Sequence 4, Application US/10280679B  
; Publication No. US20030150019A1  
; GENERAL INFORMATION:  
; APPLICANT: Large Scale Biology Corporation  
; TITLE OF INVENTION: Nonselective RNA virus Transformation Vectors  
; INVENTOR: Large Scale Biology Corporation  
; FILING DATE: 1999-10-22  
; CURRENT FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US/10/280,679B  
; FILING DATE: 2000-04-24  
; PRIOR APPLICATION NUMBER: 09/557,941  
; FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/484,341  
; FILING DATE: 1992-07-31  
; PRIOR APPLICATION NUMBER: 07/923,692  
; FILING DATE: 1990-07-22  
; PRIOR APPLICATION NUMBER: 07/600,244  
; FILING DATE: 1988-02-26  
; PRIOR APPLICATION NUMBER: 07/641,617  
; FILING DATE: 1984-01-16  
; PRIOR APPLICATION NUMBER: 07/737,899  
; FILING DATE: 1991-07-26  
; PRIOR APPLICATION NUMBER: 07/739,143  
; FILING DATE: 1991-08-01  
; PRIOR APPLICATION NUMBER: 07/310,881  
; FILING DATE: 1989-02-17  
; PRIOR APPLICATION NUMBER: 07/160,766  
; FILING DATE: 1988-02-26  
; PRIOR APPLICATION NUMBER: 07/160,771  
; FILING DATE: 1988-02-26  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO: 4  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Chinese cucumber protein alpha-trichosanthin  
US-10-280-679B-4  
Query Match 24.0%; Score 294; DB 12; Length 289;  
Best Local Similarity 34.2%; Freq. No. 1,36-27;  
Matches 82; Conservative 49; Mismatches 95; Indels 14; Gaps 9;  
QY 13 TCKKRPFTTIDYSSGSFNSHPIKOSTIPVSDQRFVVELTNGSKDXKALIDV 72  
DB 33 TSSGYVPSNLRKALPKRKKYDPLR-SSLPSS-QYXALHINVADETISVALID 69  
QY 73 TXXVYVYAGDQSYFLBDA-PRGKETHLFTGTRDRSSLPFKSGYXDLERYAGH-RDOI 130  
DB 90 TXXVYVYAGDQSYFLBDA-PRGKETHLFTGTRDRSSLPFKSGYXDLERYAGH-RDOI 148  
QY 131 PLGIXQILOSYYALRXPSSSTKXASILLIQMSEAPFPIIMKXKXINSKXSTP 190  
DB 149 PLGIXQILOSYYALRXPSSSTKXASILLIQMSEAPFPIIMKXKXINSKXSTP 204

QY 191 DXXMLEFTSMGQSGTQVQ--HSTGVNPNKRLAIXKXNFTLXNPK--VIASLALML 246  
DB 205 SLATISLNSMNSLKQXQJASTNNGCFSSPYVLINAGQVATINVDAGVTSNALID 264  
RESULT 11  
US-10-127-890-111  
; Sequence 11, Application US/10127890  
; Publication No. US2003016196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Inventor: Stephen F.  
; Student: Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; SOFTWARE: Microsoft Windows 95  
; CURRENT FILING DATE: 1999-10-27  
; APPLICATION NUMBER: US/10/127,890  
; FILING DATE: 23-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-May-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-May-1994  
; APPLICATION NUMBER: US/86/064,691  
; FILING DATE: 12-May-1986  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-Dec-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-Jun-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-Nov-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet W.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70-P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/767-9185  
; TELEFAX: 312/767-9185  
; TELETYPE: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-10-127-890-111  
Query Match 23.3%; Score 284.5; DB 12; Length 251;  
Best Local Similarity 34.0%; Freq. No. 1,66-26;  
Matches 86; Conservative 33; Mismatches 113; Indels 21; Gaps 7;  
QY 8 VTHQGTGEYFPTILRDY--VSSGSFNSHPIKOSTIPVSDQRFVVELTNGSKDX 64  
DB 5 VSSGSFNSHPIKOSTIPVSDQRFVVELTNGSKDX--FVVALSNDQ 62  
QY 65 EXTAIDVYVYVYAGDQSYFLBDA-PRGKETHLFTGTRDRSSLPFKSGYXDLERYAGH 124

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us-09-601-667c-41.rapb

QY 240 ASLALMLPVCGRPPSS 255  
DB 285 PIALMWRCKAPPPSS 300

RESULT 7

US-09-792-793A-39  
Sequence 39, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
INVENTOR: McDonald, John R.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: Patent In Ver. 2.0  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Trichosantheus killowii  
US-09-792-793A-39

Query Match 24.6%; Score 301; DB 10; Length 247;  
Best Local Similarity 34.6%; Pred. No. 1.4e-28;  
Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

QY 13 TGKEYFRFTLLRNDYSSGSGSENEFLLRQSTIPVSDAQRPVVLVLTQNGKDXNTAIDV 72  
DB 10 TSSSYGVFTSNLRALPNERKLYDIPLR-SLPGS--QRYALHLTNVADETISVALDV 66

QY 73 TNYVVAVQAGDOSTFLRDA-FRGAETHLFTGTRRSSLPFGSYXDLERYAGH-RDOI 130  
DB 67 TNYVINGRAGDOSTYFENRFAATEAKYKQAKR-KVTLFSGNTERLDYQYAKIKRENI 125

QY 131 FLGIXQILQSVAKRFGSGSTRQKRSITLILQMSAPARENFIIMRKOXINSQXSFIP 190  
DB 126 FLGIPALDSATITLTFYVNNNS--ASALMWLIQSTSPAAKYKEIQOIGKRVDK--TFLP 181

QY 191 DXYMLEETSMGQOSTQVQ--HSTQGVNNEPXRALIXGNFVTLNWXK--VIASLALML 246  
DB 182 SLATISLNSWALSQKQIOLASTNGCPESPVLINQONQVITTVDAQVTSNALIL 241

RESULT 8

US-10-375-209A-39  
Sequence 39, Application US/10375209A  
Publication No. US20030215421A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
INVENTOR: Cogging, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601E  
CURRENT APPLICATION NUMBER: US/10/375,209A  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: Patent In Ver. 2.0  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Trichosantheus killowii  
US-10-375-209A-39

Query Match 24.6%; Score 301; DB 12; Length 247;  
Best Local Similarity 34.6%; Pred. No. 1.4e-28;  
Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

QY 13 TGKEYFRFTLLRNDYSSGSGSENEFLLRQSTIPVSDAQRPVVLVLTQNGKDXNTAIDV 72  
DB 10 TSSSYGVFTSNLRALPNERKLYDIPLR-SLPGS--QRYALHLTNVADETISVALDV 66

QY 73 TNYVVAVQAGDOSTFLRDA-FRGAETHLFTGTRRSSLPFGSYXDLERYAGH-RDOI 130  
DB 67 TNYVINGRAGDOSTYFENRFAATEAKYKQAKR-KVTLFSGNTERLDYQYAKIKRENI 125

QY 131 FLGIXQILQSVAKRFGSGSTRQKRSITLILQMSAPARENFIIMRKOXINSQXSFIP 190  
DB 126 FLGIPALDSATITLTFYVNNNS--ASALMWLIQSTSPAAKYKEIQOIGKRVDK--TFLP 181

QY 191 DXYMLEETSMGQOSTQVQ--HSTQGVNNEPXRALIXGNFVTLNWXK--VIASLALML 246  
DB 182 SLATISLNSWALSQKQIOLASTNGCPESPVLINQONQVITTVDAQVTSNALIL 241

RESULT 9

US-10-127-890-6  
Sequence 6, Application US/10127890  
Publication No. US2003016196A1  
GENERAL INFORMATION:  
APPLICANT: Bacter, Marc D.  
INVENTOR: Carroll, Stephen P.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th Floor  
CITY: Chicago  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/10/127,890  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-APR-2002  
CLASSIFICATION DATA:  
CLASSIFICATION: A61K38/00 (Inventor)  
PRIORITY DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70-P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO. 6:  
SEQUENCE DESCRIPTION: 247 amino acids  
TYPES: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO. 6:  
US-10-127-890-6

Query Match 24.4%; Score 299; DB 12; Length 247;  
Best Local Similarity 34.2%; Pred. No. 2.5e-28;

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Page 3

Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;  
QY 9 THQTTGKXEFREFTLLRDYVSSGS-FSNEIPLD-RQSTIPVSDAQRFVVELTNOGKXK 66  
DB 13 TAGATVQSYTFRIVARGLTGGADVHEIPLVPRVGLPIN--QRFILVELSNHSELV 70  
QY 67 TAAIDVTNXYVVAQAGOSYFLR-DAPRGAE--THLFTGTRDRSSLPFGSYXDURV 123  
DB 71 TAAIDVTNXYVVAQAGOSYFLR-DAPRGAE--THLFTGTRDRSSLPFGSYXDURV 123  
QY 124 AGH-RDQIPGLIGXOLQSVYAL--RXPQSTXQASIIILIQMISEAARFPIIMXRX 179  
DB 130 ANLRENIETLGNPGLERIALSALYYSTGCTQLPLARSPFICIMISEAARFQYIEGEM 189  
QY 180 QXINSXSELPDXYMLETSTWQOSYOVQSTDPVFNPNXKLAIXGNFVTLXNVRXV 239  
DB 190 TRIRNRSAPDPSPVITLNSWGLSTALQESNQAFAFPDQLQRNSKRSYVDVSLI 249  
QY 240 ASALMLPVCGERPS 255  
DB 250 PRLMAYNKRAPPS 265

RESULT 5  
US-10-127-890-1  
; Sequence 1, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Inventor: Carroll, Stephen F.  
; Title of Invention: Proteins  
; Number of Sequences: 173  
; Correspondence Address:  
; Addresser: McAndrews, Held & Malloy, Ltd.  
; City: Chicago  
; State: Illinois  
; Country: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; Medium: 3.5 inch floppy disk  
; Operator: SYSTEM COMPUSYS  
; Software: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; Application Number: US/10/127,890  
; Filing Date: 23-Apr-2002  
; Classification: <Unknown>  
; Prior Application Data:  
; Application Number: US/08/646,360  
; Filing Date: 13-May-1996  
; Application Number: US/94/05348  
; Filing Date: 12-May-1994  
; Application Number: US/08/064,691  
; Filing Date: 12-May-1993  
; Application Number: US/07/988,430  
; Filing Date: 09-Dec-1992  
; Application Number: US/07/901,707  
; Filing Date: 19-Jun-1992  
; Application Number: US/07/787,567  
; Filing Date: 04-Nov-1991  
; ATTORNEY/AGENT INFORMATION:  
; Name: McAndrews, Held & Malloy, Ltd.  
; Address: 500 West Madison Street, 34th floor  
; City: Chicago, IL 60601-3000  
; Telephone: 312/707-9155  
; Telefax: 312/707-8889  
; Telecommunication Information:  
; Reference/Document Number: 200-70-F4  
; Information for SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-127-890-1  
Query Match  
30.7%; Score 376; DB 12; Length 267;  
Best Local Similarity 39.1%; Pred. No. 8,8e-36;  
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 THQTTGKXEFREFTLLRDYVSSGS-FSNEIPLD-RQSTIPVSDAQRFVVELTNOGKXK 66  
DB 13 TAGATVQSYTFRIVARGLTGGADVHEIPLVPRVGLPIN--QRFILVELSNHSELV 70  
QY 67 TAAIDVTNXYVVAQAGOSYFLR-DAPRGAE--THLFTGTRDRSSLPFGSYXDURV 123  
DB 71 TAAIDVTNXYVVAQAGOSYFLR-DAPRGAE--THLFTGTRDRSSLPFGSYXDURV 123  
QY 124 AGH-RDQIPGLIGXOLQSVYAL--RXPQSTXQASIIILIQMISEAARFPIIMXRX 179  
DB 130 ANLRENIETLGNPGLERIALSALYYSTGCTQLPLARSPFICIMISEAARFQYIEGEM 189  
QY 180 QXINSXSELPDXYMLETSTWQOSYOVQSTDPVFNPNXKLAIXGNFVTLXNVRXV 239  
DB 190 TRIRNRSAPDPSPVITLNSWGLSTALQESNQAFAFPDQLQRNSKRSYVDVSLI 249  
QY 240 ASALMLPVCGERPS 255  
DB 250 PRLMAYNKRAPPS 265

RESULT 6  
US-10-083-336A-1  
; Sequence 1, Application US/10083336A  
; Publication No. US200301665A1  
; GENERAL INFORMATION:  
; APPLICANT: Oison, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrnes, Michael P  
; APPLICANT: Hammacher, Robert W  
; APPLICANT: Hammacher, Robert W  
; APPLICANT: Hammacher, Robert W  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 576  
; TYPE: PRT  
; ORGANISM: Rickettsia communis  
US-10-083-336A-1  
Query Match  
30.7%; Score 376; DB 12; Length 576;  
Best Local Similarity 39.1%; Pred. No. 2,5e-37;  
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;  
QY 9 THQTTGKXEFREFTLLRDYVSSGS-FSNEIPLD-RQSTIPVSDAQRFVVELTNOGKXK 66  
DB 48 TAGATVQSYTFRIVARGLTGGADVHEIPLVPRVGLPIN--QRFILVELSNHSELV 105  
QY 67 TAAIDVTNXYVVAQAGOSYFLR-DAPRGAE--THLFTGTRDRSSLPFGSYXDURV 123  
DB 106 TAAIDVTNXYVVAQAGOSYFLR-DAPRGAE--THLFTGTRDRSSLPFGSYXDURV 123  
QY 124 AGH-RDQIPGLIGXOLQSVYAL--RXPQSTXQASIIILIQMISEAARFPIIMXRX 179  
DB 165 ANLRENIETLGNPGLERIALSALYYSTGCTQLPLARSPFICIMISEAARFQYIEGEM 224  
QY 180 QXINSXSELPDXYMLETSTWQOSYOVQSTDPVFNPNXKLAIXGNFVTLXNVRXV 239  
DB 225 TRIRNRSAPDPSPVITLNSWGLSTALQESNQAFAFPDQLQRNSKRSYVDVSLI 264

QY 121 ERYAGHRDQIPGLIGKILQISVAXLRKPGSGTRXQKRSITLILQMSAPARPNILMKRXQ 180  
DB 119 ERYAGHRDQIPGLIGKILQISVAXLRKPGSGTRXQKRSITLILQMSAPARPNILMKRXQ 178  
QY 181 XINSQASFLPDYVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 240  
DB 179 YINSQASFLPDYVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 238  
QY 241 SLAIVLFCGERS 254  
DB 239 SLAIVLFCGERS 252

RESULT 2  
US-09-347-064-2  
Sequence 2, Application US/09347064A  
Patent No. US20020045208A1  
GENERAL INFORMATION:  
APPLICANT: ECK, Outgen  
APPLICANT: Schmidt, Arno  
APPLICANT: Schmidt, Arno  
TITLE OF INVENTION: Recombinant Fusion Proteins Based on  
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum  
TITLE OF INVENTION: album  
FILE REFERENCE: 09282-5  
CURRENT FILING DATE: US/09/347, 064A  
EARLIER FILING DATE: 1999-07-02  
PCT/EP98/00009  
EARLIER FILING DATE: 1998-01-02  
EARLIER APPLICATION NUMBER: EP 97 10 0012.0  
EARLIER FILING DATE: 1997-01-02  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 252  
LENGTH: 252  
TYPE: PRT  
ORGANISM: Viscum album  
US-09-347-064-2

Query Match 94.1%; Score 1151; DB 9; Length 252;  
Best Local Similarity 91.3%; Pred. No. 2,2e-133;  
Matches 231; Conservative 1; Mismatches 19; Indels 2; Gaps 1;

QY 1 YERIALVYVOTGXKXRFYTLADYVSSGSFENIPLRQSTIPVSDAGRFVLVETLN 60  
DB 2 YERIALVYVOTGXKXRFYTLADYVSSGSFENIPLRQSTIPVSDAGRFVLVETLN 61  
QY 61 QGQXKXTALDVTNXYVAYADDSYFLADAPGAEHLFTGTRSSSLPFGSYXDL 120  
DB 62 QGQXKXTALDVTNXYVAYADDSYFLADAPGAEHLFTGTRSSSLPFGSYXDL 119  
QY 121 ERYAGHRDQIPGLIGKILQISVAXLRKPGSGTRXQKRSITLILQMSAPARPNILMKRXQ 180  
DB 120 ERYAGHRDQIPGLIGKILQISVAXLRKPGSGTRXQKRSITLILQMSAPARPNILMKRXQ 179  
QY 181 XINSQASFLPDYVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 240  
DB 180 YINSQASFLPDYVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 239  
QY 241 SLAIVLFCGERS 254  
DB 239 SLAIVLFCGERS 252

RESULT 3  
US-10-282-935-3  
Sequence 3, Application US/10282935  
Patent No. US20030143193A1  
GENERAL INFORMATION:  
APPLICANT: VITETTA, ELLEN S.  
APPLICANT: GHETTE, VICTOR F.  
APPLICANT: SWALSHAW, JOAN  
APPLICANT: BALDINA, ROXANA G.

QY 9 THQTXKXRFYTLADYVSSGSFENIPLRQSTIPVSDAGRFVLVETLNQGXDXTA 68  
DB 9 THQTXKXRFYTLADYVSSGSFENIPLRQSTIPVSDAGRFVLVETLNQGXDXTA 66  
QY 69 AIDVTNXYVAYADDSYFLADAPGAEHLFTGTRSSSLPFGSYXDLERYACH R 127  
DB 67 GIDVTNXYVAYADDSYFLADAPGAEHLFTGTRSSSLPFGSYXDLERYACH R 124  
QY 128 DQIPGLIGKILQISVAXLRKPGSGTRXQKRSITLILQMSAPARPNILMKRXQXNSGS 187  
DB 125 QDIPGLIGKILQISVAXLRKPGSGTRXQKRSITLILQMSAPARPNILMKRXQXNSGS 184  
QY 188 FIDPXVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 237  
DB 185 FIDPXVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 234  
QY 238 FIDPXVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 237  
DB 235 FIDPXVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 234

Query Match 37.7%; Score 461; DB 12; Length 251;  
Best Local Similarity 41.9%; Pred. No. 2.7e-48;  
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;

QY 9 THQTXKXRFYTLADYVSSGSFENIPLRQSTIPVSDAGRFVLVETLNQGXDXTA 68  
DB 9 THQTXKXRFYTLADYVSSGSFENIPLRQSTIPVSDAGRFVLVETLNQGXDXTA 66  
QY 69 AIDVTNXYVAYADDSYFLADAPGAEHLFTGTRSSSLPFGSYXDLERYACH R 127  
DB 67 GIDVTNXYVAYADDSYFLADAPGAEHLFTGTRSSSLPFGSYXDLERYACH R 124  
QY 128 DQIPGLIGKILQISVAXLRKPGSGTRXQKRSITLILQMSAPARPNILMKRXQXNSGS 187  
DB 125 QDIPGLIGKILQISVAXLRKPGSGTRXQKRSITLILQMSAPARPNILMKRXQXNSGS 184  
QY 188 FIDPXVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 237  
DB 185 FIDPXVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 234  
QY 238 FIDPXVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 237  
DB 235 FIDPXVYMLKETSQSGSTQVQSHSTGVFNNPRLAIXGNFTVLXVAXYA 234

RESULT 4  
US-10-282-935-1  
Sequence 1, Application US/10282935  
Patent No. US20030143193A1  
GENERAL INFORMATION:  
APPLICANT: VITETTA, ELLEN S.  
APPLICANT: GHETTE, VICTOR F.  
APPLICANT: SWALSHAW, JOAN  
APPLICANT: BALDINA, ROXANA G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS  
FILE REFERENCE: US/10/282, 935  
CURRENT FILING DATE: 2002-10-29  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: 60/126, 826  
PRIOR FILING DATE: 1999-03-30  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 1  
LENGTH: 251  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
US-10-282-935-1



Thu Dec 11 16:09:58 2003

us-09-601~667c-41.rag

Page 12

DZ	N-PSDB; AAWS1343.
XX	Nucleic acid encoding fusion protein containing mistletoe lectin A
XX	Protein useful for treatment of proliferative and autoimmune
PT	diseases, allergies and tumours
PX	Disclousure; Fig 11a; 115pp; German.
XX	This sequence encodes a variant mistletoe lectin A-chain, rMLA. This
CC	sequence can be used in the construction of a fusion protein which
CC	comprises an effector module that is cytotoxic intracellularly, a
CC	processing module covalently bonded to the effector module and
CC	containing a protease recognition sequence, and a binding module
CC	covalently bonded to the processing module, able to bind specifically to
CC	mistletoe lectin A-chain, thereby facilitating internalisation of the fusion
CC	protein. Such a fusion protein can be used for treating disorders
CC	involving proliferation and/or elevated activation of cells, especially
CC	autoimmune disease, allergy and tumours. The proteins can be administered
CC	e.g. by injection or topically but especially by intravenous injection,
CC	at 1 ng to 500 mg/g/d, or for ex vivo use at 1 pg to 500 ng/ml.
CC	Fusion proteins can develop toxic activity in a wide range of target
CC	cells. The processing module prevents extracellular dissociation, and
CC	fusion proteins based on mistletoe lectin A-chain are far more active
CC	than those based on ricin and do have the associated problems of
CC	non-specific toxicity. The protein may be expressed in a non-mucoglycosylated
CC	form having little in the blood where the mistletoe lectin B-chain is used,
CC	it actively assists in translocation of the ML A-chain from the
CC	endoplasmic reticulum to the cytoplasm.
XX	
XQ	Sequence 252 AA;
	Query Match 94.4%; Score 1155; DB 19; Length 252;
	Best Local Similarity 91.3%; Pred. No. 6,6e-132;
	Matches 222; Conservative 1; Mismatches 19; Indels 2; Gaps 1
OY	1 YEELATLRTQTCXKPRFTLLIDVYSSGSFNEPLMGOSTPSPGAPCVLWETM 60
Dd	1 YERILRLMTQTTEBEPFLITLDDVYSSGSFNEPLMGOSTIPVDAGPVLVLTN 60
OY	61 QGDKSDTALDVTKXYAVAYADQDGYELEDAPGAETLFTGTDRDSLEPYGSKYL 120
OY	61 QGGDSFTALDVTLVYAAYADQDGYELEDAPRAETLFTGT -RSSLPFGNSYDL 118
OY	121 ERYAHARDQPLGLIKOLISTKAKRPGSTGXDAISILLIIONTSAPAFNTLRXQ 180
OY	119 ERASHARDQPLGLIDLONSGTPARXGSLTGSSILLIIONTSAPAFNTLRHMO 178
OY	181 XINSQSLEPDYKALELSNGQSTNOVGSTIDGVPNNXSLAXGNFTLVANXAVTA 240
Dd	179 YINSQSFLPDVYMLETFSNGQSTVOGSTIDGVFNPIKLAIPEGNFVLTVNRDVA 238
OY	241 SLAIMTPEVCGERPS 254
Dd	239 SLAIMTPEVCGERRS 252

Search completed: December 11, 2003, 14:07:45  
Job time : 26.2959 secs







FT Misc-difference 483 /label= Ser, Gly  
FT Misc-difference 484 /label= Gly, Ser  
FT Misc-difference 493 /label= Gly, Tyr  
FT Misc-difference 500 /label= Asn, Ser, Thr, Lys  
FT Misc-difference 501 /label= Ser, Gly  
FT Misc-difference 502 /label= Leu, Pro  
FT Misc-difference 503 /label= Ala, Met  
FT Misc-difference 504 /label= Met, Val  
FT Misc-difference 533 /label= Pro, Phe  
FT DE19804210-AL.  
XX 12-AUG-1999.  
XX 03-FEB-1998; 98DE-1004210.  
XX 03-FEB-1998; 98DE-1004210.  
XX (BROS-) BIOSYN ARZNEIMITTEL GMBH.  
XX Morris P, Stiefel T, Voelter W, Walters P;  
XX MPI; 1999-44535/38.  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX Claim 1, Page 25-26; 78pp; German.  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (WLA)  
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
XX ribosomes in lymphokine-producing macrophages, so stimulate immunity (I) and its  
XX fragments are used to treat uncontrolled cell growth (particularly of the  
XX cancers) and if they lack cytotoxicity, to increase the strength of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a consensus sequence of the mistletoe lectin described in the  
XX specification.  
XX Sequence 533 AA;  
XX  
XX Query Match 95.1%; Score 1162.5; DB 20; Length 533;  
XX Best Local Similarity 99.2%; Pred. No. 2.3e-132;  
XX Matches 254; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 180 XINGSGFLPDYXMLETSGQSTQVGHSTGVPNNFXLALXGNFVLNAXVIA 239  
Qy 241 STAIKLFVGGRRPS8 256  
Db 240 STAIKLFVGGRRPS8 255  
RESIDUE 13  
ID AAY25973 standard; protein; 533 AA.  
XX AAY25973;  
XX 18-OCT-1999 (first entry)  
XX Mistletoe lectin protein consensus sequence 2.  
XX Mistletoe lectin, antitumour, immunostimulant; A-chain; WLA; immunity;  
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
XX cancer; cytotoxicity; antigen; isoform.  
XX Viscum album.  
XX Location/Qualifiers  
FH Key 15  
FT Misc-difference 15 /label= Asp, Glu  
FT Misc-difference 63 /label= Gly, Glu  
FT Misc-difference 66 /label= Ile, Val  
FT Misc-difference 75 /label= Leu, Ala  
FT Misc-difference 107 /label= Asp, Arg, none  
FT Misc-difference 113 /label= Asn, Thr  
FT Misc-difference 117 /label= Pro, Thr  
FT Misc-difference 114 /label= Asp, Glu  
FT Misc-difference 145 /label= Ser, Thr  
FT Misc-difference 145 /label= Phe, Tyr  
FT Misc-difference 152 /label= Thr, Ala  
FT Misc-difference 177 /label= Ala, Tyr  
FT Misc-difference 180 /label= Tyr, Asp  
FT Misc-difference 185 /label= Ala, Glu  
FT Misc-difference 219 /label= Val, Met  
FT Misc-difference 219 /label= Ile, Phe  
FT Misc-difference 224 /label= Phe, Ser  
FT Misc-difference 225 /label= Pro, Thr  
FT Misc-difference 232 /label= Thr, Ser  
FT Misc-difference 236 /label= Asp, Ser  
FT Misc-difference 240 /label= Asn, Ser  
FT Misc-difference 320 /label= Cys, Arg  
FT Misc-difference 325 /label= Gly, Asn  
FT Misc-difference 364 /label= Gly, Asp

KX	Mistletoe; iectin; antitumor; immunostimulant; A-chain; MHA; immunity;
KY	hydroxy-26S subunit; nonopsonic; antiproliferative; immune response;
KW	prophylactic; anti-infective; antineoplastic; controlled cell growth treatment;
LK	cancer; cytotoxicity; antigen; isoform.
XX	Viscum album.
OS	
XX	
Key	Location/Qualifiers
PH	Misc-difference 15
FT	/label= Asp, Glu
FT	Misc-difference 63
FT	/label= Gly, Gln
FT	Misc-difference 76
FT	/label= Ile, Val
FT	Misc-difference 75
FT	/label= Leu, Ala
FT	Misc-difference 107
FT	/label= Asp, Arg or none
FT	Misc-difference 113
FT	/label= Asn, Thr
FT	Misc-difference 117
FT	/label= Pro, Thr
FT	Misc-difference 128
FT	/label= Asp, Glu
FT	Misc-difference 141
FT	/label= Ser, Thr
FT	Misc-difference 145
FT	/label= Phe, Tyr
FT	Misc-difference 152
FT	/label= Thr, Ala
FT	Misc-difference 177
FT	/label= Ala, Tyr
FT	Misc-difference 190
FT	/label= Tyr, Asp
FT	Misc-difference 185
FT	/label= Ala, Glu
FT	Misc-difference 191
FT	/label= Val, Met
FT	Misc-difference 219
FT	/label= Ile, Phe
FT	Misc-difference 224
FT	/label= Pro, Ser
FT	Misc-difference 228
FT	/label= Pro, Thr
FT	Misc-difference 233
FT	/label= Thr, Ser
FT	Misc-difference 236
FT	/label= Asp, Ser
FT	Misc-difference 287
FT	/label= Asn, Ser
FT	Misc-difference 290
FT	/label= Cys, Arg
FT	Misc-difference 325
FT	/label= Gly, Asn
FT	Misc-difference 344
FT	/label= Gly, Asp
FT	Misc-difference 426
FT	/label= Gly, Gln
FT	Misc-difference 435
FT	/label= Val, Asp
FT	Misc-difference 439
FT	/label= Gln, Lys
FT	Misc-difference 442
FT	/label= Gly or none
FT	Misc-difference 443
FT	/label= Arg, Lys
FT	Misc-difference 464
FT	/label= Cys, Ser, Val
FT	Misc-difference 480
FT	/label= Ala, Gly
FT	Misc-difference 481
FT	/label= Gly, Ala

PT	Misc-difference 117	/label= Pro, Thr
PT	Misc-difference 134	/label= Asp, Glu
PT	Misc-difference 141	/label= Ser, Thr
PT	Misc-difference 152	/label= Phe, Tyr
PT	Misc-difference 152	/label= Thr, Ala
PT	Misc-difference 177	/label= Ala, Tyr
PT	Misc-difference 180	/label= Tyr, Asp
PT	Misc-difference 185	/label= Ala, Glu
PT	Misc-difference 219	/label= Val, Met
PT	Misc-difference 219	/label= Ile, Phe
PT	Misc-difference 224	/label= Phe, Ser
PT	Misc-difference 225	/label= Pro, Thr
PT	Misc-difference 232	/label= Thr, Ser
PT	Misc-difference 236	/label= Asp, Ser
PN	DEL9604210-AL.	
PN	12-AUG-1999.	
PD	03-FEB-1998;	98DS-1004210.
PF	03-FEB-1998;	98DS-1004210.
PR	(BIOS-) BIOSYN ARKHEMITTEL GEMH.	
PR	Morris P, Stiefel T, Voelter W, Walters P,	
PI	WPI; 1999-445335/38.	
DR	Preparation of mistletoe lectins in heterologous systems,	
DR	particularly for use as anticancer agents and immunostimulants	
XX	Claim 5; Page 30; 76pp; German.	
XX	This invention describes a novel mistletoe lectin (I) and its fragments	
XX	which have antitumor and immunostimulatory activity. The A-chain (MA)	
XX	of the mistletoe lectin binds to, and inactivates, the 28S subunit of	
XX	ribosomes. Non-cytotoxic forms of (I) activate T-cell and	
XX	lymphokine-producing macrophages, so stimulate immunity. (I) and its	
XX	fragments are used to treat uncontrolled cell growth (particularly	
XX	cancer) and if they lack cytotoxicity, to increase the strength of the	
XX	immune response, particularly to a co-administered antigen	
XX	(tumor-associated, bacterial, or viral). The method allows production of	
XX	and delivery of lectin, and its individual chains, in many different isoforms	
XX	and from various sources. The immunostimulatory products are	
XX	free from toxins present in natural mistletoe extracts. The sequence	
XX	represents a consensus sequence of the mistletoe lectin A chain (MA)	
XX	described in the invention.	
XX	Sequence 255 AA.	

```

Query Match      95.1%      Score 1165.5: DB 20: Length 255:
Best Local Similarity 99.1%      Pred. No. 8.2e-133:
Matches 254: Conservative 0: Mismatches 1: Indels 1: Gaps 1:

Dy      1 YERLLRVRHQTGXEFRTLLNDYVSGSGFNEIPLRGOSTPVSDAGRFVLELN 60
Dy      1 YERLLRVHQTGXEFRTLLNDYVSGSGFNEIPLRGOSTPVSDAGRFVLELN 60

```

Cy		6	OQDSDXALIAIVTWXXVVAQAAGGDSYFPLRADAIPGAERHLFTGTTRPESLIPEKGSYVDL	128
Dd		61	OGXDSTAAIDVTWXXVVAAVGADGVFLRAFGAETHLFTGTTRXSLSPEKGSYVDL	119
Cy		121	ERYAEHRDDIPLGIHQILQGVALRXGGSTRQARASILLIQMISAFAENPIIMXRQ	180
Dd		120	KRNASHEDQLPLGIHQILTSGSVALKMGVSSTRQANRPRLAIIXGNFTLVLTNWRXYIA	240
Cy		181	XINSXSFPPDPXWMALETSNGOSTRGYSTGRPNPRPAIXGXNFVTLNWRXYIA	279
Dd		180	XINSXSFPPDPXWMALETSMWGOSTGVGHSTGVFPNNPKRALITXGNFTLVLTNWRXYIA	239
Cy		241	SLAILFCVGERPRESS	256
Dd		240	SLAILFCVGERPRESS	255
<hr/>				
RESULT_11				
ID	AAZ5977	AAY25977	standard; protein; 255 AA.	
AC	AAZ5977;			
DC	18-OCT-1999	(first entry)		
DX	Misc:lectin A chain MCA consensus protein sequence 3.			
EX	Misc:lectoside lectin; antifungal; immunostimulant; B-chain; MCA; immunity;			
KM	Ribosome 26S subunit; non-cytotoxic; T-cell activation; immune response;			
KW	Lymphokine-producing macrophage; uncontrolled cell growth; treatment;			
XX	cancer; cytotoxicity; antigen; isoform.			
OS	Viscum album.			
XX				
FR	Key	Location/Qualifiers		
FR	Misc-difference 15	/label= Asp, Glu		
FR	Misc-difference 63	/label= Gly, Gln		
PT	Misc-difference 66	/label= Ile, Val		
PT	Misc-difference 75	/label= Leu, Ala		
PT	Misc-difference 107	/label= Asp, none		
PT	Misc-difference 113	/label= Asn, Thr		
PT	Misc-difference 117	/label= Pro, Thr		
PT	Misc-difference 134	/label= Asp, Glu		
PT	Misc-difference 141	/label= Ser, Thr		
PT	Misc-difference 145	/label= Phe, Tyr		
PT	Misc-difference 152	/label= Thr, Ala		
PT	Misc-difference 177	/label= Ala, Tyr		
PT	Misc-difference 180	/label= Tyr, Asp		
PT	Misc-difference 185	/label= Ala, Gln		
PT	Misc-difference 191	/label= Val, Met		
PT	Misc-difference 224	/label= Ile, Phe		
PT	Misc-difference 225	/label= Pro, Ser		
PT	Misc-difference 232	/label= Thr, Ser		
PT				



ID AM10021 standard; Protein; 564 AA.  
 AC AM10021;  
 XX 18-DEC-1997 (first entry)  
 XX  
 XX  
 DE Prepro mistletoe lectin.  
 XX  
 XX Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.  
 XX  
 XX Viscum album.  
 XX  
 XX EF751221-A1.  
 XX  
 XX 02-JAN-1997.  
 XX  
 XX 26-JUN-1995; 95EP-0109949.  
 XX  
 XX 26-JUN-1995; 95EP-0109949.  
 XX  
 XX (MADU ) MADUS KOEHLN AG.  
 XX  
 XX Baur A, Eck J, Lentzen H, Zinke H;  
 XX WPI; 1997-054678/06.  
 XX DR N-PSDB; AAT70473.  
 XX  
 XX Nucleic acid encoding pre-pro form of mistletoe lectin - for  
 XX therapeutic or diagnostic use  
 XX  
 XX Claim 12; Fig 4C; 30pp; German.  
 XX  
 XX Mistletoe lectin is a cytotoxic agent that has been used for tumour  
 XX therapy. It can be used in immunotoxic and medicaments. Nucleic  
 XX acid fragments can be used in diagnostic methods. Mistletoe lectin  
 XX (AAT70473) comprises an A chain (AAT70474) and a B chain (AAT70475).  
 XX  
 XX Sequence 564 AA;  
 SQ  
 Query Match 95.3%; Score 1165; DB 19; Length 564;  
 Best Local Similarity 91.8%; Pred. No. 1.2e-13;  
 Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

1 YERLRATVHTQTKKXEPFTTLRLRDYVSSGSFSENEFLRLROSTIPVSDAORFVLELTN 60  
 34 YERLRATVHTQTKKXEPFTTLRLRDYVSSGSFSENEFLRLROSTIPVSDAORFVLELTN 93  
 61 QGDSXTAIDVNNVYVAAQDQSYFLRDPAGATLFTGTTRDSSLPFGXSYDL 120  
 94 QGDSXTAIDVNNVYVAAQDQSYFLRDPAGATLFTGTTRDSSLPFGXSYDL 151  
 121 ERVAGHDQIPGIGDQILOSVALXKRPQSTXKQASIIILIQMISEARFPILMRKQ 180  
 152 ERVAGHDQIPGIGDQILOSVALXKRPQSTXKQASIIILIQMISEARFPILMRKQ 211  
 181 XINGKSEFLPDXYMLELSTWQGSQVQVSTQVFNPKALIXKGNFTLXNEXVIA 240  
 212 YINGKSEFLPDXYMLELSTWQGSQVQVSTQVFNPKALIXKGNFTLXNEXVIA 271  
 241 SLATMLFVCGERSSS 256  
 272 SLATMLFVCGERSSS 287

RESULT 8  
 ID AAM90127 standard; Protein; 564 AA.  
 AC AAM90127;  
 XX  
 XX 20-MAR-2003 (updated)  
 XX DT 30-APR-1999 (first entry)  
 XX

DE Mistletoe lectin prepro-protein.  
 XX  
 XX MW; mistletoe; lectin; M; transgenic plant; glycosylation;  
 XX dimer; immunotoxin; large-scale production; diagnosis; therapeutic;  
 XX cancer.  
 XX  
 XX Viscum album.  
 XX  
 XX EP884388-A1.  
 XX  
 XX 16-DEC-1998.  
 XX  
 XX 26-JUN-1995; 98EP-0105660.  
 XX  
 XX 26-JUN-1995; 95EP-0109949.  
 XX  
 XX 26-JUN-1995; 98EP-0105660.  
 XX  
 XX (MADU ) MADUS KOEHLN AG.  
 XX  
 XX Baur A, Eck J, Lentzen H, Zinke H;  
 XX WPI; 1999-026582/03.  
 XX DR N-PSDB; AAV74182.  
 XX  
 XX New transgenic plant expressing mistletoe lectin - useful for  
 XX producing recombinant lectin in e.g. cancer diagnosis and therapy  
 XX  
 XX Claim 1a; Fig 4c; 30pp; German.  
 XX  
 XX This invention describes a novel transgenic plant transformed with a  
 XX vector capable of encoding a mistletoe (Viscum album) lectin  
 XX also describes a polypeptide produced by a plant where the polypeptide  
 XX exhibits at least one enzymatic modification other than the glycosylation  
 XX that occurs in Viscum album or the polypeptide is a fusion protein, a  
 XX mistletoe lectin polypeptide dimer and an immunotoxin comprising the  
 XX polypeptide or the polypeptide dimer. The plants are used for large-scale  
 XX production of mistletoe lectin for diagnostic or therapeutic purposes  
 XX (e.g. in cancer therapy). This sequence represents the mistletoe lectin  
 XX used in the cloning of the transgene.  
 XX (Updated on 26-MAR-2003 to correct PF field.)  
 XX  
 XX Sequence 564 AA;  
 SQ  
 Query Match 95.3%; Score 1165; DB 20; Length 564;  
 Best Local Similarity 91.8%; Pred. No. 1.2e-13;  
 Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

1 YERLRATVHTQTKKXEPFTTLRLRDYVSSGSFSENEFLRLROSTIPVSDAORFVLELTN 60  
 34 YERLRATVHTQTKKXEPFTTLRLRDYVSSGSFSENEFLRLROSTIPVSDAORFVLELTN 93  
 61 QGDSXTAIDVNNVYVAAQDQSYFLRDPAGATLFTGTTRDSSLPFGXSYDL 120  
 94 QGDSXTAIDVNNVYVAAQDQSYFLRDPAGATLFTGTTRDSSLPFGXSYDL 151  
 121 ERVAGHDQIPGIGDQILOSVALXKRPQSTXKQASIIILIQMISEARFPILMRKQ 180  
 152 ERVAGHDQIPGIGDQILOSVALXKRPQSTXKQASIIILIQMISEARFPILMRKQ 211  
 181 XINGKSEFLPDXYMLELSTWQGSQVQVSTQVFNPKALIXKGNFTLXNEXVIA 240  
 212 YINGKSEFLPDXYMLELSTWQGSQVQVSTQVFNPKALIXKGNFTLXNEXVIA 271  
 241 SLATMLFVCGERSSS 256  
 272 SLATMLFVCGERSSS 287

RESULT 9  
 ID AAY25971 standard; Protein; 255 AA.  
 AC AAY25971;  
 XX

KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KM cancer; cytotoxicity; antigen; isoform; lectin I.  
 XX  
 XX Viscum album.  
 XX  
 XX DE19804210-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 XX  
 XX MPI; 1999-44535/38.  
 XX  
 XX N-PSDB; A4209103.  
 XX  
 XX Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX  
 XX Claim 7; Fig 1B; 78pp; German.  
 XX  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumor and immunostimulatory activity. The A-chain (MLA)  
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX and on a large scale, at any time of the year. Recombinant products are  
 XX free from toxins present in natural mistletoe extracts. This sequence  
 XX represents a mistletoe lectin I protein fragment.  
 XX  
 XX Sequence 531 AA;  
 XX  
 XX Query Match 95.3%; Score 1165; DB 20; Length 531;  
 XX Best Local Similarity 91.8%; Pred. No. 1,1e-132;  
 XX Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;  
 XX  
 XX 1 YERLRLAVTHQOTGKXERFFITLLADYVSSGSGFSENEIPILROSTIPVSDAORFVLVETLN 60  
 XX 1 YERLRLAVTHQOTGKXERFFITLLADYVSSGSGFSENEIPILROSTIPVSDAORFVLVETLN 60  
 XX 61 QGDSSTALDITNKKYVVAQAGDSYFLDPAKAEHLFTGTRDRSSIPKXSYXL 120  
 XX 61 QGDSSTALDITNKKYVVAQAGDSYFLDPAKAEHLFTGTRDRSSIPKXSYXL 118  
 XX  
 XX 121 ERYAGHROCPILGIXOLIOGVAXLAKPGSGTPOKASILLIOMISEAARFPIIMRXQ 180  
 XX 121 ERYAGHROCPILGIXOLIOGVAXLAKPGSGTPOKASILLIOMISEAARFPIIMRXQ 178  
 XX  
 XX 119 ERYAGHROCPILGIXOLIOGVAXLAKPGSGTPOKASILLIOMISEAARFPIIMRXQ 178  
 XX 119 ERYAGHROCPILGIXOLIOGVAXLAKPGSGTPOKASILLIOMISEAARFPIIMRXQ 178  
 XX  
 XX 181 XINSKXSLPDYVYMLELTSWGGQSTOVQSTDGVFNNKXLAIXGNFTLXNRYXIA 240  
 XX 181 XINSKXSLPDYVYMLELTSWGGQSTOVQSTDGVFNNKXLAIXGNFTLXNRYXIA 240  
 XX  
 XX 241 SLAINLFTVCGRRSS 256  
 XX 241 SLAINLFTVCGRRSS 254  
 XX  
 XX Db 239 SLAINLFTVCGRRSS 254

XX Mistletoe lectin I (variant) protein fragment.  
 DE  
 XX  
 XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MLA; immunity;  
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 XX cancer; cytotoxicity; antigen; isoform; lectin I.  
 XX  
 XX Viscum album.  
 XX  
 XX DE19804210-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 XX  
 XX MPI; 1999-44535/38.  
 XX  
 XX N-PSDB; A4209106.  
 XX  
 XX Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX  
 XX Disclosure; Fig 4B; 78pp; German.  
 XX  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumor and immunostimulatory activity. The A-chain (MLA)  
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 XX lymphokine-producing macrophages so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX and on a large scale, at any time of the year. Recombinant products are  
 XX free from toxins present in natural mistletoe extracts. This sequence  
 XX represents a fragment of a mistletoe lectin I protein variant.  
 XX  
 XX Sequence 532 AA;  
 XX  
 XX Query Match 95.3%; Score 1165; DB 20; Length 532;  
 XX Best Local Similarity 91.8%; Pred. No. 1,1e-132;  
 XX Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;  
 XX  
 XX 1 YERLRLAVTHQOTGKXERFFITLLADYVSSGSGFSENEIPILROSTIPVSDAORFVLVETLN 60  
 XX 1 YERLRLAVTHQOTGKXERFFITLLADYVSSGSGFSENEIPILROSTIPVSDAORFVLVETLN 60  
 XX 61 QGDSSTALDITNKKYVVAQAGDSYFLDPAKAEHLFTGTRDRSSIPKXSYXL 120  
 XX 61 QGDSSTALDITNKKYVVAQAGDSYFLDPAKAEHLFTGTRDRSSIPKXSYXL 118  
 XX  
 XX 121 ERYAGHROCPILGIXOLIOGVAXLAKPGSGTPOKASILLIOMISEAARFPIIMRXQ 180  
 XX 121 ERYAGHROCPILGIXOLIOGVAXLAKPGSGTPOKASILLIOMISEAARFPIIMRXQ 178  
 XX  
 XX 119 ERYAGHROCPILGIXOLIOGVAXLAKPGSGTPOKASILLIOMISEAARFPIIMRXQ 178  
 XX 119 ERYAGHROCPILGIXOLIOGVAXLAKPGSGTPOKASILLIOMISEAARFPIIMRXQ 178  
 XX  
 XX 181 XINSKXSLPDYVYMLELTSWGGQSTOVQSTDGVFNNKXLAIXGNFTLXNRYXIA 240  
 XX 181 XINSKXSLPDYVYMLELTSWGGQSTOVQSTDGVFNNKXLAIXGNFTLXNRYXIA 240  
 XX  
 XX 241 SLAINLFTVCGRRSS 256  
 XX 241 SLAINLFTVCGRRSS 254  
 XX  
 XX Db 239 SLAINLFTVCGRRSS 254

XX 03-FEB-1998; 98DE-1004210.  
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
XX  
XX Morris P, Stiefel T, Voelter W, Welters P;  
XX WPI; 1999-44535/38.  
XX N-PSDB; AA209104.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure; Fig 2B; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (WLA)  
XX of the mistletoe lectin binds to and inactivates the 28S subunit of  
XX ribosomes. Non-cytotoxic forms of (I) activate immunity. (I) and its  
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
XX fragments are used to treat uncontrolled cell growth (particularly  
XX cancers) and if they lack cytotoxicity, to increase the strength of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of the mistletoe lectin A1 protein.  
XX  
XX Sequence 254 AA;  
XX  
XX Query Match 95.3%; Score 1165; DB 20; Length 254;  
XX Best Local Similarity 91.8%; Pred. No. 4e-133;  
XX Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;  
XX  
XX  
XX 1 YERLRLRVTHQTGXKYEFRFTLLADYVSSGSFSNEIPILRGSTTPVSDAQRFLVVELTN 60  
DB 1 YERLRLRVTHQTGXKYEFRFTLLADYVSSGSFSNEIPILRGSTTPVSDAQRFLVVELTN 60  
XX  
XX 61 QGXSTXALIDVTNNYVAVAGQGSFTLRARAGRTHLFTGTTDRSSGLPEYKSYDL 120  
QY 61 QGXSTXALIDVTNNYVAVAGQGSFTLRARAGRTHLFTGTTDRSSGLPEYKSYDL 120  
DB 61 QGXSTXALIDVTNNYVAVAGQGSFTLRARAGRTHLFTGTTDRSSGLPEYKSYDL 120  
XX  
XX 121 ERYAGHRDIPLGIDIGSVYALAXPGSGSTRQARSILLIOMISARFNPILRRQ 180  
QY 121 ERYAGHRDIPLGIDIGSVYALAXPGSGSTRQARSILLIOMISARFNPILRRQ 180  
DB 121 ERYAGHRDIPLGIDIGSVYALAXPGSGSTRQARSILLIOMISARFNPILRRQ 180  
XX  
XX 119 ERYAGHRDIPLGIDIGSVYALAXPGSGSTRQARSILLIOMISARFNPILRRQ 178  
QY 181 XINSKSFPLDPXYMLETSWGQSTVOVSTGYFNNPKXLAIXKGNPVLTXNXXVYA 240  
DB 179 YINSKSFPLDPXYMLETSWGQSTVOVSTGYFNNPKXLAIXKGNPVLTXNXXVYA 238  
QY 241 SLAIWLPVCGRRSSS 256  
DB 239 SLAIWLPVCGRRSSS 254  
XX  
XX  
XX RESULT 4  
XX ID AAY25983 standard; Protein; 254 AA.  
XX  
XX AAY25983;  
XX  
XX 18-OCT-1999 (first entry)  
XX  
XX Mistletoe lectin A1 (variant) protein fragment.  
XX  
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; WLA; immunity;  
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
XX cancer; cytotoxicity; antigen; isoform; lectin A1.  
XX  
XX Viscum album.  
XX

XX DEL9804210-AL.  
XX  
XX 12-AUG-1999.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
XX  
XX Morris P, Stiefel T, Voelter W, Welters P;  
XX WPI; 1999-44535/38.  
XX N-PSDB; AA209107.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure; Fig 5B; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (WLA)  
XX of the mistletoe lectin binds to and inactivates the 28S subunit of  
XX ribosomes. Non-cytotoxic forms of (I) activate immunity. (I) and its  
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
XX fragments are used to treat uncontrolled cell growth (particularly  
XX cancers) and if they lack cytotoxicity, to increase the strength of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a mistletoe lectin A1 protein variant.  
XX  
XX Sequence 254 AA;  
XX  
XX Query Match 95.3%; Score 1165; DB 20; Length 254;  
XX Best Local Similarity 91.8%; Pred. No. 4e-133;  
XX Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;  
XX  
XX  
XX 1 YERLRLRVTHQTGXKYEFRFTLLADYVSSGSFSNEIPILRGSTTPVSDAQRFLVVELTN 60  
DB 1 YERLRLRVTHQTGXKYEFRFTLLADYVSSGSFSNEIPILRGSTTPVSDAQRFLVVELTN 60  
XX  
XX 61 QGXSTXALIDVTNNYVAVAGQGSFTLRARAGRTHLFTGTTDRSSGLPEYKSYDL 120  
QY 61 QGXSTXALIDVTNNYVAVAGQGSFTLRARAGRTHLFTGTTDRSSGLPEYKSYDL 120  
DB 61 QGXSTXALIDVTNNYVAVAGQGSFTLRARAGRTHLFTGTTDRSSGLPEYKSYDL 120  
XX  
XX 121 ERYAGHRDIPLGIDIGSVYALAXPGSGSTRQARSILLIOMISARFNPILRRQ 180  
QY 121 ERYAGHRDIPLGIDIGSVYALAXPGSGSTRQARSILLIOMISARFNPILRRQ 180  
DB 121 ERYAGHRDIPLGIDIGSVYALAXPGSGSTRQARSILLIOMISARFNPILRRQ 180  
XX  
XX 119 ERYAGHRDIPLGIDIGSVYALAXPGSGSTRQARSILLIOMISARFNPILRRQ 178  
QY 181 XINSKSFPLDPXYMLETSWGQSTVOVSTGYFNNPKXLAIXKGNPVLTXNXXVYA 240  
DB 179 YINSKSFPLDPXYMLETSWGQSTVOVSTGYFNNPKXLAIXKGNPVLTXNXXVYA 238  
QY 241 SLAIWLPVCGRRSSS 256  
DB 239 SLAIWLPVCGRRSSS 254  
XX  
XX  
XX RESULT 5  
XX ID AAY25979 standard; Protein; 531 AA.  
XX  
XX AAY25979;  
XX  
XX 18-OCT-1999 (first entry)  
XX  
XX Mistletoe lectin I protein fragment.  
XX  
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; WLA; immunity;  
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
XX

PT Preparation of mistletoe lectins in heterologous systems,  
PT particularly for use as anticancer agents and immunostimulants  
XX  
XX Claim 8; Fig 3b; 78pp; German.  
XX  
CC This invention describes a novel mistletoe lectin (I) and its fragments  
CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
CC of the mistletoe lectin binds to, and activates, the 28S subunit of  
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
CC lymphokine-producing macrophages, so stimulate immunity (I) and its  
CC fragments are used to treat uncontrolled cell growth (particularly  
CC cancers) and if they lack cytotoxicity, to increase the strength of the  
CC immune response, particularly to a co-administered antigen  
CC (tumour-associated, bacterial or viral). The method allows production of  
CC mistletoe lectin, and its individual chains, in many different isoforms  
CC and on a large scale, at any time of the year. Recombinant products are  
CC free from toxins present in natural mistletoe extracts. This sequence  
CC represents a fragment of the mistletoe lectin A2 protein.  
XX  
SQ Sequence 256 AA;  
SQ  
Query Match 97.6%; Score 1194; DB 20; Length 256;  
Best Local Similarity 92.6%; Pred. No. 1.2e-136;  
Matches 237; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 1 YERLRVHTQTCXEPFRITLARDVSSGSPNRIPLRGSTIPVSDAQRFLVELTN 60  
DB 1 YERLRVHTQTCXEPFRITLARDVSSGSPNRIPLRGSTIPVSDAQRFLVELTN 60  
QY 61 QGQDSXPAIDVNNVYVAVAGDQSYFLRDPAGAEVTLFTGTRRDSLLPFKGSYDL 120  
DB 61 QGQDSXPAIDVNNVYVAVAGDQSYFLRDPAGAEVTLFTGTRRDSLLPFKGSYDL 120  
QY 121 ERVAGHDDQIPGIGIOLIOSVSAARPGSSTAPAKRSIIILICWISBAARFPIIMRYQ 180  
DB 121 ERVAGHDDQIPGIGIOLIOSVSAARPGSSTAPAKRSIIILICWISBAARFPIIMRYQ 180  
QY 181 XINSQSFPLPDXYMLELSTMGQSTOVQSHSTDVGNPFRLAISTGNFVLSNRSVIA 240  
DB 181 XINSQSFPLPDXYMLELSTMGQSTOVQSHSTDVGNPFRLAISTGNFVLSNRSVIA 240  
QY 241 SLAIMLFCGERPSS 256  
DB 241 SLAIMLFCGERPSS 256  
RESULT 2  
AA25984 ID AA25984 standard; Protein; 256 AA.  
XX  
XX AA25984;  
XX  
DT 18-OCT-1999 (first entry)  
XX  
AC Mistletoe lectin A2 (variant) protein fragment.  
XX  
DE Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin A2.  
XX  
OS Viscum album.  
XX  
EN DE19804210-A1.  
XX  
XX 12-AUG-1999.  
XX  
PF 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
XX

PI Morris P, Stiefel T, Voelter W, Welters P;  
XX  
XX WPI; 1999-44535/38.  
DR N-PSDB; AA209108.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
PT particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure; Fig 6b; 78pp; German.  
XX  
CC This invention describes a novel mistletoe lectin (I) and its fragments  
CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
CC lymphokine-producing macrophages, so stimulate immunity (I) and its  
CC fragments are used to treat uncontrolled cell growth (particularly  
CC cancers) and if they lack cytotoxicity, to increase the strength of the  
CC immune response, particularly to a co-administered antigen  
CC (tumour-associated, bacterial or viral). The method allows production of  
CC mistletoe lectin, and its individual chains, in many different isoforms  
CC and on a large scale, at any time of the year. Recombinant products are  
CC free from toxins present in natural mistletoe extracts. This sequence  
CC represents a fragment of a mistletoe lectin A2 protein variant.  
XX  
SQ Sequence 256 AA;  
SQ  
Query Match 97.6%; Score 1194; DB 20; Length 256;  
Best Local Similarity 92.6%; Pred. No. 1.2e-136;  
Matches 237; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 1 YERLRVHTQTCXEPFRITLARDVSSGSPNRIPLRGSTIPVSDAQRFLVELTN 60  
DB 1 YERLRVHTQTCXEPFRITLARDVSSGSPNRIPLRGSTIPVSDAQRFLVELTN 60  
QY 61 QGQDSXPAIDVNNVYVAVAGDQSYFLRDPAGAEVTLFTGTRRDSLLPFKGSYDL 120  
DB 61 QGQDSXPAIDVNNVYVAVAGDQSYFLRDPAGAEVTLFTGTRRDSLLPFKGSYDL 120  
QY 121 ERVAGHDDQIPGIGIOLIOSVSAARPGSSTAPAKRSIIILICWISBAARFPIIMRYQ 180  
DB 121 ERVAGHDDQIPGIGIOLIOSVSAARPGSSTAPAKRSIIILICWISBAARFPIIMRYQ 180  
QY 181 XINSQSFPLPDXYMLELSTMGQSTOVQSHSTDVGNPFRLAISTGNFVLSNRSVIA 240  
DB 181 XINSQSFPLPDXYMLELSTMGQSTOVQSHSTDVGNPFRLAISTGNFVLSNRSVIA 240  
QY 241 SLAIMLFCGERPSS 256  
DB 241 SLAIMLFCGERPSS 256  
RESULT 2  
AA25980 ID AA25980 standard; Protein; 254 AA.  
XX  
XX AA25980;  
XX  
DT 18-OCT-1999 (first entry)  
XX  
AC Mistletoe lectin A1 protein fragment.  
XX  
DE Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin A1.  
XX  
OS Viscum album.  
XX  
EN DE19804210-A1.  
XX  
XX 12-AUG-1999.  
XX  
PF 03-FEB-1998; 98DE-1004210.  
XX  
XX





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us-09-601-667c-41.rpt

Page 8

QY 9 THQTVGKXEFRTLLRPDYSSGSPSNRIPILRQ-STIPVSDAORPVVHELTNOXDS-X 66  
Db 8 TKKATKTSYTOPIEALRQALASGEPRHGIYWERSTVP--DSKEFTLVELSNWAADSPV 65  
QY 67 TAAIDVNNXYVAVQAKDQSYPLR-DAPKGAETHLFTGTRDSSLPFXGXYKLERIAG 125  
Db 66 TLAVDVNNAIVVAKRTSQSEFTLEKNDPAIENLHPTI--KVTTFSSSTDLRGVHG 123  
QY 126 -HROCIPIGIXOLIGVAAEPKPG-GSTXQASGIIIIQISEAAFPDILAKKXOKIN 183  
Db 124 ERREHILLGMDLENAISALWISNINOCORALARSILIVICMVAENVAFRFIYRVGSGIS 183  
QY 184 SXKSEFLPDXYMLETSMGQSTOVQHSITD-GVFNNPKXLAIXXGNFVTLXNVR-XVIA 241  
Db 184 RAEMFRPDPMLSLKMKMSALSNVAVQSQGVSSPVELRSISNKKPVYVGSVDRIVSG 243  
QY 242 LAIMLFVC--GERPS 255  
Db 244 LAIMLFICRSTIRAS 259

Search completed: December 11, 2003, 14:01:07  
Job time : 20.7321 secs

RT genes encoding cinnamomin proteins and study of their expression  
RT submitted (JUN-2001) to the EMBL/GenBank/DBJ databases  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: AY039802; AAK82459.1; -  
DR InterPro: IPR000772; R1CIN\_B\_lectin.  
DR InterPro: IPR001574; R1P.  
DR Pfam: PF00652; R1CIN\_B\_lectin; 6.  
DR PRINTS: PR00366; SHIGARICIN.  
DR SMART: SM00458; R1CIN\_2.  
DR PROSITE: PS00231; R1CIN\_B\_lectin; 2.  
DR EMBL: AY039802; AAK82459.1; -  
DR InterPro: IPR000772; R1CIN\_B\_lectin.  
DR PROSITE: PS00231; R1CIN\_B\_lectin; 2.  
KW Hydrolase; Signal; Toxin.  
FT SIGNAL 1 32  
FT CHAIN 33 580  
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN  
SQ CINNAMOMIN II.  
SEQUENCE 580 AA; 64265 MW; 3764289ECCECF CRC64;  
Query Match 35.0%; Score 428.5; DB 10; Length 580;  
Best Local Similarity 43.8%; Pred. No. 2.2e-39;  
Matches 112; Conservative 36; Mismatches 95; Indels 13; Gaps 10.  
QY 9 TQCTCKEYRFTLLADYVSSGFSNMEFTLQ-STIPSAQRFVLTETNOGKEXT 67  
DB 40 TNAKTSTGTGTEALRQALSSSEPRGATPMDGSTVP--LSKPLVLSMAADSPV 97  
QY 68 A-AIDVTKYVVAQADSYFLRDPAGAEHLFTGTRRSLSLFPYGSYDLERYAG 125  
DB 98 ALADVTNAYVVAQADSYFLRDPAGAEHLFTGTRRSLSLFPYGSYDLERYAG 155  
QY 126 H-RDQPLGIXQLQISYALRKPQ-GSTXQARSLILQVISEARFNPILMRKXKIN 183  
DB 156 ELREKILLMDPEENASIALMTSNINQALNSGLVITQMAKAVYFETETREBSIT 215  
QY 184 SGKSLFDYKMLSEFTSWGQSTQVQSTND-GPNRPYKALIXGNFTLXNYR-XVTA 241  
DB 216 RAEFRDPMASLENNMNLSSGVQGSVODAFPNVVLSSINRQVYVDSLSHPVAVLADML 275  
QY 242 LAIMLFCV--GERPS 255  
DB 276 LAIMLFCRSSDRSS 291  
RESULT 14  
ID 006076 PRELIMINARY; PRT; 528 AA.  
DC 006076  
DT 01-NOV-1996 (Trembl) 01. Created  
DT 01-NOV-1996 (Trembl) 01. Last sequence update  
DT 01-MAR-2003 (Trembl) 23. Last annotation update  
DE Abtin-d (EC 3.2.2.22) (tRNA N-glycosidase) (fragment).  
OS Abtin precatorius (Indian licorice) (Crab's eye).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Euphorbia; Fabales; Fabaceae; Papilionoideae; Abreae; Abtin.  
NCBI\_TaxId=3816;  
RN 11  
RX SEQUENCE FROM N.A.  
RX MEDLINE=9312798; PubMed=842113; In J-Y;  
RX 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996;  
RT "Primary structure of three distinct isoforms determined by cDNA  
RT sequencing: conservation and significance.";  
RL J. Mol. Biol. 229:263-267 (1993).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: M98346; AAA32626.1; -  
DR HSP: P1140; IABR.  
DR InterPro: IPR000772; R1CIN\_B\_lectin.  
DR InterPro: IPR001574; R1P.  
DR Pfam: PF00652; R1CIN\_B\_lectin; 6.

DR Pfam: PF00652; R1P; 1.  
DR SMART: SM00458; R1CIN\_2.  
DR PROSITE: PS00231; R1CIN\_2.  
DR PROSITE: PS00275; SHIGA\_R1CIN; 1.  
KW Hydrolase; Toxin.  
FT NON TER 1 1  
FT CHAIN 528 AA; 5870 MW; 62ED42F8EPEE0B8 CRC64;  
SQ SEQUENCE 528 AA; 5870 MW; 62ED42F8EPEE0B8 CRC64;  
Query Match 34.3%; Score 419.5; DB 10; Length 528;  
Best Local Similarity 43.4%; Pred. No. 3.0e-38;  
Matches 109; Conservative 36; Mismatches 90; Indels 6; Gaps 5;  
QY 9 TQCTCKEYRFTLLADYVSSGFSNMEFTLQ-STIPSAQRFVLTETNOGKEXT 66  
DB 9 TNAKTSTGTGTEALRQALSSSEPRGATPMDGSTVP--LSKPLVLSMAADSPV 97  
QY 69 AIDVTKYVVAQADSYFLRDPAGAEHLFTGTRRSLSLFPYGSYDLERYAG-R 127  
DB 67 GIDVTNAYVVAQADSYFLRDPAGAEHLFTGTRRSLSLFPYGSYDLERYAG-R 124  
QY 128 DQPLGIXQLQISYALRKPQ-GSTXQARSLILQVISEARFNPILMRKXKIN 187  
DB 125 ELREKILLMDPEENASIALMTSNINQALNSGLVITQMAKAVYFETETREBSIT 215  
QY 188 FLPDYKMLSEFTSWGQSTQVQSTND-GPNRPYKALIXGNFTLXNYR-XVTA 246  
DB 185 FQDPMASLENNMNLSSGVQGSVODAFPNVVLSSINRQVYVDSLSHPVAVLADML 244  
QY 247 FVC 249  
DB 245 FVC 247  
RESULT 15  
ID 009722 PRELIMINARY; PRT; 549 AA.  
DC 009722  
DT 01-MAR-2001 (Trembl) 16. Created  
DT 01-MAR-2001 (Trembl) 16. Last sequence update  
DT 01-OCT-2002 (Trembl) 22. Last annotation update  
DE Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (tRNA  
DE N-glycosidase) (fragment).  
OS Cinnamomum camphora (Camphor tree).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
NCBI\_TaxId=11429;  
RN 11  
RX SEQUENCE FROM N.A.  
RX Xie L, Liu W -Y, Wang F -D;  
RX 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996;  
RT "Molecular cloning of cinnamomin A', B-chain and the expression,  
RT purification, characterization and mutagenesis of the A'-Chain.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: AF595548; AAF68978.2; -  
DR HSP: P02879; ZAM1.  
DR InterPro: IPR000772; R1CIN\_B\_lectin.  
DR InterPro: IPR001574; R1P.  
DR Pfam: PF00652; R1CIN\_B\_lectin; 5.  
DR PRINTS: PR00366; SHIGARICIN.  
DR SMART: SM00458; R1CIN\_2.  
DR PROSITE: PS00231; R1CIN\_B\_lectin; 2.  
KW Hydrolase; Toxin.  
FT NON TER 1 1  
FT CHAIN 549 AA; 60648 MW; 02607E607CA4480 CRC64;  
SQ SEQUENCE 549 AA; 60648 MW; 02607E607CA4480 CRC64;  
Query Match 34.3%; Score 419.5; DB 10; Length 549;  
Best Local Similarity 43.4%; Pred. No. 2.1e-38;  
Matches 111; Conservative 36; Mismatches 94; Indels 13; Gaps 10.

DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DR	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Abrin B (RBN A-glycosidase) (RC 3.2.3.22) (Fragment).
GN	RIP.
OS	Abrus precatorius (Indian licorice) (Crab's eye).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gnemlosperma; Eudicotyledons; Rosales; Rubiales; Fabaceae; Leguminosales; Abruseae; Abrus.
OX	NCBI_TaxId=3816;
RN	[1] _
RP	SEQUENCE FROM N.A.
RX	TEISSIE-LEAF;
RY	MEDLINE=91201329; PubMed=2016300;
RT	Evensen G., Mathiesen A., Sundan A.
SA	"Direct molecular cloning and expression of two distinct abrin A-
SL	chains.";
ST	J. Biol. Chem. 266:6848-6852(1991).
CC	-1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNIT. IT IS MORE TOXIC THAN RIBIN.
CC	-1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
CC	-1- CATALYTIC ACTIVITY: ENDOHEXDRYLASIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
CC	-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC	-1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC	-1- FAMILIAL: BLOTCHER, MATELIER AND PLANTS RIBOSOME-INACTIVATING
CC	RNMI, Y54872; CAY3854.1.) ..
DR	InterPro: IPRO01574; RIP.
DR	Pfam: Pf00161; RIP; 1.
DR	PRINTS: PR00396; SHIGALICIN.
DR	PROSITE: PS00275; SHIGA_RICIN; 1.
FW	Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
KW	CHAIN 1 252
FT	NON TER 252
QD	SEQUENCE 252 AA; 29309 MW; BHF046B9392B5DE CMC64;

Query Match Similarity	36.24%	Score 443;	DB 10;	Length 252;
Best Local Similarity	43.64%	Pred. No. 1,66-41;		
Matches 106;	Conservative 34;	Mismatches 97;	Indels 6;	Gaps 5;
OY	THGTEKKEPFFITLLRDVSGSFNSFNIPLRQSTITPSPDAQFVLWEINQKQKSNXTA	68		
Db	1 TGAQSTGQSGTIDAKRNLKGLHRIPLVADPFTVHERKRIIVHNSRSESLSEV	67		
OY	69 AIDPMNNVVAQSGOSYFLPAPARAGATFLPFGTBRDSSCLSPYSGYSDLEVRGK-R	127		
Db	68 GIDVNNVVAVPAQSGOSYFLPAPASASTYLFQGL-QRTSLRDSQYGLDEVRKMQRR	125		
OY	128 DQTFPGIXQLQSYPAKEPFGSGTFRKQASRIILLIQWISSEAAFNPIIMXKRXINSXS	187		
Db	126 RQTSIGDALTFALSPISFGASMDERKATLLVLIQWSEAKRIIRISNVGQVGRIGRA	185		
OY	188 FLDKXKMLRFSMWCQSGYQVQSGTDVQVPMKXALAXXGKPFLLXN-RXVSIISAILM	246		
Db	186 FQDPRMLSLNNQNLISGQVQSSVQTFPFAVTLVRVNNQPVAYDSLTHQGVAVATLML	245		
OY	247 FVC 249			
Db	246 FVC 248			
PRELIMINARY	PRELIMINARY;	PRT;	580 AA.	
AC	Q94BW3			
DT	01-DEC-2001 (TREMBL)rel. 19, Created			
DT	01-DEC-2001 (TREMBL)rel. 19, Last sequence update)			

DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Type 2 ribosome-inactivating protein cinnamomum III precursor
DS	(EC 3.2.2.22) (RNA N-Glycosylase).
OS	Cinnamomum camphora (camphor tree).
CC	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC	Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX	NCBI_TaxID=13429;
PF	SEQUENCE FROM N.A.
RA	Yang Q., Gong Z.Z., Liu W.Y.;
RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT	genes encoding cinnamomum proteins and study of their expression
RT	patterns.";
RL	Submitted (JUN-2001) to the EMBL/GenBank/ODBC databases.
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-DGLUCOSIDIC BOND AT ONE
CC	SPECIFIC ADENOSINE ON THE 28S RNM.
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR	EMBL; AY039803; AK83460.1;
DR	InterPro; IPR00772; Ricin_B_Lectin.
DR	InterPro; IPR001574; RIR
DR	Pfam; PF00162; Ricin_B_Lectin; 6.
DR	Pfam; PF00162; Ricin_B_Lectin; 6.
DR	PRINTS; PR00136; SHIGARICIN.
DR	SMART; SM00458; RCIN; 2.
DR	PROSITE; PS50231; RICIN_B_LECTIN; 2.
DM	Hydrolase; Signal; Toxin.
FT	SIGNAL
FT	CHAIN
FT	1 3 580
FT	3 32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III.
FT	SEQUENCE 580 AA; 64421 NM; 940D10F0LE7B558 GC64;
Query Match	35.0%; Score 428.5; DB 10; Length 580;
Pos. local similarity	41.8%; Pred. No. 2,2e-39;
Matches 112;	Conservative 37; Mismatches 94; Indels 13; Gaps 10.

Cy	9	THATGCGEERFRTLLRQVSSGSPNEILLRG	STTPSDAQRFLVELNQAGAS-X	86
Db	40	TKNAKKTSTGCTALRALQALASGEPGILPWRKSTVP	-DSKFLVLELSNADSDSV	97
Cy	67	TAADIDTNNVAVAAQAGCGSTFIR	DAPKGAETHLFTGTTRDSSLTPKQGXQLERYAG	125
Db	96	THAVDITNAGVAVAAQAGSGSTQKRGSEILLI	IQMISEAAQFPNLTMRKXQXN	183
Cy	126	-HNDGTEIGXGLQSLQVAAKXG	-GSTQKRGSEILLI	183
Db	156	ERESEILLMDPLENNKISLWVITSLNQQLRALRSL	LVYQWAEAVFRFIRYVESST	245
Cy	184	SGASLEDPXMYELRSTSGGCGSTQVQSTG	-GVNRPKRLAIKXNFTLNNVY-XV	241
Db	216	RAEMRPPDPMISLEKMGALSNAVOOSNOGQVSS	PVELLSISNKPYYGVGSIDVRIAG	275
Cy	242	LAINLFCV	-GERSPS	255
Db	276	LAINLFLGRSTGRASS	291	

RESULT 13

Q9ABM4	1D	Q9ABM4	PRELIMINARY	FRT	580 AA.
AC	Q9ABM4	Q9ABM4			
DB	Q9ABM4	Q9ABM4			
DT	01-DEC-2001	(TFEMBL:1.19, Created)			
DT	01-DEC-2001	(TFEMBL:1.19, last sequence update)			
DT	01-MAR-2003	(TFEMBL:1.21, last annotation update)			
DE	Type 2 ribosome-inactivating protein cinnaomun II precursor				
DE	(EC 3.2.2.22) (cRN: N-glycosidase)				
OS	Cinnamomum camphora (Camphor tree)				
OC	Spermatophyta; Vasculariferae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.				
OX	NCBI_TaxID=13429;				
RA	SEQUENCE FROM N.A.				
RT	Yang Q., Gong Z.Z., Liu W.Y.;				
RA	Molecular Cloning of three type 2 RIP (ribosome-inactivating protein)				

QY 9 TQTTGKXEFRTTLADYVSSGSFSENEILRQSTIPVSDAKRFVAVELTNGQDXNTA 68  
DB 9 TEGATSGYKQFLEAKRERL-RGGLIHDIIVLPDPT-TLQENNRITLVELNSDTESEIV 66  
QY 69 AIDVTNXYVAVYAGQSGYFLDAPRGAETLFTGTTPRSGSLPRGSGYDLEKACH-R 127  
DB 67 GIDVTNAYVAVYAGQSYFLDAPRGSADVLFTGT--DQSLPFGYGVGLERNAHQSR 124  
QY 128 DQIPGLIGXOLIOSVAXLXPGSGSTRQKARSILILQWISGAARPNPILMXRQXINSGX 187  
DB 125 QQIPGLIGXOLMTGISFFSGQNDKEKATLIVIIQWVAAALPRYISNRYVSIQGTGA 184  
QY 188 FLDPXVMELETSGQSGTQVQSHSTQGVFNNPKRLAIXXGNFTLANVXK----- 237  
DB 185 FQDPAKMSLENNMNLNRGVQSGVQDTFFNQ-----VTLNINRNPYVDSLSH 234  
QY 238 -VINSALMTFVC 249  
DB 235 PTVAVALMTFVC 247

## RESULT 9

Q96237

ID Q96237 PRELIMINARY; FRT; 251 AA.

AC Q96237, 1997 (TRENDEL, 02, Created)  
DT 01-FEB-1997 (TRENDEL, 02, Last sequence update)  
DE PCNNAc-1-E164A/R167L protein (EC 3.2.2.22) (PNN N-glycosidase)  
DE (Fragment)  
OS Abrys precatorius (Indian licorice) (Crab's eye).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrys.  
NCBI TaxID=3816;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=seed; PubMed=8307038;  
RA Chih-hung H. Lee M.C. Chen J.K.  
RT "Cloning and expression of three abrys x-chains and their mutants  
derived by site-specific mutagenesis in Escherichia coli.";  
RL Bur. J. Biochem. 219:83-87(1994).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL; X76722; CA54140.1; -  
DR HSSP; P11440; IABR.  
DR InterPro; IPR001574; RIP.  
DR PRINTS; PR00161; RIP; 1.  
DR PROSITE; PRO0396; SHIGARCTIN.  
KM Hydroxylase; toxin.  
FT NON TER 1  
FT NON TER 251  
SQ SEQUENCE 251 AA; 28055 MW; 6f64755CDBAF97E CRC64;

Query Match 37.6%; Score 460; DB 10; Length 251;  
Best Local Similarity 41.9%; Pred. No. 1.9e-43;  
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;

QY 9 TQTTGKXEFRTTLADYVSSGSFSENEILRQSTIPVSDAKRFVAVELTNGQDXNTA 68  
DB 9 TEGATSGYKQFLEAKRERL-RGGLIHDIIVLPDPT-TLQENNRITLVELNSDTESEIV 66  
QY 69 AIDVTNXYVAVYAGQSGYFLDAPRGAETLFTGTTPRSGSLPRGSGYDLEKACH-R 127  
DB 67 GIDVTNAYVAVYAGQSYFLDAPRGSADVLFTGT--DQSLPFGYGVGLERNAHQSR 124  
QY 128 DQIPGLIGXOLIOSVAXLXPGSGSTRQKARSILILQWISGAARPNPILMXRQXINSGX 187  
DB 125 QQIPGLIGXOLMTGISFFSGQNDKEKATLIVIIQWVAAALPRYISNRYVSIQGTGA 184  
QY 188 FLDPXVMELETSGQSGTQVQSHSTQGVFNNPKRLAIXXGNFTLANVXK----- 237

DB 185 FQDPAKMSLENNMNLNRGVQSGVQDTFFNQ-----VTLNINRNPYVDSLSH 234  
QY 238 -VINSALMTFVC 249  
DB 235 PTVAVALMTFVC 247

## RESULT 10

Q96235

ID Q96235 PRELIMINARY; FRT; 251 AA.

AC Q96235, 1997 (TRENDEL, 02, Created)  
DT 01-FEB-1997 (TRENDEL, 02, Last sequence update)  
DE PCNNAc-1-E164A/R167L (EC 3.2.2.22) (PNN N-glycosidase)  
DE (Fragment)  
OS Abrys precatorius (Indian licorice) (Crab's eye).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrys.  
NCBI TaxID=3816;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=seed; PubMed=8307038;  
RA Chih-hung H. Lee M.C. Chen J.K. Chen J.K. Chen J.K.  
RT "Cloning and expression of three abrys x-chains and their mutants  
derived by site-specific mutagenesis in Escherichia coli.";  
RL Bur. J. Biochem. 219:83-87(1994).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL; X76644; CA54092.1; -  
DR HSSP; P11440; IABR.  
DR InterPro; IPR001574; RIP.  
DR PRINTS; PR00161; RIP; 1.  
DR PROSITE; PRO0396; SHIGARCTIN.  
KM Hydroxylase; toxin.  
FT NON TER 1  
FT NON TER 251  
SQ SEQUENCE 251 AA; 27997 MW; 3B60351839AEP7E CRC64;

Query Match 37.1%; Score 454; DB 10; Length 251;  
Best Local Similarity 41.5%; Pred. No. 9.1e-43;  
Matches 105; Conservative 34; Mismatches 88; Indels 26; Gaps 6;

QY 9 TQTTGKXEFRTTLADYVSSGSFSENEILRQSTIPVSDAKRFVAVELTNGQDXNTA 68  
DB 9 TEGATSGYKQFLEAKRERL-RGGLIHDIIVLPDPT-TLQENNRITLVELNSDTESEIV 66  
QY 69 AIDVTNXYVAVYAGQSGYFLDAPRGAETLFTGTTPRSGSLPRGSGYDLEKACH-R 127  
DB 67 GIDVTNAYVAVYAGQSYFLDAPRGSADVLFTGT--DQSLPFGYGVGLERNAHQSR 124  
QY 128 DQIPGLIGXOLIOSVAXLXPGSGSTRQKARSILILQWISGAARPNPILMXRQXINSGX 187  
DB 125 QQIPGLIGXOLMTGISFFSGQNDKEKATLIVIIQWVAAALPRYISNRYVSIQGTGA 184  
QY 188 FLDPXVMELETSGQSGTQVQSHSTQGVFNNPKRLAIXXGNFTLANVXK----- 237  
DB 185 FQDPAKMSLENNMNLNRGVQSGVQDTFFNQ-----VTLNINRNPYVDSLSH 234  
QY 238 -VINSALMTFVC 249  
DB 235 PTVAVALMTFVC 247

RESULT 11  
ID Q98760 PRELIMINARY; FRT; 252 AA.  
AC Q98760, 1998 (TRENDEL, 08, Created)  
DT 01-NOV-1998 (TRENDEL, 08, Created)

Thu Dec 11 16:10:00 2003

us-09-601-667c-41.rspt

Page 4

FT RA To M.-Sed Song S.K.;  
PT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
CC - - CATALYTIC ACTIVITY ENZYMOLOGISTS OF THE N-GLYCOSIDIC BOND AT ONE  
CC - - STABILIZING BINDINGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC - - STABILIZING BINDINGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL; AF080916; LAM64934.1; ..  
DR Interpro: IPR001574; RFP.  
DR Pfam: PF00161; RIP; ..  
DR PRINTS; PR00386; SHGARGCIN.  
KW Hydrolase; toxin.  
FT NON TER 1  
PT TER 251  
FT SEQUENCE 251 AA; 28090 MW; A11774809125B8 CRC64;

Query Match	79.5%;	Score 977;	DB 10;	Length 251;
Best Local Similarity	80.6%;	PIdent. No. 8.2e-102;		
Matches 20;	Conservative	7;	Mismatches 36;	Indels 6; Gaps 3
Qy	1	YERLRLVTHMTCSEYRFLITLIDVSSGSPENILPLRGSTIPVSSAGFVLELN	60	
Db	1	YERLRLVTHMTCSEYRFLITLIDVSSGSPENILPLRPS-IPVSSAGFVLELN	59	
Qy	61	Q--GDUSNAIDVYNYVVAAGAGSYFLDAPGAEHLFTGYTRDRESSLPKASY	117	
Db	60	QLRKEDSLTSLNDVNYLVYVAAGAGSYFLRNDLGRHHLRVT--RSLPDSHSL	117	
Qy	118	XDLEHYAGRPDIFLIXDLQISYVALYEXGSGSPKQASILLIOMISLAAERNPILMR	177	
Db	118	ADLEHYAGRHDFILREPLRLHYSALDLYGSGSPQASIIIVCOMISLAAERNPILMR	177	
Qy	178	XKQILNIGSYPLDYMFLFLTSGGCGSTQGHSTGRRELATKXNTKTLNXPX	237	
Db	178	ARLYNIGSYPLDYMFLFLTSSGCGSTQGVSTDGVNPFRLGISTGNFVNLNVAD	237	
Qy	238	VIRASLAINLPVC	249	
Db	238	VIRSLGIMVPC	249	

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RESULT 7
Q38761          PRELIMINARY;          PRT;          252 AA.
ID   Q38761; Q96234;
AC   Q38761; Q96234;
DT   01-NOV-1996 (PRELIMINARY, 01, Created)
DT   01-NOV-1996 (PRELIMINARY, 01, Last sequence update)
DR   01-OCT-2002 (PRELIMINARY, 22, Last annotation update)
DR   R1C1A-A-chain type 73 (EC 3.2.2.22) (R1C1A-N-91ycosidase)
DS   (segment).
OS   Abrus precatorius (Indian licorice) (Crab's eye).
OC   Spatiotricha, Vitidiales; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC   eucosids I; Fabales; Fabaceae; Papilionoideae; Abrease; Abrus.
CX   NCBI_TaxID:31816;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=leaf;
RA   Evensen G., Mathiesen A., Sundan A.;
RL   Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
RN   [2]
RP   TISSUE=seed;
RC   TISSUE=seed;
RA   MEDLIN:94119756; PubMed:8307038;
RA   Chah-Hung H., Lee M.-C., Chen Y.-K., Lin J.-Y.;
RA   Cloning and expression of three abrin A-chains and their mutants
RA   derived from Abrothamnus biocoloratus in Escherichia coli."
RA   J Biol Chem 273:93183-97(1998)
CC   -1. CATALYTIC ACTIVITY: ENDOGALACTOSYL OF THE N-GLYCOSIDIC BOND AT ONE
CC   SPECIFIC ADDRESSING TO THE 28S RRNA.
CC   -1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR   EMBL; X54873; CA93655.1; -.
DR   EMBL; X76720; CA654138.1; -.
DR   HSPB; P1140; 1ABR.

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DR	InterPro:	IPR001574;	RIP.
DR	Pfam:	PF00161;	RIP; 1
DR	PRINTS:	PR00396;	SHEGRCIN.
DR	PROSITE:	PS00275;	SHEGRCIN; 1.
KR	NCBI:	PF00161;	RIP; 1
FT	NON REP.	252	252
SO	SEQUENCE	252 AA;	1878239 NW; 1878B8E3JAAECF CRC64;
Query Match		38.2%;	Score 467; DB 10; Length 252;
Match Local Similarity		42.3%;	Fvec: N0.3-e-44;
Matches 10'; Conservative		3;	Mismatches 86; Indels 26; Gaps 6;

QY THQTQGEKFEFFFTILTRRYVSSGSNSELPLMKQSTIVSDKQRYVATLNNQSKSYTA 58  
Db TSASQSVKQFTEARRRR-RGSLHDPVLPDPT-FLQENRRYIVALSNDSTSEV 67  
QY AIDVNNXYVAKQADDSYFLDAPRQAEFTPLGTTRDRSLPBGYSXOLERYVGH-R 127  
Db 69 GIDVTAIVYARAGQSTFGLDAPSSADYLPFGI-DHNSLPFYQGLDRMHR 125  
QY 68 QOIPILGTLTHGISFPGSGDNDEKATITIVIGWAAAPFYSNRVAVSIOTSTA 185  
Db 126 FLEEDYVLELETSFGSGSTOVGHSTDFVFNPKXKLAIXGNFVTLXNVX- 237  
QY 188 FQDPAALILNNNDLSRGVGSYQDTFPNQ-VLTINREPIVYDLSLH 235  
Db 186  
QY 238 -VIAELAIIMFVC 249  
Db 236 PTVAIVLIMFVC 248

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RESULT 8
Q96236 PRELIMINARY; PRT: 251 AA.
ID Q96236
AC Q96236;
DT 01-FEB-1997 (EMBLrel, 02, Created)
PT 01-FEB-1997 (TrEMBL, 02, Sequence update)
PF 01-FEB-1997 (EMBL, 02, Fast annotation update)
DE Abtin A chain (EC 3.2.2.22) (E14A) (RRN N-glycosidase)
   (Fragment)
GN PCDNAc-1-E14A.
OS Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OC NCBI_taxid=3816;
OM
OR
RX MEDLINE=94139756; PubMed=8307038;
RC TISSUE=SEED;
RT "Cloning and expression of three abrin A-chains and their mutants
   derived by site-specific mutagenesis in Escherichia coli.";
RL Eur. J. Biochem. 219:183-87(1994).
CC -1- CHAIN-INITIAL ACETYLATION. -1- N-GLYCOSIDIC BOND AT ONE
   -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: X76721; CAA54119.1; -
DR HSSP; P1140; 1ABR.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolase; Toxin.
FT
FT NON_TER 1
FT TER 251
SQ SEQUENCE 251 AA; 28040 MW; D5F7CB182D0EC93 CRC64;
Query Match 37.7%; Score 461; DB 10; Length 251;
Basic Local Similarity 41.9%; Pred. No. 1,5e-43;
Matches 106; Conservative 34; Indels 26; Gaps

```

DE Lectin chain A isoform 1 (EC 3.2.2.22) (rRNA N-glycosidase)  
 DS (Fragment)  
 OS Viscum album subsp. coloratum  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Santalales; Viscaceae; Viscum.  
 OX NCBI\_TaxId=159976;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2156752; PubMed=11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RM Do M.-S., Song S.K.; Sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum)."  
 RL Mol. Cells 12:215-220(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC EMBL: AF069244; JMW4532.1; .  
 CC DDB: J01001574; RIP.  
 CC RefSeq: NC\_001394; RIP.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR Hydrolase; Toxin.  
 KW NON TER 1  
 FT NON TER 254  
 FT NON TER 254  
 SQ SEQUENCE 254 AA; 28446 MW; 6DB5CB18FAFE0 CRC64;

Query Match 89.5%; Score 1094; DB 10; Length 254;  
 Best Local Similarity 85.5%; Pred. No. 5.2e-115;  
 Matches 219; Conservative 8; Mismatches 27; Indels 2; Gaps 1;

QY 1 YERLRVHTGTCGTFPRITLIDNVYSGSFNEIPLAQSTIPYSDAPRYVLEIN 60  
 DB 1 YERLRVHTGTCGTFPRITLIDNVYSGSFNEIPLAQSTIPYSDAPRYVLEIN 60  
 QY 61 QGDXKXTALIDVTNXYVAYAOQSYFLDAPGAEFTLFTGTRDSSLPFGSYXDL 120  
 DB 61 QGDXKXTALIDVTNXYVAYAOQSYFLDAPGAEFTLFTGTRDSSLPFGSYXDL 120  
 DB 61 QGDSITAIIDVTNLYVAYAOQSYFLDAPGAEFTLFTGTRDSSLPFGSYXDL 118  
 QY 121 ERYAGRDQIPGIXQLIQSYALXPGSSTXQASITLILQISEARFNPIMXKXQ 180  
 DB 119 ERYAGRDQIPGIRELLIQSYALXPGSSTXQASITLILQISEARFNPIMXKXQ 178  
 QY 181 XINSGKSPDPKXMLEFTSMQGSITQVHSTGVFNNKRLAIXGFTLXNRYIA 240  
 DB 179 YISSGSPDPKXMLEFTSMQGSITQVHSTGVFNNKRLAIXGFTLXNRYIA 238  
 QY 241 SLAINLFCVCEPRSSS 256  
 DB 239 SLAINLFCVCEPRSSS 254

RESULT 5  
 QBLK04 PRELIMINARY; PRT; 249 AA.  
 ID QBLK04  
 DT 01-OCT-2002 (TRENBERG) 22, Created  
 DT 01-OCT-2002 (TRENBERG) 22, Last sequence update  
 DT 01-MAR-2003 (TRENBERG) 23, Last annotation update  
 DE Lectin chain A isoform 2 (EC 3.2.2.22) (rRNA N-glycosidase)  
 OS Viscum album subsp. coloratum  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Santalales; Viscaceae; Viscum.  
 OX NCBI\_TaxId=159976;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,

RX MEDLINE=2156752; PubMed=11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RM Do M.-S., Song S.K.; Sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum)."  
 RL Mol. Cells 12:215-220(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC EMBL: AF069244; JMW4532.1; .  
 CC DDB: J01001574; RIP.  
 CC RefSeq: NC\_001394; RIP.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR Hydrolase; Toxin.  
 KW NON TER 1  
 FT NON TER 249  
 FT NON TER 249  
 SQ SEQUENCE 249 AA; 27821 MW; 3C5870F838BDAB5 CRC64;

Query Match 86.2%; Score 1054; DB 10; Length 249;  
 Best Local Similarity 83.9%; Pred. No. 1.6e-110;  
 Matches 209; Conservative 13; Mismatches 25; Indels 2; Gaps 1;

QY 1 YERLRVHTGTCGTFPRITLIDNVYSGSFNEIPLAQSTIPYSDAPRYVLEIN 60  
 DB 1 YERLRVHTGTCGTFPRITLIDNVYSGSFNEIPLAQSTIPYSDAPRYVLEIN 60  
 QY 61 QGDXKXTALIDVTNXYVAYAOQSYFLDAPGAEFTLFTGTRDSSLPFGSYXDL 120  
 DB 61 QGDXKXTALIDVTNXYVAYAOQSYFLDAPGAEFTLFTGTRDSSLPFGSYXDL 118  
 QY 121 ERYAGRDQIPGIXQLIQSYALXPGSSTXQASITLILQISEARFNPIMXKXQ 180  
 DB 119 ERYAGRDQIPGIRELLIQSYALXPGSSTXQASITLILQISEARFNPIMXKXQ 178  
 QY 181 XINSGKSPDPKXMLEFTSMQGSITQVHSTGVFNNKRLAIXGFTLXNRYIA 240  
 DB 179 YISSGSPDPKXMLEFTSMQGSITQVHSTGVFNNKRLAIXGFTLXNRYIA 238  
 QY 241 SLAINLFCV 249  
 DB 239 SLAINLFCV 247

RESULT 6  
 QBLK04 PRELIMINARY; PRT; 251 AA.  
 ID QBLK04  
 DT 01-OCT-2002 (TRENBERG) 22, Created  
 DT 01-OCT-2002 (TRENBERG) 22, Last sequence update  
 DT 01-MAR-2003 (TRENBERG) 23, Last annotation update  
 DE Lectin chain A isoform 3 (EC 3.2.2.22) (rRNA N-glycosidase)  
 OS Viscum album subsp. coloratum  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Santalales; Viscaceae; Viscum.  
 OX NCBI\_TaxId=159976;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2156752; PubMed=11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RM Do M.-S., Song S.K.;  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC EMBL: AF069244; JMW4532.1; .  
 CC DDB: J01001574; RIP.  
 CC RefSeq: NC\_001394; RIP.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR Hydrolase; Toxin.  
 KW NON TER 1  
 FT NON TER 249  
 FT NON TER 249  
 SQ SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,

Matches 231: Conservative 3; Mismatches 20; Indels 2; Gaps 1;

QY 1 YERLRLRVTHQGTGKEFRITLLRDYVSSGSFNSNEIPILROSTIFVSDAQRFVLVELTN 60  
DB 1 YERLRLRVTHQGTGKEFRITLLRDYVSSGSFNSNEIPILROSTIFVSDAQRFVLVELTN 60  
QY 61 QGDSKSTALIDVTNXYVVAQAGQSYFLDAPGATHTLFTGTDDSSIPKSGSYXL 120  
DB 61 QGDSKSTALIDVTNXYVVAQAGQSYFLDAPGATHTLFTGTDDSSIPKSGSYXL 118  
QY 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 180  
DB 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 178  
QY 119 ERYAGRRDQIPLGIDQLGOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 240  
DB 119 ERYAGRRDQIPLGIDQLGOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 238  
QY 179 YINSGSFLPDVYVMELETSMGQSTVOVSHSTGVPNNPKRLAIXGNFVLNVRVIA 240  
DB 179 YINSGSFLPDVYVMELETSMGQSTVOVSHSTGVPNNPKRLAIXGNFVLNVRVIA 238  
QY 241 SLAINLFCGRPSS 256  
DB 239 SLAINLFCGRPSS 254

## RESULT 2

Q8W243 PRELIMINARY; PRT; 565 AA.

AC Q8W243: 2002 (TRENBERG). 20. Created.  
DT 01-MAR-2002 (TRENBERG). 20. Last sequence update.  
RT 01-OCT-2002 (TRENBERG). 20. Last sequence update.  
RU VCA Isoform 2 (EC 3.2.2.22) (rRNA N-glycosylase).  
OS Viscum album subsp. coloratum.  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OX Santalales; Viscaceae; Viscum.  
NX NCBI\_TaxID=159976;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Park W.-B., Liu S.;  
RT Cloning of Viscum album subsp. coloratum (Korean mistletoe)."  
RT Biochem. Biophys. Res. Commun. 289:100-104 (2002).  
RU -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: AF369961; AL04017.1; -.  
DR InterPro: IPR000772; Ricin\_B lectin.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00652; Ricin\_B lectin; 6.  
DR Pfam: PF00161; RIP; 1.  
DR PRINTS: PR00396; SHIGAZICIN.  
DR SMART: SM00458; RICIN; 2. LECTIN; 2.  
DR PROSITE: PS00231; RICIN\_B LECTIN; 2.  
NX Hydrolyase; Signal; Toxin.  
KM HYDROLASE; 23.  
FT CHAIN 23 POTENTIAL.  
FT CHAIN 23 VCA ALPHA CHAIN.  
FT CHAIN 309 565 VCA BETA CHAIN.  
SQ SEQUENCE 565 AA; 62401 MW; 394E3994DM05F11 CRC64;

Query Match 91.3%; Score 1116; DB 10; Length 565;  
Best Local Similarity 87.8%; Pred. No. 5,1e-117;  
Matches 224; Conservative 4; Mismatches 26; Indels 2; Gaps 1;

QY 1 YERLRLRVTHQGTGKEFRITLLRDYVSSGSFNSNEIPILROSTIFVSDAQRFVLVELTN 60  
DB 1 YERLRLRVTHQGTGKEFRITLLRDYVSSGSFNSNEIPILROSTIFVSDAQRFVLVELTN 93  
QY 61 QGDSKSTALIDVTNXYVVAQAGQSYFLDAPGATHTLFTGTDDSSIPKSGSYXL 120  
DB 61 QGDSKSTALIDVTNXYVVAQAGQSYFLDAPGATHTLFTGTDDSSIPKSGSYXL 151  
QY 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 180  
DB 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 211

QY 181 XINSGSFLPDVYVMELETSMGQSTVOVSHSTGVPNNPKRLAIXGNFVLNVRVIA 240  
DB 212 YINSGSFLPDVYVMELETSMGQSTVOVSHSTGVPNNPKRLAIXGNFVLNVRVIA 271  
QY 241 SLAINLFCGRPSS 256  
DB 272 SLAINLFCGRPSS 287

## RESULT 3

Q8KH7 PRELIMINARY; PRT; 249 AA.

AC Q8KH7: 2002 (TRENBERG). 21. Created.  
DT 01-JUN-2002 (TRENBERG). 21. Last sequence update.  
RT 01-OCT-2002 (TRENBERG). 21. Last sequence update.  
RU Viscum album (Indian) mRNA for Mistlec lectin chain A, isoform 2."  
OS Viscum album (European mistletoe).  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OX Santalales; Viscaceae; Viscum.  
NX NCBI\_TaxID=3972;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rissotto, West N., Singh T.P.;  
RT Viscum album (Indian) mRNA for Mistlec lectin chain A, isoform 2."  
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RU -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: AY081148; AL087005.1; -.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP; 1.  
NX HYDROLASE; Toxin.  
FT NON-TER 1  
FT NON-TER 249  
SQ SEQUENCE 249 AA; 27944 MW; 69FA767309A833 CRC64;

Query Match 91.0%; Score 1113; DB 10; Length 249;  
Best Local Similarity 88.8%; Pred. No. 3,6e-117;  
Matches 223; Conservative 3; Mismatches 23; Indels 2; Gaps 1;

QY 1 YERLRLRVTHQGTGKEFRITLLRDYVSSGSFNSNEIPILROSTIFVSDAQRFVLVELTN 60  
DB 1 YERLRLRVTHQGTGKEFRITLLRDYVSSGSFNSNEIPILROSTIFVSDAQRFVLVELTN 60  
QY 61 QGDSKSTALIDVTNXYVVAQAGQSYFLDAPGATHTLFTGTDDSSIPKSGSYXL 120  
DB 61 QGDSKSTALIDVTNXYVVAQAGQSYFLDAPGATHTLFTGTDDSSIPKSGSYXL 118  
QY 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 180  
DB 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 178  
QY 119 ERYAGRRDQIPLGIBELIOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 240  
DB 119 ERYAGRRDQIPLGIBELIOSVALLKPKGSTRQARSLILQWISBAARPNFILMRXQ 238  
QY 241 SLAINLFCGR 251  
DB 239 SLAINLFCGR 249

RESULT 4  
Q8LK06 PRELIMINARY; PRT; 254 AA.  
AC Q8LK06: 2002 (TRENBERG). 22. Created.  
DT 01-OCT-2002 (TRENBERG). 22. Last sequence update.  
RT 01-MAR-2003 (TRENBERG). 23. Last annotation update.



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# OK protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 19,7321 seconds  
(without alignments)  
3347,915 Million cell updates/sec

Title: US-09-601-667C-41  
Score: 12.9  
Sequence: 1 YERKALRYHOTGKHYFR.....XTASLAIMLFCGEPSSS 256

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.muc:\*  
8: sp.outgroup:\*  
9: sp.outgroup:\*  
10: sp.plant:\*  
11: sp.virus:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriopl:\*  
17: sp.archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1147	93.8	531	10	Q8RXH6
2	1116	91.3	555	10	Q8W243
3	1113	91.0	249	10	Q8RXH7
4	1024	82.5	244	10	Q8LXOC
5	1024	82.5	251	10	Q8LXOC
6	977	79.5	251	10	Q8LXOC
7	467	38.2	252	10	Q8R761
8	461	37.7	251	10	Q8E237
9	460	37.6	251	10	Q8E236
10	454	37.1	251	10	Q8E235
11	443	36.2	252	10	Q8R760
12	428.5	35.0	580	10	Q94BW3
13	428.5	35.0	580	10	Q94BW4
14	426	34.8	528	10	Q8F076
15	419.5	34.3	549	10	Q8FV22
16	418.5	34.2	551	10	Q94BW5

17	380	31.1	547	10	Q9W6E9	Q9W6E9 abrus prec
18	374	30.6	570	10	Q41358	Q41358 sambucus ni
19	370	30.3	541	10	Q41174	Q41174 ricinus com
20	367.0	30.3	540	10	Q24115	Q24115 sambucus ni
21	367.0	29.6	544	10	Q24115	Q24115 sambucus ni
22	362.5	29.6	555	10	Q04071	Q04071 sambucus ni
23	361	29.1	592	10	Q8W287	Q8W287 iris hollan
24	356	29.1	573	10	Q8W288	Q8W288 iris hollan
25	350.5	28.7	563	10	Q04367	Q04367 sambucus ni
26	347	28.4	566	10	Q04072	Q04072 sambucus ni
27	345	28.2	569	10	P93543	P93543 sambucus ni
28	339	27.7	563	10	Q94582	Q94582 sambucus ni
29	338	27.6	563	10	Q8C712	Q8C712 sambucus ni
30	334.5	27.4	564	10	Q9C634	Q9C634 polygonatum
31	327	26.3	589	10	Q8C712	Q8C712 polygonatum
32	327	26.3	589	10	Q8C712	Q8C712 polygonatum
33	286	24.2	247	10	Q8R761	Q8R761 trichosan
34	286	24.2	270	10	Q8C712	Q8C712 trichosan
35	296	24.2	277	10	Q8C712	Q8C712 trichosan
36	296	24.2	289	10	Q41216	Q41216 trichosan
37	294	24.0	277	10	Q8C711	Q8C711 trichosan
38	289.5	23.7	300	10	Q04357	Q04357 iris hollan
39	289	23.6	275	10	Q8H114	Q8H114 gymostemma
40	288	23.5	277	10	Q8H115	Q8H115 gymostemma
41	288	23.5	603	10	Q9W653	Q9W653 polygonatum
42	286.5	23.4	277	10	Q8C710	Q8C710 gymostemma
43	286.5	23.4	277	10	Q8C710	Q8C710 gymostemma
44	286.5	23.4	277	10	Q8C710	Q8C710 gymostemma
45	276.5	22.6	298	10	Q04358	Q04358 iris hollan

## ALIGNMENTS

### RESULT 1

Q8RXH6 PRELIMINARY; EST; 531 AA.

Q8RXH6: 1002 (TRENDEL 21, Created)

Q8RXH6: 01-JUN-2002 (TRENDEL 21, Last annotation update)

Q8RXH6: 01-MAR-2003 (TRENDEL 23, Last annotation update)

Q8RXH6: Lactin chain A isoform 1 (EC 3.2.2.22) (RNA N-glycosidase)

Q8RXH6: Viscum album (European mistletoe).

Q8RXH6: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Santalales; Viscaceae; Viscum.

Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

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Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

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Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

Q8RXH6: NCBI\_TaxID=3972;

Query Match 93.8%; Score 1147; DB 10; Length 531;  
Best Local Similarity 90.2%; Pred. No. 1.5e-120;

Thu Dec 11 16:10:00 2003

us-09-601-667c-41.rsp

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DR HSP; A804560; BAB19677.1; -.
DR HSP; P16094; IARC.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGRACIN.
DR PROSITE; PS00275; SHIGA RICHIN; 1.
KV Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
  toxin; Signal.
FT SIGNAL. 1 21
FT CDS 1 21
FT NAME 1 21
FT NAME SITE 185 185
FT CARBOHYD 103 103
FT CARBOHYD 110 110
FT CARBOHYD 252 252
SQ SEQUENCE 286 AA; 31771 MW; 4EPD4966E04DA1 CRC64;

Query Match 21.94; Score 267.5; DB 1; Length 286;
Best Local Similarity 31.64; Pred. No. 4.8e-22;
Matches 75; Conservative 45; Mismatches 102; Indels 15; Gaps 8;

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DB 40 YKRTISRNALPNAGIYNIPLVPS--ISGSRYLIMQLSYEGNTTVAVDVTVNY 96
QY 77 VVAYQAGDSYFLDA-PRGAEHLFTGTTDRSSLPKGSYDLERYA-GHDDQIFLG 134
DB 97 IWGYLVNGTSYFNETDAQIAKVFQGT--KSTLPYSGNYQLOSVAREHDSIFLGF 154
QY 135 XOLIOSYXALXPGSGSTRXQANSILLIOMISEARFNPIMRXQINS-GKSPLEPKY 193
DB 155 MALDSALSTLY--YDSKSAFLAFLVLIQTALAKRYKI--EKQILIRISYKPOLA 209
QY 194 MELETYSNGQSTQV--HETDGVNPPRLAIXKNTYTLANRYVIAISALMLFV 248
DB 210 AISENENSLSKQIQIAKNNNGQFQPKIINDKGIQLEVTNVSIVVTVNIMLL 266
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HEX 34 46  
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STRAND 70 76  
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STRAND 100 101  
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HEX 251 252  
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290 AA; 31788 MW; E966CD9C031A42DB CRC64;  
SEQUENCE

30-MAY-2000 (Rel. 39, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
DE Type I ribosome-inactivating protein trichosanthes precursor (rRNA  
N-glycosidase) (EC 3.2.2.22) (RIP) (Trichosanthes)  
TCA.  
OS Trichosanthes anguina (Snake gourd)  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Equisetopsida; Angiosperms; Euphorbiales; Euphorbiaceae; Core eudicots; Rosidae;  
CC Euphorbia; Euphorbiaceae; Euphorbiales; Euphorbiaceae; Trichosanthes.  
CC NCBI\_TaxID=50544;  
KN [1]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=CV, Anguina; Tissue=seed;  
RX MEDLINE=99132006; PubMed=991318;  
RA Chow L.-P., Chow M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,  
Lin Y.-Y.;  
RA "Purification, characterization and molecular cloning of trichosanthes,  
a novel type I ribosome-inactivating protein from the seeds of  
Trichosanthes anguina (Euphorbiaceae)."  
RT Biochem. J. 338:211-219 (1999).  
RU P10266.  
SP SEQUENCE OF 20-264.  
RC Tissue=seed;  
RA Chow L.-P., Kamo M., Lin J.-Y., Wang S.-H., Yano Y., Tsung A.;  
RT "Amino acid sequence of trichosanthes, a ribosomal-inactivating  
protein from Trichosanthes anguina seeds."  
RL J. Biomed. Sci. 3:178-186 (1996).  
CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN  
RIBOSOMES.  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
-1- specificity; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC -1- TYPE 1 RIP SUBFAMILY.  
CC This SWISS-Prot entry is copyrighted. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use, by non-profit institutions as long as its content is in no way  
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requires a license agreement (see <http://www.ebi.ac.uk/submit/submit.html>)  
or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
CC EMBL: A0505066; J0505066.1; -  
CC HSP: P31185; IHRV.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PRINTS: PS00275; SHIGA\_RICIN.  
DR PROSITE: PS00275; SHIGA\_RICIN.  
KW Plant defense; protein synthesis inhibitor; Hydrolase; Toxin;  
KW Glycoprotein; Signal.  
FT SIGNAL 1 29  
FT CHAIN 20 264  
FT PROPEP 265 294  
FT ACT SITE 177 177  
FT ACT SITE 180 180  
FT CARBOHYD 70 70  
FT CARBOHYD 220 220  
FT CONFLICT 51 51  
FT CONFLICT 65 65  
FT CONFLICT 84 84  
FT CONFLICT 152 152  
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Query Match 22.6%; Score 276.5; DB 1; Length 294;  
Best Local Similarity 33.2%; Pred. No. 56-23;  
Matches 80; Conservative 39; Mismatches 107; Indels 15; Gaps 7;

13 TXXXYYFFITLLDDYVSSSSFFNEIFLRQSTIFVSDAQRFLVELNGXSDXDAIV 72  
29 TXXXSSFFITLLDDYVSSSSFFNEIFLRQSTIFVSDAQRFLVELNGXSDXDAIV 85

CC eucristalis I; Cucurbitales; Cucurbitaceae; Momordica.  
OX NCBI\_TaxID=3672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=seed;  
RX MEDLINE=95027170; PubMed=1408771;  
RT Molecular, biological, and preliminary structural analysis of  
RT "Membrin" is a ribosome inactivating protein from Momordica  
RT balsamina, is homologous to other plant proteins.";  
RL Nucleic Acids Res. 20:4662-4663(1992).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC TYPE 1 RIP SUBFAMILY.  
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CC -----  
DR EMBL; 212175; CAAB16.1; .  
DR EMBL; 52560; S2550  
DR EMBL; 52560; S2550  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; P00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Plant defense; protein synthesis inhibitor; Hydrolase; Toxin; Signal;  
KW 3D-structure.  
FT SIGNAL 1 23  
FT CHAIN 24 286  
FT ACCT SITE 181  
SQ SEQUENCE 286 AA; 32031 MW; 3889F18A6E25966 C6C64;  
Query Match Best Local Similarity 33.0%; Score 281; DB 1; Length 286;  
Best Local Similarity 33.9%; Pred. No. 1.5e-23;  
Matches 78; Conservative 44; Mismatches 88; Indels 20; Gaps 9;  
OY 13 TGVKFFETLADRYSSSGSPSN--ELPDRGTFPVSADQFVAVELTMOGDSKXTA 69  
OY 73 KATKTEFE--DEPFAALTFPSHKVDYDLNIST--ISDSRFLDLSVAITATISA 86  
OY 107MTVAVVAAQAGQSPVAPRAQRAHFLPOTRSTSPSPKSYXDLSEVAVG-R 127  
OY 87 IDTVNVVVAARREDVSPFSEPAVNIILFGR-KTILPTGVNEMLCQ-AAKRR 143  
OY 128 DQPIPGXDLQSYVALKPGQSTPRQASLILQLQISAAAFNFIIMKQKXNGKS 187  
OY 144 ENIDGJPAISALATLTPYNAQSPSA--LVLTQTTAAARKKTEFVAVVY-ATN 199  
DY 188 FLDPGVVLELTSNGQSTGV--QSTGVFNNVKKALIKGVETLVKNV 235  
DY 200 FKNALATLSLENQSLSKQITLAKQNGQKFNVDLKFRTSPGVNV 249  
DB 200 FKNALATLSLENQSLSKQITLAKQNGQKFNVDLKFRTSPGVNV 249  
RESULT 12  
RIP1 BRADI  
ID RIP1 BRADI STANDARD; PRT; 290 AA.  
AC P3185; 1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 41, Last annotation update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
FE (EC 3.9.2.22 (BD)) Hydrolyzing protein bryodin 1 precursor (EC 3.9.2.22 (BD))  
OS Bryonia dioica (Seed bryodin).  
CS Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucristalis I; Cucurbitales; Cucurbitaceae; Bryonia.  
OX NCBI\_TaxID=3672;  
RN [1]  
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
RX TISSUE=seed;  
RX MEDLINE=9728081; PubMed=911598;  
RX Sgall C.B., Neubauer M., Klee H.E., Chang C.Y., Einspahr H.M.,  
RX Sgall C.B., Neubauer M., Klee H.E., Chang C.Y., Einspahr H.M.,  
RT Molecular, biological, and preliminary structural analysis of  
RT "Membrin" is a ribosome inactivating protein from the plant  
RT Bryonia dioica.";  
RL Biochemistry 36:1095-1103(1997).  
CC (2)  
CC SEQUENCE FROM N.A.  
CC Sgall C.B.,  
RT "Membrin" and expression of a gene encoding bryodin 1 from Bryonia  
RT dioica." and expression of a gene encoding bryodin 1 from Bryonia  
RT dioica." and expression of a gene encoding bryodin 1 from Bryonia  
RP Plant number US551110, 30-JUL-1996.  
RP [1]  
RP SEQUENCE OF 24-66.  
RX TISSUE=seed;  
RX MEDLINE=8932691; PubMed=2753596;  
RX Monouchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Sorio M.,  
RX Lajp D.;  
RT N-terminal sequence of some ribosome-inactivating proteins.";  
RT Int. J. Pept. Protein Res. 53:263-267(1989).  
RL  
RL  
RP SEQUENCE OF 24-43.  
RX TISSUE=Seed;  
RX MEDLINE=95151812; PubMed=7849072;  
RX Sgall C.B., Gawlak S.L., Chace D., Wolfe E.A., Mixan B.,  
RX Marguard H.;  
RT Characterization of ribosome-inactivating proteins isolated from  
RT Bryonia dioica and their utility as carcinoma-reactive  
RT immunocjugates.";  
RL Biochem. Chem. 5:423-429(1994).  
CC -1- PROTEIN SYNTHESIS INHIBITOR IN ANIMAL CELLS  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -1- FM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO  
CC PRODUCE A SHORTER PROTEIN.  
CC -1- BIOTECHNOLOGY: Especially useful as immunotoxin for  
CC pharmacological applications as it has low toxicity in rats and  
CC mice but is potent once inside target cells.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC TYPE 1 RIP SUBFAMILY.  
CC  
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CC -----  
DR EMBL; 224930; NOT\_ANNOTATED\_CDS.  
DR EMBL; 514831; S16493  
DR PDB; 1BR7; 04-MAR-98.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; P00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;  
KW 3D-structure; Multigene family; Glycoprotein; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 286  
FT ACCT SITE 181  
FT ACCT SITE 181  
FT ACCT SITE 212  
FT CARBOHYD 214 214  
FT CARBOHYD 250 250  
FT MYOGEN 212 212  
FT CONFLICT 61 65  
FT STRAND 25 28  
N-LINKED (GLCNAc, . . .) (POTENTIAL).  
N-LINKED (GLCNAc, . . .) (POTENTIAL).  
E-K: REDUCES ACTIVITY 10-FOLD.  
RSSIS -> LRHXI (IN REF. 3).

**Biol.** Pharm. Bull. 20:711-713(1997).

[2] SEQUENCE OF 24-<sup>STO</sup>. MEDLINE=92065821; PubMed=19111000;  
EX MedlinePlus=19111000; Nakabayashi K., Ogiwara Y.;  
DR "The amino acid sequence of an abortifacient protein,  
RT Karazutsumi," Chem. Pharm. Bull. 39:1244-1249(1991).  
CL  
LL -1- FUNCTION: ABORTION-INDUCTING PROTEIN. IT INACTIVATES EUKARYOTIC  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S ribosomal subunit.  
CC -1- SIMILARITY: RELATED TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC -1- RIP SUBSTRATE.  
CC -----  
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CC or send an email to licenses@isb-sib.ch)  
CC -----  
CC EMBL accession: BA221766.1 ;  
CD PIR: JCS606; JC5606  
DR PIR: J03093; J03093.  
DR HSSP: P09989; IMRZ.  
DR Interpro: IPRO01574; R.F.  
DR Pfam: PF00161; RFP\_1.  
DR PRINTS: PS00396; SHIGARCIN.  
DR PROSITE: PS00295; SHIGA\_RICH\_1.  
KM Plant defense Antiviral; Protein synthesis inhibitor; Hydrolase;  
EM Signal; Potential POTENTIAL.

FT	CHAIN	24	270	KASABURI-N.A.
FT PROPEP		271	289	REMOVED IN MATURE FORM.
FT ACT SITE		183	183	BY SIMILARITY.
SQ	SEQUENCE	289 AA; 11704 MW; 883DE32142887825 CRC64;		
Query Match		24.5%; Score 300; DB 1; Length 289;		
Best Local Similarity		35.4%; Pred. No. 1.2e-35;		
Matches		85; Conservativity 46; Mismatches 95; Indels 14; Gaps 9		
Qy		13	TKAEYREFITLIDVSSGSSENFELFROSTIYPSVDAPRVETLPMCKQKSTALDIV 72	
Db		33	TSSTGVTFINNAKALPEKRLDIFLDR SLTGSQ--QRAHLILHIVADSTISVALDIV 89	
Qy		73	KNRYVVAQAGGSGSFLPRA-PGAEFTLPTOTTRDSSLEFPGSGYDELRPAGH-RDQI 130	
Db		90	INIVYWGVRKQGISFENSAEATAPKAYVFNCAK-KTLTPYSGNVEKTLDAKQIEEM 148	
Qy		131	PLGIQLQSGVAARXGSGSTFQAQSITLTIQVISAPEENVTLIMRKRQXINSQSLP 190	
Db		149	PLGIPLPDLSITITLTFYNNNS--NAAALWLTQSTSAARXKTEIEQVIGEVDR--TFEP 204	
Qy		191	DXYMLELSTSMQSGSTVQ--HSTGVGVNNEKRLAIXGNFTLVANXK--VIASLALM 246	
Db		205	SLATLSEMSNLSKQIQIASTNOCPEFVYVILNNQKQVITLVADGQVTSNMLL 266	
RESULT 11				
RIP2 WOMA				
ID	RIP2 WOMA	STANDARD;	FRT;	286 AA.
AC	P29339;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ribosome-inactivating protein mormecin II precursor (rRNA			
DE	N-glycosidase) (EC 3.2.2.22).			
OS	Monotropa balsamina (Belted gourd) (Balsam pear).			
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			

Best Local Similarity 36.6%; Fred. No. 1.6e-29;  
Matches 89; Conservative 37; Mismatches 99; Indels 18; Gaps 9;

QY 13 TGEKFRFTLTADYSSGS--FSENEPLAQSTTFVSDMORFVLELNQCKXKTAID 71  
Db 32 TGEATFTYINLNTYVIGTFRVYDIEVLNNAAGLA--RFQVILINNGESYVALD 88  
QY 72 VTNXVYVAYAGDQSGYFLADAPRGAETHLPTFTEDSLSPKSGYXDLARVAGH--RDQ 129  
Db 89 VNNVYVAYAPAGNTAYFLADASTFANNVLAQINHTV--LPVGSYDGLSTPAGRISREN 146  
QY 130 ILGLXQDIQSYVAL--KXPQGSTQKASLILILQWISSEARPNFIMEXQKXNSGS 187  
Db 147 IELGPEELISAGNNFHNHFGTSV--PRAFTVILQTVSEAPRKIKQVSE--NVGTX 201  
QY 188 FLDPXVLELETSNGQSTQVQ--HSTQGVNNEKXALXGNFTLXNRX-VIASLAI 244  
Db 202 KRPDPAPLSLQNNMOSLSQDILQKTRQGRAPFELFTVSTPTVIVNAPVAKQIAL 261  
QY 245 MWP 247  
Db 262 LLY 264

RESULT 9  
RPT TRIKI STANDARD; PRT; 289 AA.

AC 609383; 1998 (Rel. 10, Created)  
DT 01-NOV-1998 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ribosome-inactivating protein alpha-trichosanthin precursor  
DE (tRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).  
OS Trichosanthes kirilowii (Mongolian snake-gourd).  
OC Bukariyoc; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosoids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
NCBI TaxID=3677;  
RX 111  
RP SEQUENCE FROM N.A.  
RC STRAIN=Maximowicz; PubMed=1993291.  
RA Shaw P.C., Yung W.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;  
RT "Cloning of trichosanthin cDNA and its expression in *Escherichia*  
RT coli.";  
RT Gene 97:267-272 (1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Maximowicz; TISSUE=Leaf;  
RA MEDLIN=9025790; PubMed=2341400;  
RX Chow T., Pelaman R.A., Lovett M., Patak M.;  
RT Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a  
RT trichosanthin homolog from *Trichosanthes kirilowii*.  
RL J. Biol. Chem. 265:8670-8674 (1990).  
RN [3]  
RP SEQUENCE OF 24-270.  
RC STRAIN=Maximowicz; TISSUE=Tuberous root;  
RA MEDLIN=9025789; PubMed=2341399;  
RX Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,  
RA Wu P., Hwang K., Patak M.;  
RT "Primary amino acid sequence of alpha-trichosanthin and molecular  
RT models for abrin A-chain and alpha-trichosanthin.";  
RL J. Biol. Chem. 265:8665-8669 (1990).  
RN [4]  
RP SEQUENCE OF 24-270.  
RC TISSUE=Tuberous root;  
RA Wang Y., Qian R.O., Gu Z.W., Jin S.W., Zhang L.O., Xia Z.X.,  
RA Tian G.Y., Ni C.Z.;  
RT "Scientific evaluation of Tian Hua Fan (THF): history, chemistry and  
RT application.";  
RL Pure Appl. Chem. 58:789-798 (1996).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).

EX MEDLINE=94344957; PubMed=8066085;  
RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;  
RT "Structure of trichosanthin at 1.88-A resolution.";  
RL Proteins 19:14-15 (1994).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
RA Huang O., Liu S., Tang Y., Jin S., Wang Y.;  
RT "Studies on crystal structures, active-centre geometry and  
RT dequating mechanism of two ribosome-inactivating proteins.";  
RL Biochem. J. 309:285-298 (1995).  
CC 1- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS  
CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT  
CC INACTIVATES ENZYMOLOGIC 60S RIBOSOMAL SUBUNTS.  
CC 1- CATALYTIC ACTIVITY: Enzymolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC 1- SPECIFICITY: SPECIFIC TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC 1- THE N-TERMINUS OF THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
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CC -----  
DR EMBL: M4638; M463207.1; -  
DR PIR: J00562; M463206.1; -  
DR PDB: 1MRK; 07-FEB-95.  
DR PDB: 1TCS; 10-JUL-95.  
DR PDB: 1J4G; 28-JAN-03.  
DR PDB: 1NLI; 21-JAN-03.  
DR PDB: 1QD2; 24-APR-00.  
DR InterPro: IPR001574; R/P.  
DR Pfam: PF00161; R/P. 1.  
DR PRINTS: PR00396; SMOGACTIN.  
DR PROSITE: PS00273; SMOGACTIN; 1.  
DR Plant Database: Trichosanthin; Protein synthesis inhibitor; Hydrolase;  
KW SIGNL. Signal. 3D structure.  
FT CHAIN 24 270  
FT PROPEP 271 289  
FT ACT SITE 183 183  
FT BY SIMILARITY 183 183  
FT I P L -> L (IN REF. 4).  
FT MISSING (IN REF. 4).  
FT CONFLICT 87 87  
FT CONFLICT 82 84  
FT CONFLICT 132 92  
FT CONFLICT 142 144  
FT CONFLICT 149 150  
FT CONFLICT 215 216  
FT CONFLICT 231 231  
FT CONFLICT 234 234  
FT CONFLICT 246 266  
FT CONFLICT 247 247  
FT STRAND 25 28  
FT TURN 30 31  
FT HELIX 34 46  
FT TURN 47 47  
FT STRAND 50 54  
FT TURN 55 56  
FT STRAND 57 66  
FT HELIX 66 69  
FT STRAND 70 79  
FT STRAND 78 79  
FT STRAND 82 88  
FT STRAND 89 92  
FT STRAND 93 99  
FT TURN 100 101  
FT STRAND 102 105

MISSING IN MATURE PROTEIN.  
BY SIMILARITY.  
I P L -> L (IN REF. 4).  
MISSING (IN REF. 4).  
Y -> V (IN REF. 4).  
V -> V (IN REF. 4).  
K -> S (IN REF. 4).  
MS -> S (IN REF. 4).  
O -> T (IN REF. 2).  
S -> T (IN REF. 2).  
MISSING (IN REF. 4).  
T -> M (IN REF. 2).







EX MEDLINE-96374222; PubMed-8780513;  
RA Day P.J., Ernest S.R., Prankel A.E., Monzinger A.F., Pascal J.M.,  
RA Moirina-Svintch M.C., Robertus J.D.;  
RT "Structure and activity of an active site substitution of ricin A  
RT chain";  
RL Biochemistry 35:11098-11103(1996).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
RX MEDLINE-97240820; PubMed-9068280;  
RA Fan X., Hollis T., Svintch M., Day P., Monzinger A.F., Milne G.W.,  
RA Robertus J.D.;  
RT "Structure-based identification of a ricin inhibitor";  
RL J Mol Biol 266:1043-1049(1997).  
RN [14]  
RP MCTGENESIS.  
RX MEDLINE-93165632; PubMed-1287657;  
RA Kin Y., Robertus J.D.;  
RT "Analysis of several key active site residues of ricin A chain by  
RT mutagenesis and X-ray crystallography";  
RL Protein Eng 5:775-779(1992).  
CC -1- FUNCTION: Ricin is a glycoprotein toxin to animal cells and to a less  
CC extent to plants. It is a dimeric protein consisting of two subunits,  
CC A and B. The A chain is responsible for inhibiting  
CC protein synthesis through the catalytic inactivation of 60S  
CC ribosomal subunits. It acts as a glycosidase that removes a  
CC specific adenine residue from an exposed loop of 28S ribosomal  
CC RNA. As this loop is involved in the binding of elongation  
CC factors, the modified ribosomes are unable to support protein  
CC synthesis. The A chain can inactivate a few thousand ribosomes  
CC per minute, thus inactivating them faster than the cell can make  
CC new ones. A single A-chain molecule can therefore kill an animal  
CC cell. The B chain binds to cell receptors and facilitates the  
CC entry into the cell of the A chain; B chains are also responsible  
CC for cell agglutination (lectin activity). It binds to beta D  
CC galactose residues on the cell surface.  
CC CATALYTIC ACTIVITY: Endoglycosidase of the N-glycosidic bond at one  
CC adenine residue in 28S rRNA.  
CC -1- Specific adenosine on the 28S rRNA.  
CC -1- SUBUNIT: Disulfide-linked dimer of A and B chains.  
CC -1- DOMAIN: The B chain is composed of two domains, each domain  
CC consists of 3 homologous subdomains (alpha, beta, gamma).  
CC -1- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 271.  
CC MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.  
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIF SUPERFAMILY.  
CC -1- SIMILARITY: CONTAINS 2 EGGNOUGH2 RIF SUPERFAMILY.  
CC -1- SIMILARITY: CONTAINS 2 EGGNOUGH2 RIF SUPERFAMILY.  
CC WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).  
CC -1- DATABASE: NMR-PROTEIN Spoilicht;  
CC NOTE-1: Issue 31 of February 2003;  
CC WWW="http://www.expasy.org/spotlight/articles/spf1031.html".  
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CC  
CC EMBL: Y01179; CAA26939.1; -  
CC EMBL: X52908; CAA37095.1; -  
CC EMBL: X02388; CAA26230.1; -  
CC EMBL: A12892; CAA01058.1; -  
CC PIR: A24041; RLCSD.  
CC  
CC PDB: 2A4I; 31-JAN-94.  
CC PDB: 1APG; 31-JAN-94.  
CC PDB: 1PMF; 31-OCT-93.  
CC PDB: 1IFS; 14-JAN-98.  
CC PDB: 1IF7; 14-JAN-98.  
CC PDB: 1IF6; 14-JAN-98.  
CC PDB: 1IFC; 31-OCT-93.  
CC PDB: 1OBT; 16-JUN-97.  
CC PDB: 1OBT; 16-JUN-97.  
CC PDB: 1BRS; 02-SEP-98.

DR PDB; 1BR6; 02-SEP-98.  
DR PDB; 1IL3; 16-JAN-02.  
DR PDB; 1IL4; 16-JAN-02.  
DR PDB; 1IL9; 16-JAN-02.  
DR Glycosylated; P02879; Ricin\_B\_lectin.  
DR Interfero; P02052; Ricin\_A\_lectin.  
DR Interfero; P02052; Ricin\_A\_lectin.  
DR P1am; P02051; R1P\_1\_lectin; 6.  
DR PRINTS; P000396; SHIGARICIN.  
DR SMART; SMO0458; SHIGARICIN.  
DR PROSITE; P500231; RICIN\_B\_LECTIN; 2.  
DR PROSITE; P500275; SHIGA\_RICIN; 1.  
KV Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
KV Glycoprotein; Lectin; Signal; 3D-structure.  
FT SIGNAL 1 35  
FT CHAIN 1 35  
FT LINKER PEPTIDE 306 342  
FT CHAIN 2 315 576  
FT DOMAIN 321 448  
FT DOMAIN 451 575  
FT REPEAT 331 373  
FT REPEAT 374 414  
FT REPEAT 417 449  
FT REPEAT 462 497  
FT REPEAT 501 540  
FT REPEAT 543 570  
FT ACT SITE 212 316  
FT DISULFID 334 353  
FT DISULFID 377 394  
FT DISULFID 465 478  
FT DISULFID 504 521  
FT CARBOHYD 45 45  
FT CARBOHYD 271 271  
FT CARBOHYD 409 409  
FT CARBOHYD 449 449  
FT CONFLICT 546 547  
FT STRAND 43 47  
FT TURN 49 50  
Query Match 30.7%; Score 376; DE 1; Length 576;  
Best Local Similarity 39.1%; Pred. No. 1, 1e-33; Indels 12; Gaps 8;  
Matches 100; Conservative 43; Mismatches 101;  
DB 9 THQGTAKYRFRPILLDVYSSGS-FNSRFL-RGTPPSDAGCPVULKNGGKDX 66  
DB 48 TKGVQSTNFRVAKGRKLGNDVRLHIVPKVGLPIN--QFVLHLSNMAELAV 105  
DB 67 TALLDPTKYVAVYQADQSYLR-CARGAK--THFTGTRRDSAPFVGSYDLEK 123  
DB 106 TLADLTAVVYGVYAGNSAYFPFNDQDEAYTHFT-DVQRVYTFVFGNYRLEDL 164  
DB 124 AGH-FQGPFGIYVLIOSYVAL--EYFGSTXQASJILLICWISNAPFPLMKRX 179  
DB 165 AGNINRNLKIDNGLPEVLSALVYITGSLDPLTASFLICIMISNAPFVIGSRK 224  
DB 180 QXINSXSLFEDYVWMLBFTSGGQSTOVHSTGVNRPXSLAKXNPFVLYXVRY 239  
DB 225 TIKRNSAPDPSVTLNLSGSLALNQSQAPASPIQLQRNNSKTSYVDVSLI 284  
DB 240 ASLAVTFPCRPS 255  
DB 285 PIALAVYKCAPPS 300  
RESULT 6  
AGGL\_RICCO STANDARD, FRT, 564 AA.  
ID AGGL\_RICCO  
AC P06750;



CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.  
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL: X55667; CA39202.1; -.  
 CC  
 CC PIR: S16022; S16022.  
 CC  
 CC HSRP: P1140; 1ABR.  
 CC  
 CC InterPro: IPR000772; Ricin\_B\_lectin.  
 CC  
 CC Pfam: PF00682; Ricin\_B\_lectin; 6.  
 CC  
 CC PRINTS: PR00396; SHIGARICIN.  
 CC  
 CC SMART: SM00458; RICIN. 2.  
 CC  
 CC PROSITE: PS00275; SHIGA\_RICIN; 1.  
 CC  
 CC PROSITE: PS00275; SHIGA\_RICIN; 2.  
 CC  
 CC DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 CC Glycoprotein; Lectin; Signal; Pyroglutamate carboxylic acid.  
 CC  
 CC KW SIGNAL 1 34  
 CC FT CHAIN 1 35 285  
 CC FT PEPTIDE 286 295  
 CC FT CHAIN 296 562  
 CC FT PEPTIDE 563 572  
 CC FT DOMAIN 437 544  
 CC FT REPEAT 317 359  
 CC FT REPEAT 360 400  
 CC FT REPEAT 403 435  
 CC FT REPEAT 448 483  
 CC FT REPEAT 487 526  
 CC FT REPEAT 529 562  
 CC FT ACT\_SITE 198 198  
 CC FT DISULFID 281 303  
 CC FT DISULFID 320 339  
 CC FT DISULFID 343 360  
 CC FT DISULFID 453 460  
 CC FT DISULFID 490 507  
 CC FT MOD\_RES 35 35  
 CC  
 CC FT CARBOHYD 234 234  
 CC FT CARBOHYD 395 395  
 CC FT CARBOHYD 435 435  
 CC  
 CC SQ SEQUENCE 562 AA; 62817 MW; 1FD0BC707BA678 CEC64;  
 CC  
 CC Query Match 34.8%; Score 126; DB 1; Length 562;  
 CC Best Local Similarity 42.4%; P-Val 3.2e-39; Indels 6; Gaps 5;  
 CC Matches 105; Conservative 36; Mismatches 98;  
 CC  
 CC 9 THQTGKGFYFPTILLRDYVSGSGSNEFLPLOSITVSDQRFVATLNOGQDXTA 68  
 CC 43 TEATSSQYKOFIFLRLQRL-TGLIHDIPLVLPDPT-TVEENRRIYVLENSERSSEIV 100  
 CC  
 CC 69 AIDVNNKYVAVNQKQDQSYFLADPARGATLFTGTIDSSLPFGXSYXDLERVAGH-8 127  
 CC 101 GIDVNNKYVAVNQKQDQSYFLADPARGATLFTGTIDSSLPFGXSYXDLERVAGH-8 158  
 CC 128 DQIPGICXOLQSYVXALXKSGSTKXASLILQMSLSPAPPLIRKXKXINSK3 187  
 CC 159 ERLSLGQLTHAIFSLSGANSDEKATLIVIQMSLSPAPPLIRKXKXINSK3 218  
 CC  
 CC 188 FLIDKYVLELETSWCOOSTQVQSTDEVNPNKRLXIXXNPVLTANV-RATVLSIAIM 246  
 CC 219 FQEDPAATSLIENWMDLISGVQVQSTDEVNPNKRLXIXXNPVLTANV-RATVLSIAIM 278  
 CC  
 CC 247 FVC 249

Db 279 FVC 281  
 |||  
 RESULT 4  
 ABRS ABRS STANDARD; PRT: 527 AA.  
 DT 06-077; E81374; (Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 18-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Abirin-B precursor [Contains: Abirin-B chain (rRNA N-glycosidase)  
 DE (EC 3.2.2.22); Abirin-B chain]  
 OS Abrus precatorius (Indian locoweeds) (Crab's eye)  
 CC Eukaryote; Vitellinase; Streptophyta; Tracheophyta;  
 CC Spermatophytes; Angiosperms; Rosales; Rosidae;  
 CC Myrtilales; Fabiales; Fabaceae; Papilionoideae; Abrease; Abrus  
 CC [1]\_taxid=3816;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9112798; PubMed=842313;  
 RA Hung C.-H., Lee M.-C., Lee T.-C., Lin Y.-Y.;  
 RT "Primary structure of three distinct isabrinins determined by cDNA  
 RT sequencing. Conservation and significance.";  
 RL J. Mol. Biol. 229:263-267 (1993).  
 RN [2]  
 RP SEQUENCE OF 260-527.  
 RX MEDLINE=93169023; PubMed=7763422;  
 RA Kimura M., Sumitama T., Funatsu G.;  
 RT "Type complete amino acid sequences of the B-chains of abirin-B and  
 RT abirin-B, toxic proteins from the seeds of Abrus precatorius.";  
 RL Biochem. Biotechnol. Biochem. 57:166-169 (1993).  
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN  
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL  
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.  
 CC ABRIN-A IS MORE TOXIC THAN RICIN.  
 CC FUNCTION: THE B CHAIN IS A BRADYCYCLIN-SPECIFIC LECTIN THAT  
 CC BINDS TO THE SURFACE OF ABRIN TO THE CELL MEMBRANE THAT  
 CC INHIBITS BRADYCYCLIN.  
 CC -1- FUNCTION: THE B CHAIN IS A BRADYCYCLIN-SPECIFIC LECTIN THAT  
 CC BINDS TO THE SURFACE OF ABRIN TO THE CELL MEMBRANE THAT  
 CC INHIBITS BRADYCYCLIN.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.  
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.  
 CC  
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 CC  
 CC EMBL: M98345; AAA3625.1; -.  
 CC  
 CC PIR: S32430; S32430.  
 CC  
 CC HSRP: P1140; 1ABR.  
 CC  
 CC InterPro: IPR000772; Ricin\_B\_lectin.  
 CC  
 CC Pfam: PF00682; Ricin\_B\_lectin; 6.  
 CC  
 CC PRINTS: PR00396; SHIGARICIN.  
 CC  
 CC SMART: SM00458; RICIN. 2.  
 CC  
 CC PROSITE: PS00275; SHIGA\_RICIN; 1.  
 CC  
 CC PROSITE: PS00275; SHIGA\_RICIN; 2.  
 CC  
 CC DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 CC Glycoprotein; Lectin; Pyroglutamate carboxylic acid.  
 CC  
 CC KW CHAIN 1 250  
 CC FT PEPTIDE 251 260  
 CC FT CHAIN 261 527  
 CC  
 CC FT CHAIN 261 527  
 CC ABRIN-B CHAIN.

FT TURN 10 11  
 FT STRAND 14 28  
 FT STRAND 34 32  
 FT TURN 34 32  
 FT STRAND 36 38  
 FT TURN 42 43  
 FT HELIX 47 49  
 FT STRAND 51 57  
 FT TURN 63 69  
 FT STRAND 70 72  
 FT TURN 75 79  
 FT STRAND 83 86  
 FT TURN 88 93  
 FT STRAND 94 97  
 FT HELIX 100 101  
 FT TURN 103 106  
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 FT TURN 115 119  
 FT STRAND 124 126  
 FT STRAND 129 129  
 FT HELIX 131 142  
 FT TURN 143 144  
 FT HELIX 148 167  
 FT STRAND 168 168  
 FT TURN 169 180  
 FT STRAND 182 182  
 FT TURN 185 196  
 FT HELIX 197 197  
 FT TURN 198 207  
 FT STRAND 212 220  
 FT TURN 222 223  
 FT STRAND 226 231  
 FT TURN 232 233  
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 FT STRAND 248 258  
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 FT STRAND 282 284  
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 FT TURN 296 297  
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 FT HELIX 311 313  
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 FT STRAND 393 395  
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 FT STRAND 410 411  
 FT STRAND 413 415  
 FT HELIX 417 421  
 FT STRAND 422 423

FT STRAND 424 428  
 FT TURN 432 433  
 FT HELIX 435 437  
 FT STRAND 439 441  
 FT TURN 443 444  
 FT STRAND 446 446  
 FT TURN 450 453  
 FT STRAND 452 455  
 FT TURN 464 465  
 FT STRAND 467 472  
 FT TURN 474 475  
 FT STRAND 478 480  
 FT HELIX 483 484  
 FT STRAND 486 487  
 FT TURN 490 492  
 FT STRAND 493 496  
 FT TURN 497 501

Query Match 38.2% Score 467; DB 1; Length 528;  
 Best Local Similarity 42.3%; Pred. No. 8, 4e-44;  
 Matches 107; Conservative 34; Mismatches 66; Indels 26; Gaps 6;

QY 9 THQTTXKXEPPTLLRDVYSSGSFNEIPILKQSTIPVSDAQPVLVEITNGQXSYTA 68  
 DB 9 TEGATSSQYKQFTALREBRL-RGQLHDIPIVLPDPT-TLOERNYITVELNSDTSIEV 66  
 QY 69 AIDVTXVYVAYQADQSYFLDAPGAEHTLFTTTSDBSLSPFGSYXDLERYAGH-R 127  
 DB 67 GIDVTAVYVAYPACQSYFLDAPSSASDYLFTGR--DQSLPFGYGLERMAHQSR 124  
 QY 126 DQILGTXQLQSYVAKAKXGQSTQKQASILLIOMTSPAPRNPILMYRQXINSQXS 187  
 DB 125 QQILGTXQLHNGISFPFGSGNDREKATLYIIVQVAAAFRYSNRYVSGTGTVA 184  
 QY 188 FLDPXVMELETSQCSQSTQVGHSTGVNPNPRLAIXGNFVLANVX----- 237  
 DB 185 FQPPAMTSLLENMMDLSRGVSVQDTFPPQ-----VLTININPVIYDLSH 234  
 QY 238 -VILASLAINLFC 249  
 DB 235 FTVAVLALMLPVC 247

RESULT 3  
 ID ABC ABCR STANDARD; PRT; 562 AA.  
 AC P28550;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Abirin-c precursor (contains: Abirin-c A chain (rRNA N-glycosidase)  
 DE Abirin-c 3.2.2.22; Abirin-c B chain;  
 DE Abirin-c precursor (human stromal) (Crabtree eye)  
 CC Eukaryotes; Viridales; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicotyledons;  
 CC Eucosids I; Fabales; Fabaceae; Papilionoideae; Abrus; Abrus.  
 CC NCBI Taxid:3816;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=9126957; PubMed=2050149;  
 RA Wood K.A., Lord J.M., Wawrzyniak E.J., Patack M.,  
 RT "Preproabirin: genomic cloning, characterization and the expression of  
 the A-chain in *Bescheria coli*.";  
 RI 1992; 13:1221-1229;  
 CC Eukaryotes; Viridales; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicotyledons;  
 CC Eucosids I; Fabales; Fabaceae; Papilionoideae; Abrus; Abrus.  
 CC NCBI Taxid:3816;  
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,124 OF 28 S RNA. THE  
 B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE  
 BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.  
 CC CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
 specific adenosine on the 28S RNA.  
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.



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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 4.3929 Seconds  
(without alignments)  
2736,539 Million cell updates/sec

Title: US-09-601-667C-41

Perfect score: 1223.1761RLRVTHTGTGKVFRR.....XVTLASLAIMLPVCGERPSS 256

Sequence: 176RLRVTHTGTGKVFRR.....XVTLASLAIMLPVCGERPSS 256

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Displaying first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1165	95.3	254	1	MIA VISAL
2	467	38.2	528	1	ABR4 ABRR
3	426	34.8	562	1	ABR4 ABRR
4	404.5	33.1	527	1	ABR4 ABRR
5	376	30.7	576	1	RICI RICCO
6	370.5	30.3	564	1	AGGL RICCO
7	339	27.7	563	1	NIGB SAMI
8	326	26.7	282	1	RIP2 BRDI
9	307	24.6	289	1	RIP2 BRDI
10	289	24.3	282	1	RIP2 BRDI
11	289	24.3	282	1	RIP2 BRDI
12	278.5	22.8	290	1	RIP1 BRDI
13	276.5	22.6	294	1	RIP1 TRIAN
14	273.5	22.4	316	1	RIP2 GBLU
15	267.5	21.9	286	1	RIP1 CUCFI
16	253.5	20.7	277	1	RIP1 MOMCH
17	244.5	20.0	286	1	RIP1 LUFEC
18	239.5	19.6	250	1	RIPB LUFEC
19	233.5	19.1	278	1	RIPB MIRN
20	191.5	15.7	261	1	RIP1 MIRN
21	184	15.3	323	1	RIP1 MIRN
22	184	15.3	323	1	RIP1 MIRN
23	168	13.7	253	1	RIP7 SAPOR
24	166	13.6	253	1	RIP7 SAPOR
25	162	13.2	299	1	RIP6 SAPOR
26	157	12.8	292	1	RIP2 SAPOR
27	138.5	11.3	310	1	RIP2 PHYLA
28	131	10.7	293	1	RIP0 DIACH
29	127	10.4	236	1	RIP3 SAPOR
30	126	9.8	280	1	RIP1 HORVO
31	111.5	9.1	315	1	SLVA BRDI
32	111.5	9.1	315	1	SLVA BRDI
33	110	9.0	280	1	RIP2 HORVO

#### ALIGNMENTS

##### RESULT 1

ID MIA VISAL STANDARD; PRT: 254 AA.

AC P81446; 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE Beta-galactoside specific lectin I A chain (MIA) (ML-1 A) (RNA N-

glycosidase) (EC 3.2.2.22) (Unreviewed)

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

CC Santalales; Santalaceae; Viscum.

CX NCBI\_TaxID=972;

NP [1]

RP SEQUENCE.

RC MEDLINE=9714581; PubMed=8980141;

RA Soier W.H., Stoeva S., Schwaborn C., Wilhelm S., Striebel T.,

RE Voelter W.;

RT PDB=1A99; 15-DEC-1998

CC Complete amino acid sequence of the A chain of mistletoe lectin I.;

CC FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN

CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL

CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE

CC INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR

CC CELL AGGLUTINATION (LECTIN ACTIVITY)

CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SUBUNIT Disulfide-linked dimer of A and B chains.

CC -1- FRANKLINICIN: Due to its immunomodulatory effects it is being

CC used in the treatment of cancer cells and be an effective treatment for solid

CC tumors.

CC -1- MISCELLANEOUS: TWO ISOMERS OF MIA EXIST: GLYCOSYLATED FORM MIA

CC AND NON-GLYCOSYLATED FORM MIA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC PIR: P00018; PD0018.

DR HSP; P1140; IABR.

DR Interfero; IPRO01574; RIP.

DR Plant defensin; Hydrolyase; Toxin; Repeat; Glycoprotein; Lectin.

DR Plant defensin; Hydrolyase; Toxin; Repeat; Glycoprotein; Lectin.

FT ACT SITE 165 165

FT ACT SITE 165 165

FT CARBOHYD 112 112

FT CARBOHYD 112 112

FT VARIANT 15 15

FT VARIANT 15 15

FT VARIANT 66 66

FT VARIANT 66 66

FT VARIANT 112 112

FT VARIANT 112 112

FT VARIANT 116 116

FT VARIANT 116 116

FT VARIANT 133 133

FT VARIANT 133 133

FT VARIANT 140 140

FT VARIANT 140 140

FT VARIANT 144 144

FT VARIANT 144 144

FT VARIANT 151 151

FT VARIANT 151 151

Thu Dec 11 16:09:59 2003

us-09-601-667c-41.rpt

Page 8

Db 144 ENIDIGLPLSSAITTLFFYMAQAPSA--LIVLIQTREARFPKIEHVAKYV--ATN 199  
QY 188 FLBDXYMLBLETWGOOSTOY--OHSIDYFNNPKXLAIXXGNFTLXNV 235  
Db 200 KPNLAIISLENQMSALSQIFLAONQCKFPNFPVDIKPTGERFOYTVV 249

Search completed: December 11, 2003, 13:55:48  
Job time : 8.95754 secs



Thu Dec 11 16:09:59 2003

us-09-601-667c-41.rpt

Page 7

QY 131 EGIKQIQLISVVALRPGSGSTRKQARSILLILQITSPAKRNPITMRKQKXINSGLFP 190  
Db 126 PLEIPLADSDSLITITFTNNNS--ASALMVLQSTSSAKRFEEOIGGRVDX--FEIP 181  
QY 151 DAYVLEETISWGQSTQV--HSTGVFNNPKRLAIKXGNFTLVNXX--VTASLAWL 246  
Db 152 STATISSEMSMALSKQIDISTNNNGQFEFFVVLNACHQSVITVMDAGVTSNILL 241

FIGURE 13  
TC5606  
Karasuvin C - *Trichosanthes kirilowii* var. *japonica*  
N;comains: karasuvin A  
C;Species: *Trichosanthes kirilowii* var. *japonica*  
C;date: 23-Sep-1997 #sequence \_revision 23-Sep-1997  
C;accession: TC5606; TC5033  
R;Mutizami, H.; Iida, K.; Kondo, T.; Ogihara, Y.

A: Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protein  
 A: Reference number: JCS606; MUID:97356562; PMID:9212998

A1Accession: J5606  
A1Molecule type: DNA  
A1Residues: 1-289 <M1Z>  
A1Cross-references: DBJ01A00066; MID:24329630; PIDN:BA2176.; | PII:9232831  
R1Condo, T., Makiuchi, H., Takeeda, T., Gishara, Y.  
R1Citat. Pharm. Bull. 19, 1485-1489, 1966  
A1Title: Amino acid sequences and ribosome-inactivating activities of karasaurin-B and karasaurin-A  
A1Reference number: JCS052; MID:97108848; MID:9531169

A:RECOMBINATION:UC5013  
A:FUNCTION:RNA N-glycosylase  
A:Molecule type: protein  
A:Residues: 22-270 <ON>  
C:Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abortifacient, and antitumor activities.  
F:32-270/Product: RNA N-glycosylase homology  
F:32-270/Product: karasulin A Sterans predicted <MA>  
F:27-266/Domains: rRNA N-glycosidase homology <RN>

Query Match:	24.5%;	Score 300;	DB 2;	Length 289;
Best Local Similarity	35.4%;	Pred. No. 5.3e-25;		
Matches	85;	Conservative	46;	Mismatches 95;
			Indels	14;
			Gaps	9

QY	1	TKCEPEFTLLNAYVSSGSPNEIPLROSTIVSNAPCVLYEIMCKOXSATIDV	72
QY	33	TSSTGYAFISINRFLAPEERLEIDPEFLR-STLEGS--GRALAIHNVYADETISVAIDV	89
QY	73	TKXVYVACGDSYELTDA-PYGAETHLPTFTRRSLSLEPFSGXLYERFAGH-RDOI	130
QY	90	INWYVDSYRAGSYTFSEFNASTARSKALIKYAKOAR-KTLYSGVMEKQIADAKREI	148
QY	131	ELGICGLQSYPAKSTFGSEKROKRAKILLQMISEIAPNRYLREKQINSQSGSFI	204
QY	149	PLGELDALDAITFLTFYVANS--ASALIMVLLSTSEBNAKFEISQIGRQYDK-TLIP	204
QY	191	EKMHELEMSWQSTQVQ-HSTGVFNPPKALIXKSNVTLKXNR--VLSIAIHL	246
QY	205	SLAIISEMSALSQCIQIASNNGOFEETPVLINAGKQVITINVDAGVTSNIIALL	264

RESULT 14  
 JC4840  
 rRNA N-glycosidase (EC 3.2.2.22) trichoangulina - snake gourd  
 C.Species: Trichoanthus angulina (snake gourd)  
 C.Date: 15-Aug-1996 #sequence\_revision 24-Oct-1997 #text\_change 05-Dec-1997  
 C.ID: JC4840; J07070; J06677  
 C.Xref: X08201, X08202, X08203, X08204, X08205, X08206, X08207, X08208, X08209, X08210, X08211, Wang, S.H.; Teno, Y.; Tsugita, A.  
 Aloned. Sci. 3: 178-186, 1996  
 A.Title: Amino acid sequence of trichoangulina, a ribosomal-inactivating protein from  
 A.Reference number: JC4840  
 A.Accession: JC4840  
 A.Molecule type: protein  
 A.Residues: 1-132, '8', '134-245 <CHOI>

A:Experimental source: seed  
A:Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Tabl.  
R/Klone, L.P.; Kamo, M.; Lin, C.Y.; Ueno, Y.; Tsugita, A.  
A:Submitted to JPIID, August 1995  
A:Description: Amino acid sequence of trichangutina, a ribosomal-inactivating protein fr  
A:Reference number: JT0677  
A:Accession: JT0701

A:Residues: 1-50, 'V', #5-245 <CHO2>  
 A:Superfamily: rRNA\_N-glycosylase, rRNA\_N-glycosylase  
 Keywords: glycoprotein, glycosidase, hydrolase, phosphoprotein, seed  
 E:4-2/2:Domain: rRNA\_N-glycosidase homology <RNG>  
 F:51,201:Binding site: carbohydrate (asn) (covalent), #status experimenta  
 F:70,156:Active site: 'Yr, Glu, Arg #status predicted  
 F:135:Binding site: phosphate (Ser) (covalent) by casein kinase II, #st  
 F:135:Binding site: phosphate (Ser) (covalent) by casein kinase II, #st

Query Match	23.7%	Score 289.5;	DB 2;	Length 245;
Best Local Similarity	34.4%;	Pred. No. 6e-24;		
Matches	83;	Conservative 37;	Mismatches 106;	Indels 15;
			Gaps	7

[illegible]

```

RESULT 15
S25560
rRNA-N-glycosidase (BC 3.2.2.22) monomordin II - balsam apple
C:Species: Monomordica balsamina (balsam apple)
C:Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 20-Aug-1999
C:Accession: S25560
R:Orig:1990, M., Becker, M.
Nucleic Acids Res. 20, 4662, 1992
A:Title: Monomordin II, a ribosome inactivating protein from Monomordica balsamina, is homol
A:Reference number: S25560, MUID:93027170, PMID:1408771
A:Accession: S25560
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-285 <ORF>
A:Cross-references: EMBL:Z12175; NID:g19525; PIDD:CAA7816.1; PID:g19526
A:Superfamily: rRNA-N-glycosidase; rRNA-N-glycosidase homology
A:Keywords: glycosidase; hydrolase
A:7-27-264/Domain: rRNA-N-glycosidase homology <RNG>

```

Query Match	23.0%	Score 2841	DB 23	Length 286.
Best Local Similarity	33.9%	Pred. No. 6,3e-323		
Matches	789	Conservative 44	Mismatches 88	Indels 20; Gaps
Cy	13	TCXCYFFITLLADYVSSGSPFN--ETPLKOSTIPVSDAOFVVELTNSGMDXSTKA	69	
Dy	13	TAKTIVTTL--EGRFAFTPLSKTKDILPALSTL--ISDRSFFILDLTSAIEATL	86	
Cy	70	IVTNYVVVAQGVQSGSYFLPAQPGAFHFCPTQTRSGFLPFGVSGVNRVAC--S	127	
Dy	87	IVTVVVVAARRDVSYPKSPPEAKNVLFPKTR--KTLFPGYCNVETGCT--ANKR	143	
Cy	128	DDPLGIGXDLISGKXALMLNGSGTQVARSILLIIMDSNAAPFLIMXKQINSKGS	187	

Oy 13 TCKEYFFETLLRDVYSSGSFSENEPIILKOSTIPVSDAQRFVLVELTNGKSDXTAIDV 72  
 Db 10 TSSSYGVFISLNRKLPERRKLYDIPLR-STLPGS--QRYALHLNVADETTVAIDV 66  
 Oy 73 TTXVYVADQDSYFLNDA-PRGAEHLFTGTRRRESLPKXSYDLEARYGH-ROCI 130  
 Db 67 TTVYVAGYADDSYFLNDA-PRGAEHLFTGTRRRESLPKXSYDLEARYGH-ROCI 125  
 Oy 131 PGIKXLIOSYVAKRPGSGTQKRSIIHLIQISEAFRFTLWKKXCKXNGKSEFLP 190  
 Db 126 PGLPDLSDATTLTFYVNAAS--AASALMTLIQSTSEAFRFTLWKKXCKXNGKSEFLP 181  
 Oy 191 DXYMLELFTSGQSTQVQ--HSTQGVNNEKALIXGNFVLKXVYK--VIASLAIW 246  
 Db 182 SLATISLHNSWALSLSQIOLASTNGQFSEVVLINAGNORVITINAGVTSNIALLL 241

## RESULT 11

RNA N-glycosidase (BC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian snake  
 N:Alternate names: alpha-TCS; type I ribosome-inactivating protein  
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
 C:Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text change 23-Mar-2001  
 C:Accession: J0566; A36274; J01093; A36273; J00003  
 R:Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.

A:Title: Cloning of trichosanthin cDNA and its expression in *Bacterichia coli*.  
 A:Reference number: J0566; PMID:9113657; PMID:1999291  
 A:Accession: J0566

A:Molecule type: mRNA  
 A:Accession: J0566  
 A:Cross-references: GB:934858; NID:9170536; PIDN:AAA34207.1; PID:9170537  
 A:Experimental source: tuber  
 R:Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatek, M.  
 J: Biol. Chem. 265: 8670-8674, 1990  
 A:Title: Isolation and DNA sequencing of a gene encoding alpha-trichosanthin, a type I rth  
 A:Reference number: A36274; PMID:9026790; PMID:2341400  
 A:Accession: A36274  
 A:Molecule type: DNA  
 A:Residues: 1-233, 'T', 235-246, 'W', 248-289 <CH>  
 A:Cross-references: GB:905434; NID:9170534; PIDN:AAA34206.1; PID:9170535  
 R:Zhang, R.G.; Wang, B.; Shao, Z.; Yang, X.R.  
 A:Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.  
 A:Reference number: J01093; PMID:94271613; PMID:8003348  
 A:Accession: J01093  
 A:Molecule type: DNA

A:Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <CH>  
 A:Cross-references: GB:970176; NID:9547149; PIDN:AAA31048.1; PID:9547149  
 R:Collins, E.V.; Robertus, J.D.; Lipevski, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Huan  
 J: Biol. Chem. 265: 8665-8669, 1990  
 A:Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abn  
 A:Reference number: A36273; PMID:9026789; PMID:2341193  
 A:Accession: A36273  
 A:Molecule type: protein  
 A:Residues: 24-270 <CO>  
 R:Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z.  
 Pure Appl. Chem. 58: 789-798, 1986  
 A:Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application  
 A:Reference number: J00003  
 A:Accession: J00003

A:Molecule type: Protein  
 A:Residues: 24-56, 'V', 58-59, 'T', 61-71, 'T', 73-81, 85-86, 'L', 88-92, 'DAGPAAV', 93-142, 'GL'  
 A:Experimental source: tuber  
 R:Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.  
 submitted to the Brookhaven Protein Data Bank, July 1994  
 A:Reference number: A67091; PDB:1MRJ  
 A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-  
 R:Hung, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, July 1994  
 A:Reference number: A67092; PDB:1MRK  
 A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24-

R:Hung, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, December 1994  
 A:Reference number: A6711; PDB:1MRK  
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-2:  
 R:Hung, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, December 1994  
 A:Reference number: A6712; PDB:1MRK  
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-2:  
 R:Hung, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, December 1994  
 A:Reference number: A6713; PDB:1MRK  
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-2:  
 R:Hung, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, December 1994  
 A:Reference number: A6714; PDB:1MRK  
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-2:  
 R:Hung, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, December 1994  
 A:Reference number: A6715; PDB:1MRK  
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-2:

Oy 13 TCKEYFFETLLRDVYSSGSFSENEPIILKOSTIPVSDAQRFVLVELTNGKSDXTAIDV 72  
 Db 3 TSSSYGVFISLNRKLPERRKLYDIPLR-STLPGS--QRYALHLNVADETTVAIDV 69  
 Oy 73 TTXVYVADQDSYFLNDA-PRGAEHLFTGTRRRESLPKXSYDLEARYGH-ROCI 130  
 Db 67 TTVYVAGYADDSYFLNDA-PRGAEHLFTGTRRRESLPKXSYDLEARYGH-ROCI 125  
 Oy 131 PGIKXLIOSYVAKRPGSGTQKRSIIHLIQISEAFRFTLWKKXCKXNGKSEFLP 190  
 Db 126 PGLPDLSDATTLTFYVNAAS--AASALMTLIQSTSEAFRFTLWKKXCKXNGKSEFLP 181  
 Oy 191 DXYMLELFTSGQSTQVQ--HSTQGVNNEKALIXGNFVLKXVYK--VIASLAIW 246  
 Db 182 SLATISLHNSWALSLSQIOLASTNGQFSEVVLINAGNORVITINAGVTSNIALLL 241

## RESULT 12

karasurin - Mongolian snake-gourd  
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
 C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 12-Apr-1995  
 C:Accession: J00393; P00163

R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.  
 Chem. Pharm. Bull. 39: 1244-1249, 1991  
 A:Title: The complete amino acid sequence of an abortifacient protein, karasurin.  
 A:Reference number: J00393; PMID:9005921; PMID:1914000  
 A:Accession: J00393  
 A:Molecule type: protein  
 A:Residues: 1-247 <TO>  
 A:Note: a sequence which lacks Ala-247 is also shown in this publication  
 C:Superfamily: RNA N-glycosidase  
 C:Keywords: abortifacient  
 F/4-243/Domain: RNA N-glycosidase homology <RNG>

Query Match 24.5%; Score 300; DB 2; Length 247;  
 Best Local Similarity 35.4%; Pred. No. 4.3e-25;  
 Matches 89; Conservative 46; Mismatches 95; Indels 14; Gaps 9;  
 Oy 13 TCKEYFFETLLRDVYSSGSFSENEPIILKOSTIPVSDAQRFVLVELTNGKSDXTAIDV 72  
 Db 10 TSSSYGVFISLNRKLPERRKLYDIPLR-STLPGS--QRYALHLNVADETTVAIDV 66  
 Oy 73 TTXVYVADQDSYFLNDA-PRGAEHLFTGTRRRESLPKXSYDLEARYGH-ROCI 130  
 Db 67 TTVYVAGYADDSYFLNDA-PRGAEHLFTGTRRRESLPKXSYDLEARYGH-ROCI 125

Db 106 TLALDVYNAVYVGRASNSAFPHFDNQEDAEATHTLFT-DVQNRVTFAGFGNDRLBQL 164  
Qy 124 AGH-ADQIPYGLXOLQSYKYL---RPGSTRQKQARSITLILQIMISBAAREPILMBXR 179  
Db 165 AGHLENTBELNGPLSEHLSALYYSTGCTGPTLAKSFWCIQIMISBAAREPILMBXR 224  
Qy 180 QXINSGKSPDPXYMLEFTSMQOQSTOVQSHSTGTPNNPRLAIXGNFTLXNRYX 239  
Db 225 TRIRNRSAPDPSVITLSENGRSLSTALOESNGAPASPTOLOSRNRSFQVYDVSILI 284  
Qy 240 ASIALMFLVCGERPS 255  
Db 285 PITALMYRCAPPSS 300

## RESULT 8

S62627

agglutinin I precursor - European elder

C/Species: Sambucus nigra (European elder)

C/Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Aug-1999

C/Accession: S62627; S62619

R/van Damme, E.J.M.; Barre, A.; Rouge, P.; van Leuven, F.; Pauwels, W.J.

Eur. J. Biochem. 235, 128-137, 1996

R/Title: The Nucleo(alpha,beta-galactinase-binding lectin from elderberry (Sambucus nigra)

A/Reference: PubMed:8631315

A/Accession: S62627

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-570 &lt;VAN&gt;

A/Cross-references: EMBL:U27122; NID:G1141772; FIDN:MAC9158.1; PID:G1141773

A/Accession: S62619

A/Status: preliminary

A/Molecule type: protein

A/Residues: 29-39/309-319 &lt;VAA&gt;

A/Superfamily: ricin; rRNA N-glycosidase homology

F/37-253/Domain: rRNA N-glycosidase homology &lt;RNG&gt;

Query Match

Best Local Similarity 30.6%; Score 374; DB 2; Length 570;

Matches 95; Conservative 45; Mismatches 106; Indels 12; Gaps 8;

Qy 8 VHQGTQXK-VERPITLADYVSGSFSN-EIPLAQSTIPVSDAKOPVYALNQGKDS 65  
Db 37 VSFNLTGADYEPFLALQEVYLTQNTAFDLPVLPAPES-QVSDNPFVYALNNSGDT 95  
Qy 66 XTALDVYNAVYVQADQSYELDAPRAATHLFTGTRRSLSLFPYGSYDLERYV 125  
Db 96 VTALIDVQVLYVAFSSMKSPFSGSTAVQKDLFTVDTQE-ELNFTGNTSLRQVG 153  
Qy 126 H-RDQIPYGLXOLQSYKYL---RPGSTRQKQARSITLILQIMISBAAREPILMBXR 181  
Db 154 FGRVYIFLAGKSLQGISLRTYTLTGQIKRLAGLVILQWSEARLFXILKRLTS 213  
Qy 182 INSGKSPDPXYMLEFTSMQOQSTOVQSHSTGTPNNPRLAIXGNFTLXNRYX 239  
Db 214 ITDAEFTPTDLMISNNNSSEELQADQPGGIFAGVQLDRNNNSIEVTFRLFE 273  
Qy 239 IASIALMFLVCGERPS 255  
Db 274 LTYTALMYRCAPPSS 300

## RESULT 9

R1CSAG

agglutinin precursor - castor bean

N/Contains: rRNA N-glycosidase (BC 3.2.2.22)

C/Species: Ricinus communis (castor bean)

C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

C/Accession: A24261; A24210

R/Kobayashi, H.M.; Lamb, T.P.; Pappin, D.J.C.; Lord, J.M.

Biochem. J. 260, 15682-15686, 1988

A/Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.

A/Reference: PubMed:8635949; PMID:2393130

A/Accession: A24261  
A/Molecule type: mRNA  
A/Residues: 1-564 <NOB>  
A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701  
R/Kobayashi, H.M.; Yoshikawa, Y.; Funatsu, G.  
Biochem. Biophys. Acta 872, 277-285, 1986  
A/Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin  
A/Accession: A24210  
A/Status: preliminary

## RESULT 10

JCS032

karasurin-B - Trichosanthes kirilowii var. japonica

C/Species: Trichosanthes kirilowii var. japonica

C/Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 23-May-1997

C/Accession: JCS032

R/Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.

Biochem. Biophys. Acta 139, 1485-1489, 1996

A/Title: Amino acid sequence and ribosome-inactivating activities of karasurin-B and K

A/Reference: PubMed:8951169

A/Accession: JCS032

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-147 &lt;NOB&gt;

A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701

A/Accession: JCS032

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-147 &lt;NOB&gt;

A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701

A/Accession: JCS032

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-147 &lt;NOB&gt;

A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701

A/Accession: JCS032

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-147 &lt;NOB&gt;

A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701

A/Accession: JCS032

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-147 &lt;NOB&gt;

A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701

A/Accession: JCS032

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-147 &lt;NOB&gt;

A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701

A/Accession: JCS032

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-147 &lt;NOB&gt;

A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701

A/Accession: JCS032

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-147 &lt;NOB&gt;

A/Cross-references: GB:M2089; NID:9169700; FIDN:AAA3869.1; PID:9169701

A/Accession: JCS032

A/Status: preliminary

Query Match 24.7%; Score 302; DB 2; Length 247;  
Best Local Similarity 35.4%; Pred. No. 2, 6e-25;  
Matches 85; Conservative 46; Mismatches 95; Indels 14; Gaps 9;





A:Accession: S13429  
A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 'B',2-528 <HUN>

A:Notes-references: GB:M69344; NID:g166294; PIDN:AAA12624.1; EID:g166295  
A:Note: the coding region for the sequence shown is preceded by an ATG codon  
R:Kamatsu, G., Taguchi, Y.; Kameono, M.; Yanaka, H.  
Agric. Biol. Chem. 53, 1095-1097, 1989

A>Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from  
A:Reference number: U70202

A:Accession: J70202

A:Molecule type: protein

A:Residues: 1-201,203-251 <FUN>

A:Notes: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
R:Evensen, G.; Mathiesen, A.; Sundan, A.  
FEBS Lett. 266, 6848-6852, 1990

A>Title: DNA cloning, expression and characterization of two distinct abrin B-chains.

A:Reference number: A39761; MIDB:J101329; PMID:2016500

A:Accession: A39761

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 'B',2-251 <EVZ>

A:Cross-references: GB:X54872

A:Note: residues 1-8 were derived from the synthesized primer  
R:Kimura, M.; Sumizawa, T.; Funatsu, G.  
Biotechnol. Biochem. 57, 166-169, 1993

A:Cross-references: GB:X54873; MIDB:J165022; PMID:7753422

A:Reference number: JCI338; MIDB:J3165022; PMID:7753422

A:Contents: seeds

A:Accession: JCI338

A:Molecule type: protein

A:Residues: 261-347,'T',349-351,'A',353-357,'L',359-528 <RM>

A:Experimental source: seed

R:Evensen, G.; Mathiesen, A.; Sundan, A.  
submitted to the EMBL Data Library, October 1990

A:Description: Direct Molecular Cloning of two distinct abrin B-chains.  
A:Reference number: J14471

A:Accession: J14471

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 'ME',2-251 <EV2>

A:Cross-references: EMBL:X54873; NID:g16090; PIDN:CA38655.1; PIG:g16091

K:Chow, Y.L.; Chow, L.P.; Tsuyita, A.; Lin, J.Y.  
FEBS Lett. 309, 115-118, 1992

A>Title: The complete primary structure of abrin-a B chain.  
R:Kamatsu, G.; Taguchi, Y.; Kameono, M.; Yanaka, H.  
Agric. Biol. Chem. 53, 1095-1097, 1989

A:Accession: J24133

A:Molecule type: protein

A:Residues: 265-297,'Y',299-426,'V',428-466,'P',468-482,'L',484-528 <CB>  
R:Lin, S.H.; Chow, L.P.; Chen, Y.C.; Liaw, Y.C.; Lin, J.Y.  
Eur. J. Biochem. 240, 564-569, 1996

A>Title: Probing the domain structure of abrin-a by tryptic digestion.  
A:Reference number: S74110; MIDB:J9708945; PMID:8856055

A:Accession: S74110

A:Molecule type: protein

A:Residues: 1-201,203-251 <LIN>

A:Experimental source: seed

A:Accession: S74111

A:Molecule type: protein

A:Residues: 262-276,'X',278-280,329-348,369-388,399-418 <LN>

A:Experimental source: seed

A:Comment: abrin-a is more toxic than ricin. The toxin consists of an A chain, which inhibits  
catalytic receptors on the cell surface. The A and B chains are linked by a single disulfide  
C:Superfamily: ricin; rRNA-N-glycosidase homology  
C:Protein family: duplication; glycoprotein; glycosylase; hydrolase; lectin; pyroglyutamic acids  
P:7-246/DNA: rRNA-N-glycosidase homology <RG>  
P:261-528/Product: abrin-a chain B status experimental <RC>  
P:263-325,326-369,369-407,414-449,449-483,493-528/Region: 40-residue repeats  
F:1/Modified site: pyrroloindole carboxylic acid (Gln) #status experimental  
F:7/7,119,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
P:164,167/Active site: Glu, Arg #status predicted

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F/242/-269,286/-305,328/-346/-417/-430,456/-473/Duplicate bonds: #status predicted
F/286,312/Binding site: N-acetylglucosaminase (Aap, Aen) #status predicted
F/361,401/Binding site: Carboxyglutamate (Aap) (covAen) #status experimental
F/500,521/Binding site: N-acetylglucosamine (Aap, Aen) #status predicted

Query Match      18.2%; Score 467; DB 1; Length 528;
Local Similarity 42.2%; Pred. No. 8,96-11;
Matches 107; Conservative 34; Mismatches 66; Indels 26; Gaps 6;

QY 9 THQTGKXEPFFITLNRAYVSSGSFSENIPLAQSTIVSDAQFVYVLTNQGDSKTA 68
Db 9 TCGATSVSSKQFTEKLRLR-IGGLIHDIPLVLDPE- TLQSNRYIVLWESNDSTSEYV 66

QY 69 AIDYKXVYVAQADQSYFLKDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 127
Db 69 AIDYKXVYVAQADQSYFLKDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 127

QY 67 GIDYVNVYVAHNRGQSYFLRDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 124
Db 67 GIDYVNVYVAHNRGQSYFLRDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 124

QY 125 QQPLPGLQALPHGISFPGSGNDNEKALTLIVLQWAEAPFVYSNRVRSIQGTGA 184
Db 125 QQPLPGLQALPHGISFPGSGNDNEKALTLIVLQWAEAPFVYSNRVRSIQGTGA 184

QY 188 FLPEDVYELSTVSGQSYTOVQHSIDV/FNNPRLAIXGKVFPLNVX- 237
Db 188 FQPDADAIETLNMWDMSRQVESYQDTPEQ-----VLTNINSEPVYDSLSH 234

QY 238 -VTSALMLFVC 249
Db 235 PTVVALLMLFVC 247

RESULT 3
C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N/Contains: abrin N-glycosidase (BC 3.2.2.22)
C/Spectrum: Abrus precatorius (Indian licorice)
C/Date: 21-Feb-1992 Resequene, revision 31-Dec-1993 #text-change 20-Aug-1999
R/Accession: C39761
R/Accession: C39761
R/Title: Direct molecular cloning and expression of two distinct abrin A-chains
A/Reference number: A39761; MIM:31201329; MIM:2016300
A/Accession: C39761
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Svensen, G.; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A/Reference number: S14471
A/Accession: S14471
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Cross-References: EMBL:X54872; NID:G15088; PIDN:CA338654.1; PID:G16089
A/Superfamily: ricin; RNA N-glycosidase homology
A/Keywords: duplication; glycosidase; hydrolase; lectin; toxin
P1-251/Product: abrin (clone 7.2) chain A #status predicted <CH>
P1-246/Domain: RNA N-glycosidase homology; RNA N-glycosidase
P164,167/Active site: Glu, Arg #status predicted

Query Match      36.2%; Score 443; DB 2; Length 251;
Best Local Similarity 43.6%; Pred. No. 8,96-11;
Matches 106; Conservative 34; Mismatches 97; Indels 6; Gaps 5;

QY 9 THQTGKXEPFFITLNRAYVSSGSFSENIPLAQSTIVSDAQFVYVLTNQGDSKTA 68
Db 9 TCGATSVSSKQFTEKLRLR-IGGLIHDIPLVLDPE- TLQSNRYIVLWESNDSTSEYV 66

QY 69 AIDYKXVYVAQADQSYFLKDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 127
Db 69 AIDYKXVYVAQADQSYFLKDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 127

QY 67 GIDYVNVYVAHNRGQSYFLRDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 124
Db 67 GIDYVNVYVAHNRGQSYFLRDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 124

QY 125 QQPLPGLQALPHGISFPGSGNDNEKALTLIVLQWAEAPFVYSNRVRSIQGTGA 184
Db 125 QQPLPGLQALPHGISFPGSGNDNEKALTLIVLQWAEAPFVYSNRVRSIQGTGA 184

QY 188 FLPEDVYELSTVSGQSYTOVQHSIDV/FNNPRLAIXGKVFPLNVX- 237
Db 188 FQPDADAIETLNMWDMSRQVESYQDTPEQ-----VLTNINSEPVYDSLSH 234

QY 238 -VTSALMLFVC 249
Db 235 PTVVALLMLFVC 247

RESULT 3
C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N/Contains: abrin N-glycosidase (BC 3.2.2.22)
C/Spectrum: Abrus precatorius (Indian licorice)
C/Date: 21-Feb-1992 Resequene, revision 31-Dec-1993 #text-change 20-Aug-1999
R/Accession: C39761
R/Accession: C39761
R/Title: Direct molecular cloning and expression of two distinct abrin A-chains
A/Reference number: A39761; MIM:31201329; MIM:2016300
A/Accession: C39761
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Svensen, G.; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A/Reference number: S14471
A/Accession: S14471
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Cross-References: EMBL:X54872; NID:G15088; PIDN:CA338654.1; PID:G16089
A/Superfamily: ricin; RNA N-glycosidase homology
A/Keywords: duplication; glycosidase; hydrolase; lectin; toxin
P1-251/Product: abrin (clone 7.2) chain A #status predicted <CH>
P1-246/Domain: RNA N-glycosidase homology; RNA N-glycosidase
P164,167/Active site: Glu, Arg #status predicted

Query Match      36.2%; Score 443; DB 2; Length 251;
Best Local Similarity 43.6%; Pred. No. 8,96-11;
Matches 106; Conservative 34; Mismatches 97; Indels 6; Gaps 5;

QY 9 THQTGKXEPFFITLNRAYVSSGSFSENIPLAQSTIVSDAQFVYVLTNQGDSKTA 68
Db 9 TCGATSVSSKQFTEKLRLR-IGGLIHDIPLVLDPE- TLQSNRYIVLWESNDSTSEYV 66

QY 69 AIDYKXVYVAQADQSYFLKDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 127
Db 69 AIDYKXVYVAQADQSYFLKDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 127

QY 67 GIDYVNVYVAHNRGQSYFLRDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 124
Db 67 GIDYVNVYVAHNRGQSYFLRDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 124

QY 125 QQPLPGLQALPHGISFPGSGNDNEKALTLIVLQWAEAPFVYSNRVRSIQGTGA 184
Db 125 QQPLPGLQALPHGISFPGSGNDNEKALTLIVLQWAEAPFVYSNRVRSIQGTGA 184

QY 188 FLPEDVYELSTVSGQSYTOVQHSIDV/FNNPRLAIXGKVFPLNVX- 237
Db 188 FQPDADAIETLNMWDMSRQVESYQDTPEQ-----VLTNINSEPVYDSLSH 234

QY 238 -VTSALMLFVC 249
Db 235 PTVVALLMLFVC 247

RESULT 3
C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N/Contains: abrin N-glycosidase (BC 3.2.2.22)
C/Spectrum: Abrus precatorius (Indian licorice)
C/Date: 21-Feb-1992 Resequene, revision 31-Dec-1993 #text-change 20-Aug-1999
R/Accession: C39761
R/Accession: C39761
R/Title: Direct molecular cloning and expression of two distinct abrin A-chains
A/Reference number: A39761; MIM:31201329; MIM:2016300
A/Accession: C39761
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Svensen, G.; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A/Reference number: S14471
A/Accession: S14471
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Cross-References: EMBL:X54872; NID:G15088; PIDN:CA338654.1; PID:G16089
A/Superfamily: ricin; RNA N-glycosidase homology
A/Keywords: duplication; glycosidase; hydrolase; lectin; toxin
P1-251/Product: abrin (clone 7.2) chain A #status predicted <CH>
P1-246/Domain: RNA N-glycosidase homology; RNA N-glycosidase
P164,167/Active site: Glu, Arg #status predicted

Query Match      36.2%; Score 443; DB 2; Length 251;
Best Local Similarity 43.6%; Pred. No. 8,96-11;
Matches 106; Conservative 34; Mismatches 97; Indels 6; Gaps 5;

QY 9 THQTGKXEPFFITLNRAYVSSGSFSENIPLAQSTIVSDAQFVYVLTNQGDSKTA 68
Db 9 TCGATSVSSKQFTEKLRLR-IGGLIHDIPLVLDPE- TLQSNRYIVLWESNDSTSEYV 66

QY 69 AIDYKXVYVAQADQSYFLKDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 127
Db 69 AIDYKXVYVAQADQSYFLKDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 127

QY 67 GIDYVNVYVAHNRGQSYFLRDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 124
Db 67 GIDYVNVYVAHNRGQSYFLRDAFRAEATLFTGTTRSDSLPPKQSYKOLERYVGH-R 124

QY 125 QQPLPGLQALPHGISFPGSGNDNEKALTLIVLQWAEAPFVYSNRVRSIQGTGA 184
Db 125 QQPLPGLQALPHGISFPGSGNDNEKALTLIVLQWAEAPFVYSNRVRSIQGTGA 184

QY 188 FLPEDVYELSTVSGQSYTOVQHSIDV/FNNPRLAIXGKVFPLNVX- 237
Db 188 FQPDADAIETLNMWDMSRQVESYQDTPEQ-----VLTNINSEPVYDSLSH 234

QY 238 -VTSALMLFVC 249
Db 235 PTVVALLMLFVC 247

RESULT 3
C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N/Contains: abrin N-glycosidase (BC 3.2.2.22)
C/Spectrum: Abrus precatorius (Indian licorice)
C/Date: 21-Feb-1992 Resequene, revision 31-Dec-1993 #text-change 20-Aug-1999
R/Accession: C39761
R/Accession: C39761
R/Title: Direct molecular cloning and expression of two distinct abrin A-chains
A/Reference number: A39761; MIM:31201329; MIM:2016300
A/Accession: C39761
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Svensen, G.; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A/Reference number: S14471
A/Accession: S14471
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Cross-References: EMBL:X54872; NID:G15088; PIDN:CA338654.1; PID:G16089
A/Superfamily: ricin
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Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 7.95754 Seconds  
(without alignments) 3093.817 Million cell updates/sec

Title: US-09-601-667C-41

Sequence: 1 YERLRRTVHTQTTGKHEFRF.....XVTSAGLAIMLVGGERPSS 256

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616622 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1: PIR 76:\*  
2: PIR 76:\*  
3: PIR 76:\*  
4: PIR 76:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1165	95.3	254	2 PD0018	mistletoe lectin I
2	467	38.2	528	1 TZLSA	abrin-a precursor
3	443	36.2	251	2 C39761	abrin (clone 7.2)
4	426	34.8	528	2 S32431	abrin-d precursor
5	404	33.4	562	2 S16022	abrin-c precursor
6	372	30.7	576	2 S12450	abrin-b precursor
7	374	30.6	570	2 S62827	ricin B precursor
8	370.5	30.3	564	1 RRC5AG	agglutinin B, beta chain
9	302	24.7	247	2 JC0532	karsurin-B - tritic
10	301	24.6	289	1 RRTGT	karsurin-A - tritic
11	300	24.5	247	2 JC0533	karsurin-C - tritic
12	289.5	23.7	245	2 JC0480	karsurin - Mongol
13	289.5	23.7	245	2 JC0480	karsurin - Mongol
14	281	23.0	286	2 S25560	RNA N-glycosidase
15	273	22.4	286	2 S25560	RNA N-glycosidase
16	273	22.4	286	2 S25560	RNA N-glycosidase
17	273	22.4	286	2 S25560	RNA N-glycosidase
18	273	22.4	286	2 S25560	RNA N-glycosidase
19	253.5	20.7	268	1 S25560	RNA N-glycosidase
20	244.5	20.0	277	2 S22494	RNA N-glycosidase
21	239.5	19.6	250	2 JN0106	RNA N-glycosidase
22	233.5	19.1	278	2 A39817	RNA N-glycosidase
23	191.5	15.7	261	2 JH0401	antiviral protein
24	189	15.5	313	2 S17757	RNA N-glycosidase
25	181	14.8	294	2 S28421	abrin (clone 3.7)
26	172.5	14.1	106	2 B39761	RNA N-glycosidase
27	168	13.7	253	2 S28539	RNA N-glycosidase
28	166	13.6	253	2 S28539	RNA N-glycosidase
29	162	13.2	253	2 S29331	RNA N-glycosidase

30	162	13.2	283	2 S05205	RNA N-glycosidase
31	159	13.0	253	2 S28541	RNA N-glycosidase
32	157	12.8	252	1 RLOHG2	RNA N-glycosidase
33	150	12.3	272	2 JC0481	betavulgin - beet
34	141	11.5	253	2 S45922	RNA N-glycosidase
35	138	11.5	253	2 S45922	RNA N-glycosidase
36	133	10.7	250	2 S1932	RNA N-glycosidase
37	127	10.4	236	2 S1932	RNA N-glycosidase
38	123.5	10.1	289	2 T12573	30X ribosome inact
39	120	9.8	281	2 B38664	shiga-like toxin -
40	112.5	9.2	320	2 S42608	protein synthesis
41	112	9.2	280	2 JC0546	Shiga-like toxin cha
42	111.5	9.1	315	1 A26626	Shiga-like toxin C
43	111.5	9.1	315	1 XUBP93	Shiga-like toxin I
44	111.5	9.1	315	2 JN0725	Shiga-like toxin I
45	111.5	9.1	315	2 A53887	Shiga-like toxin I

#### ALIGNMENTS

##### RESULT 1

PD0018  
mistletoe lectin I A chain - Viscum album (fragment)

C/Date: 03-Jul-1998 #sequence, revision 10-Jul-1998 #text\_change 26-Aug-1999

E/Accession: PD0018 #Accession: R. Vukobratovic, A. Stoeva, S. Betzel, C. Voelter, W.

Biochem. Biophys. Res. Commun. 261:159-170, 1998 of mistletoe lectin I from Viscum alb

A/Title: Primary structure and molecular weight of mistletoe lectin I from Viscum alb

A/Reference number: PD0018, MUID:98308123, PMID:9642133

A/Accession type: protein

A/Residues: 1-254 <SSC>

C/Superfamily: ricin; RNA N-glycosidase homology

F/-246/Domain: RNA N-glycosidase homology <RMG>

Query Match 95.3%; Score 1165; DB 2; Length 254;

Best Local Similarity 91.8%; Pred. No. 5.4e+120;

Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

1 YERLRRTVHTQTTGKHEFRFRLILRLRYSSGSSNEPLRLGSLTIPYLMARPLYELTN 60

1 YERLRRTVHTQTTGKHEFRFRLILRLRYSSGSSNEPLRLGSLTIPYLMARPLYELTN 60

61 QGQSTVLAIDVNNVYVAQAGQGFRLPAPRAETHLFGRTDRLSPKSGYD 120

61 QGQSTVLAIDVNNVYVAQAGQGFRLPAPRAETHLFGRTDRLSPKSGYD 118

121 EYVGRDQIPDIXIOLIGVALKPRGSTRQKRSHTLILQMSAPRNPILMKRQ 180

119 EYVGRDQIPDIXIOLIGVALKPRGSTRQKRSHTLILQMSAPRNPILMKRQ 178

181 XNCGSEFLPYVMELEISNCOQSTVQHSIDGVFANPRLAIPRONVILNVDVLA 240

179 XNCGSEFLPYVMELEISNCOQSTVQHSIDGVFANPRLAIPRONVILNVDVLA 238

241 SIAIMFYCGERPSS 256

239 SIAIMFYCGERPSS 254

##### RESULT 2

TZLSA precursor - Indian jicoria (fragment)

RNA N-glycosidase (fragment)

C/Date: 31-Dec-1993 #sequence, revision 11-Aug-1997 #text\_change 16-Jul-1999

R/Accession: S32429, J02002, A39761, J01398, S34472, S24133, S74110, S74111

J. Mol. Biol. 229: 263-267, 1993

A/Title: Primary structure of three distinct isobabins determined by cDNA sequencing. CC

A/Reference number: S32429, MUID:9313798, PMID:842133

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Page 8

Oy	237	XVIAALIMFVC	249
		: : :	
Db	235	QVXPTALKEVC	247

Search completed: December 11, 2003, 14:48:52  
Job time : 35.4124 secs



Thu Dec 11 16:09:57 2003

us-09-601-667c-40.rapb

Page 7

STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70-P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 111:  
US-10-127-890-111  
Query Match 10.8%; Score 284.5; DB 12; Length 251;  
Best Local Similarity 34.0%; Pctd. No. 4,6e-23;  
Matches 86; Conservative 33; Mismatches 113; Indels 21; Gaps 7;  
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QY 65 SKTALIDVTXVYVAYOGAGSYAFEDAPRGAEFTLFTGTRDRSLPFGSYDLEHYA 124  
63 LAELIADVTSVYVGVQVRNSYFEDAPDAVEGLFKVTKTR--LHFGSYSLGEXK 120  
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QY 125 GHDDQIPGIXQI--IQSVYALRPGSGTQKASITLILQWISGAARF---NPILMR 177  
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QY 178 XKQKINSKGSFLPDXYMLETISWQOSTOVQHS--TDGVFNRPXRLAIXGNFVTLXNR 236  
181 FQGRIR-----PANNITSLERKNGKLSFQIRISGANGMSAEVLEBRANGKXYVTAVD 234  
Db  
QY 237 XYTASLAINPFC 249  
238 QVPRKILKFCV 247

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Strudnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
BETTER, MARC D.  
CITY: Chicago  
STREET: 500 West Madison Street, 34th floor  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70-P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 102:  
US-10-127-890-102  
Query Match 10.7%; Score 280.5; DB 12; Length 251;  
Best Local Similarity 33.6%; Pctd. No. 1.3e-22;  
Matches 85; Conservative 34; Mismatches 113; Indels 21; Gaps 7;  
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Db  
QY 65 SKTALIDVTXVYVAYOGAGSYAFEDAPRGAEFTLFTGTRDRSLPFGSYDLEHYA 124  
63 LAELIADVTSVYVGVQVRNSYFEDAPDAVEGLFKVTKTR--LHFGSYSLGEXK 120  
Db  
QY 125 GHDDQIPGIXQI--IQSVYALRPGSGTQKASITLILQWISGAARF---NPILMR 177  
121 AIREETDLGIEPLRIGIKLDENALIDNYKTEILASLLVVIQWVSAARFTIENQINN 180  
QY 178 XKQKINSKGSFLPDXYMLETISWQOSTOVQHS--TDGVFNRPXRLAIXGNFVTLXNR 236  
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us-09-601-667c-40.rapb

Page 5

QY 13 TCKEYFFFTLLADYVSSGSENFEPILKOSTIPVSDAQRVUVELTNOXKSDXTALIDV 72  
DB 10 TSSSYGVFISNLRKALPSEKXIDYDIPLR--SGLPSS--CRYALHILTNVADETISVADY 66  
QY 73 TTXVYVAYQADQSYFLDA--PRGAEHLFTGTRDRSSLPFGXSYDLEKRYAGH-RDQI 130  
DB 67 TNYVMEYRAGDSTYFEMASATBAKAVFDQAMR-KYLLPYSGNTERLOTMAKIRENI 125  
QY 131 PGLXQLOSYVALKXPGSTRXQNSIILIONISEARPNFLIMEXKQXINSKXSLP 190  
DB 126 PGLPDLDSATITLTFYNNNS--AASLAWLIGSTSEKAKXFEIQOIGKVDK--TFEP 181  
QY 191 DXYMLELETSNGQOSTQVQ--HSTGVFNPKRYALIXXGNFTYLANVX--VIASIALML 246  
DB 182 SLATISSENSWALSQOIQASTNNGQFSFVVLINAGNOVATITNVDAGVVTSNIALLL 241  
RESULT 10  
US-10-375-209A-39  
Sequence 39, Application US/10375209A  
Publication No. US20030215421A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 2020-601E  
CURRENT FILING DATE: 2003-02-24  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Trichosanthea killipowii  
US-10-375-209A-39  
Query Match 11.5%; Score 201; DB 12; Length 247;  
Best Local Similarity 34.8%; Pred. No. 1-6-24;  
Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;  
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DB 10 TSSSYGVFISNLRKALPSEKXIDYDIPLR--SGLPSS--CRYALHILTNVADETISVADY 66  
QY 73 TTXVYVAYQADQSYFLDA--PRGAEHLFTGTRDRSSLPFGXSYDLEKRYAGH-RDQI 130  
DB 67 TNYVMEYRAGDSTYFEMASATBAKAVFDQAMR-KYLLPYSGNTERLOTMAKIRENI 125  
QY 131 PGLXQLOSYVALKXPGSTRXQNSIILIONISEARPNFLIMEXKQXINSKXSLP 190  
DB 126 PGLPDLDSATITLTFYNNNS--AASLAWLIGSTSEKAKXFEIQOIGKVDK--TFEP 181  
QY 191 DXYMLELETSNGQOSTQVQ--HSTGVFNPKRYALIXXGNFTYLANVX--VIASIALML 246  
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US-10-127-890-6  
Sequence 6, Application US/10127890  
Publication No. US20030166156A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studentika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McGraw-Hill, H. & M. Co., Ltd.  
STREET: 500 West Madison Street, 34th floor

QY 13 TCKEYFFFTLLADYVSSGSENFEPILKOSTIPVSDAQRVUVELTNOXKSDXTALIDV 72  
DB 10 TSSSYGVFISNLRKALPSEKXIDYDIPLR--SGLPSS--CRYALHILTNVADETISVADY 66  
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QY 191 DXYMLELETSNGQOSTQVQ--HSTGVFNPKRYALIXXGNFTYLANVX--VIASIALML 246  
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Sequence 4, Application US/10280679B  
Publication No. US20030150019A1  
GENERAL INFORMATION:  
APPLICANT: American Biotechnology Corporation  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McGraw-Hill, H. & M. Co., Ltd.  
STREET: 500 West Madison Street, 34th floor

Thu Dec 11 16:09:57 2003

us-09-601-667c-40.rapb

Page 4

1 / CURRENT FILING DATE: 2002-10-29  
2 / PRIOR APPLICATION NUMBER: 09/538,873  
3 / PRIOR FILING DATE: 2000-03-30  
4 / PRIOR APPLICATION NUMBER: 60/126,826  
5 / PRIOR FILING DATE: 1999-03-30  
6 / NUMBER OF SEQ ID NOS: 23  
7 / SOFTWARE: Patent In Ver. 2.1  
8 / SEQ ID NOS: 1-23  
9 / LENGTH: 267  
10 / TYPE: PRT  
11 / ORGANISM: Artificial Sequence  
12 / FEATURES:  
13 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
14 / US-10-282-935-1

15 / Query Match 14.3% Score 376; DB 12; Length 267;  
16 / Best Local Similarity 39.1%; Pred. No. 3.2e-33;  
17 / Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

18 / QY 9 THQTGXYRFRITLADYSSGS-FSNRIPL-RSTIPVSDAGRPVLVETLWCKDXX 66  
19 / DB 13 TGAATVOSTYRFRITLADYSSGS-FSNRIPL-RSTIPVSDAGRPVLVETLWCKDXX 70  
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21 / DB 71 TLAIDVTNXXVYVAGDQOSYPLR-DAPRGAE-THTFTGTRDSSLPKSGYXDLERY 129  
22 / QY 124 AGH-RDQIPGIXXOLIOSYXAL---KPGGSTRXOARSILLIOMISAPRNPILMRX 179  
23 / DB 130 AGH-RDQIPGIXXOLIOSYXAL---KPGGSTRXOARSILLIOMISAPRNPILMRX 189  
24 / QY 180 QXINSKXFLPXVMELETSWQOSTOVGHSTGVFNNPXRALIXGNFTLXNRYXT 239  
25 / DB 190 TRIRYRNSADPSVITLWNSGSLTALIOESNQGAFSPLOLRNNSGFSYDVSIIL 249  
26 / QY 240 ASALIMLVYCGRRSS 255  
27 / DB 250 PIALMYRCAPPSS 265

28 / RESULT 8  
29 / US-10-127-890-1  
30 / Application US/10127890  
31 / Publication No. US2003016136A1  
32 / GENERAL INFORMATION:  
33 / APPLICANT: Bacter, Marc D.  
34 / Carcoli, Stephen F.  
35 / Studinka, Gary M.  
36 / TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
37 / Proteins  
38 / NUMBER OF SEQUENCES: 173  
39 / CORRESPONDENCE ADDRESS:  
40 / ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
41 / STREET: 500 West Madison Street, 34th floor  
42 / CITY: Chicago  
43 / STATE: Illinois  
44 / COUNTRY: USA  
45 / ZIP: 60661  
46 / COMPUTER READABLE FORM:  
47 / MEDIUM TYPE: Floppy disk  
48 / OPERATING SYSTEM: PC-DOS/MS-DOS  
49 / SOFTWARE: Patent In Release #1.0, Version #1.25  
50 / CURRENT APPLICATION DATA: US/010127/890  
51 / FILING DATE: 12-MAY-1994  
52 / APPLICATION NUMBER: US/010127/890  
53 / CLASSIFICATION: C12N000023  
54 / OTHER INFORMATION: <Unknow>  
55 / PRIOR APPLICATION DATA:  
56 / APPLICATION NUMBER: US/08/646/360  
57 / FILING DATE: 13-MAY-1996  
58 / APPLICATION NUMBER: PCT/US94/05348  
59 / FILING DATE: 12-MAY-1994

1 / APPLICATION NUMBER: US 08/064,691  
2 / FILING DATE: 12-MAY-1993  
3 / APPLICATION NUMBER: US 07/988,430  
4 / FILING DATE: 09-DEC-1992  
5 / APPLICATION NUMBER: US 07/901,707  
6 / FILING DATE: 19-JUN-1992  
7 / APPLICATION NUMBER: US 07/787,567  
8 / FILING DATE: 04-NOV-1991  
9 / NAME: McAndrews, John M.  
10 / REGISTERED ADDRESS: 3040 S. M.  
11 / TELECOMMUNICATION INFORMATION:  
12 / TELEPHONE: 312/707-8889  
13 / TELEFAX: 312/707-9155  
14 / INFORMATION FOR SEQ ID NO. 1:  
15 / SEQUENCE CHARACTERISTICS:  
16 / LENGTH: 267 amino acids  
17 / TYPE: amino acid  
18 / TOPOLOGY: linear  
19 / US-10-127-890-1

20 / Query Match 14.3% Score 376; DB 12; Length 267;  
21 / Best Local Similarity 39.1%; Pred. No. 3.2e-33;  
22 / Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

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26 / DB 71 TLAIDVTNXXVYVAGDQOSYPLR-DAPRGAE-THTFTGTRDSSLPKSGYXDLERY 129  
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28 / DB 130 AGH-RDQIPGIXXOLIOSYXAL---KPGGSTRXOARSILLIOMISAPRNPILMRX 189  
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30 / DB 190 TRIRYRNSADPSVITLWNSGSLTALIOESNQGAFSPLOLRNNSGFSYDVSIIL 249  
31 / QY 240 ASALIMLVYCGRRSS 255  
32 / DB 250 PIALMYRCAPPSS 265

33 / RESULT 9  
34 / US-09-792-793A-39  
35 / Sequence 39, Application US/09792793A  
36 / Publication No. US20020168370A1  
37 / GENERAL INFORMATION:  
38 / APPLICANT: McAndrews, John R.  
39 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
40 / FILE REFERENCE: 25020-601D  
41 / CURRENT APPLICATION NUMBER: US/09/792,793A  
42 / FILING DATE: 2001-02-22  
43 / NUMBER OF SEQ ID NOS: 93  
44 / SOFTWARE: Patent In Ver. 2.0  
45 / SEQ ID NOS: 1-93  
46 / LENGTH: 247  
47 / TYPE: PRT  
48 / ORGANISM: Trichosanthus kirilowii  
49 / US-09-792-793A-39  
50 / Query Match 11.5% Score 301; DB 10; Length 247;  
51 / Best Local Similarity 34.6%; Pred. No. 6.6e-25;  
52 / Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

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SEQ ID NO 8  
LENGTH: 252  
TYPE: PRT  
ORGANISM: Viscum album  
US-09-347-064-8

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Best Local Similarity 91.3%; Pct. No. 4 4e-120;  
Matches 232; Conservative 1; Mismatches 19; Indels 2; Gaps 1;

QY 1 YERLRVTHQTCXEFREFTLLRDVSSGSFSEIEPLRQSTIPVSDAQREVLVETLN 60  
DB 1 YERLRVTHQTCXEFREFTLLRDVSSGSFSEIEPLRQSTIPVSDAQREVLVETLN 60  
QY 61 QGDSITAIIDVTNNKYVAQAQGSYFLRDARQAEHLFTGTTDRKSLIPKGSYXDL 120  
DB 61 QGDSITAIIDVTNNKYVAQAQGSYFLRDARQAEHLFTGTTDRKSLIPKGSYXDL 118  
QY 121 ERYAGRDQIPDGIQXIGVAAIAKPGSGSTXORSTILLCYISEAARPNILMXAQ 180  
DB 119 ERYAGRDQIPDGIQXIGVAAIAKPGSGSTXORSTILLCYISEAARPNILMXAQ 178  
QY 181 XINSGXSLPDXYMLELTSWGQSTQVQHSIDGVNPNKRLAIXGNPVTLANRYVIA 240  
DB 179 YINSGXSLPDXYMLELTSWGQSTQVQHSIDGVNPNKRLAIPGNFVTLNRYDVIA 238  
QY 241 SLATMLPVCGERP 254  
DB 239 SLATMLPVCGERP 252

RESULT 5  
US-09-347-064-2  
Sequence 2, Application US/09347064A  
Patent No. US20020045208A1  
GENERAL INFORMATION:  
APPLICANT: Beck, Jürgen  
INVENTOR: Beck, Jürgen  
APPLICANT: Beck, Jürgen  
TITLE OF INVENTION: Recombinant Fusion Proteins Based on  
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum  
FILE REFERENCE: 09282-5  
CURRENT APPLICATION NUMBER: US/09/347,064A  
CURRENT FILING DATE: 1999-07-02  
EARLIER APPLICATION NUMBER: PCT/EP98/00009  
EARLIER FILING DATE: 1998-01-02  
EARLIER APPLICATION NUMBER: EP 97 10 0012.0  
EARLIER FILING DATE: 1997-01-02  
NUMBER OF SEQ ID NOS: 38  
SOURCE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 252  
TYPE: PRT  
ORGANISM: Viscum album  
US-09-347-064-2

Query Match 43.8%; Score 1151; DB 9; Length 252;  
Best Local Similarity 91.3%; Pct. No. 1,2e-119;  
Matches 231; Conservative 1; Mismatches 19; Indels 2; Gaps 1;

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DB 2 YERLRVTHQTCXEFREFTLLRDVSSGSFSEIEPLRQSTIPVSDAQREVLVETLN 61  
QY 61 QGDSITAIIDVTNNKYVAQAQGSYFLRDARQAEHLFTGTTDRKSLIPKGSYXDL 120  
DB 62 QGDSITAIIDVTNNKYVAQAQGSYFLRDARQAEHLFTGTTDRKSLIPKGSYXDL 119  
QY 121 ERYAGRDQIPDGIQXIGVAAIAKPGSGSTXORSTILLCYISEAARPNILMXAQ 180  
DB 120 ERYAGRDQIPDGIQXIGVAAIAKPGSGSTXORSTILLCYISEAARPNILMXAQ 179

QY 181 XINSGXSLPDXYMLELTSWGQSTQVQHSIDGVNPNKRLAIXGNPVTLANRYVIA 240  
DB 180 YINSGXSLPDXYMLELTSWGQSTQVQHSIDGVNPNKRLAIPGNFVTLNRYDVIA 239  
QY 241 SLATMLPVCGERP 253  
DB 240 SLATMLPVCGERP 252

RESULT 6  
US-10-282-935-3  
Sequence 3, Application US/10282935  
Patent No. US20030143193A1  
GENERAL INFORMATION:  
APPLICANT: VITETTA, ELLEN S.  
INVENTOR: VITETTA, ELLEN S.  
APPLICANT: SHALISHAM, JOAN  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
FILE REFERENCE: US20030143193A1  
CURRENT APPLICATION NUMBER: US/10/282,935  
CURRENT FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: 09/538,873  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: 60/126,826  
PRIOR FILING DATE: 1999-03-30  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 351  
LENGTH: 251  
TYPE: PRT  
ORGANISM: Abrus precatorius  
US-10-282-935-3

Query Match 17.6%; Score 461; DB 12; Length 251;  
Best Local Similarity 41.9%; Pct. No. 9,9e-43;  
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;  
QY 9 TQATGKXEFRTLLRDVSSGSFSEIEPLRQSTIPVSDAQREVLVETLNQKXKXTRA 68  
DB 9 TQATGKXEFRTLLRDVSSGSFSEIEPLRQSTIPVSDAQREVLVETLNQKXKXTRA 66  
QY 69 AIDVTNNKYVAQAQGSYFLRDARQAEHLFTGTTDRKSLIPKGSYXDLRYVIAH-R 127  
DB 67 GIVTNNAVVAARQGSYFLRDARQAEHLFTGTTDRKSLIPKGSYXDLRYVIAH-R 124  
QY 128 DQEPDGIQXIGVAAIAKPGSGSTXORSTILLCYISEAARPNILMXAQKINSKXS 187  
DB 125 QDPIGLQALHGISFREGGNNNEKXRTLLVLDQVAAAARFRTISNVVSVISQVGA 184  
QY 188 PLDXYMLELTSWGQSTQVQHSIDGVNPNKRLAIXGNPVTLANRYVIA 240  
DB 186 PLDXYMLELTSWGQSTQVQHSIDGVNPNKRLAIXGNPVTLANRYVIA 237  
QY 238 PLATMLPVCGERP 249  
DB 235 PLATMLPVCGERP 247

RESULT 7  
US-10-282-935-1  
Sequence 1, Application US/10282935  
Patent No. US20030143193A1  
GENERAL INFORMATION:  
APPLICANT: VITETTA, ELLEN S.  
INVENTOR: VITETTA, ELLEN S.  
APPLICANT: SHALISHAM, JOAN  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
FILE REFERENCE: US20030143193A1  
CURRENT APPLICATION NUMBER: US/10/282,935

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Page 2

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QY 391 VQTLDTYTGCGMAGNDTAPREVTITGPRDLCMESNKGXSVWETCCSSQXNXXALYXD 450
DB 121 VQTLDTYTGCGMAGNDTAPREVTITGPRDLCMESNKGXSVWETCCSSQXNXXALYXD 179
QY 451 GSIRPKQNDQCLTGGRDSVSVIVINIVSCSXKXQKWFTEKXALINLKKXXXDVYQA 510
DB 180 GSIRPKQNDQCLTGGRDSVSVIVINIVSCSXKXQKWFTEKXALINLKKXXXDVYQA 239
QY 511 NPKLRITIIYPATGKFNQMWLPV 533
DB 240 NPKLRITIIYPATGKFNQMWLPV 262

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Beck, Jürgen
APPLICANT: Schmidt, Arno
APPLICANT: Schaefer, Jörg
TITLE OF INVENTION: Ribosome-Inactivating Proteins Based on
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 267
ORGANISM: Vascum album
US-09-347-064-4

Query Match
Best Local Similarity 91.6%; P-adj. 1.4e-132; Length 267;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;

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DB 1 DDTGCSAEPVTRIVGRGKGVYVDDPTGCGNQLMREKSNDDPQVLTREDYTR 60
QY 331 NSGCLTYGTVAGYVYVNFPCNTAVREATTQVIXKXGIIINPSNVLVLAASGIKETTL 390
DB 61 NSGCLTYGTVAGYVYVNFPCNTAVREATTQVIXKXGIIINPSNVLVLAASGIKETTL 120
QY 391 VQTLDTYTGCGMAGNDTAPREVTITGPRDLCMESNKGXSVWETCCSSQXNXXALYXD 450
DB 121 VQTLDTYTGCGMAGNDTAPREVTITGPRDLCMESNKGXSVWETCCSSQXNXXALYXD 179
QY 451 GSIRPKQNDQCLTGGRDSVSVIVINIVSCSXKXQKWFTEKXALINLKKXXXDVYQA 510
DB 180 GSIRPKQNDQCLTGGRDSVSVIVINIVSCSXKXQKWFTEKXALINLKKXXXDVYQA 239
QY 511 NPKLRITIIYPATGKFNQMWLPV 533
DB 240 NPKLRITIIYPATGKFNQMWLPV 262

RESULT 3
US-10-083-336A-1
Sequence 3, Application US/10083336A
Patent No. US20030181655A1
GENERAL INFORMATION:
APPLICANT: Olsson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Vennemacher, Robert W
US-10-083-336A-1

TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (R1D 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 576
ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match
Best Local Similarity 49.2%; P-adj. 7.2e-128; Length 576;
Matches 264; Conservative 76; Mismatches 176; Indels 21; Gaps 12;

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DB 106 TLAIDYTVAYVYVAGADQSFYR-DAPRGE--THTFTGTRDSLPXSYXDERY 164
QY 124 AGH-RDQIPGIXOLIQSYXAL--RXSGSTRKQARSITLQWISSEARRPILWEXR 179
DB 165 AGH-RDQIPGIXOLIQSYXAL--RXSGSTRKQARSITLQWISSEARRPILWEXR 224
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QY 240 ASLAWLVCGRSSDVRVYVIRVYAD--DYTCASAEPTVIRVGRKXKXVYVD 296
DB 285 TRIMYRSAPDSVITLNNKRLSTLQENQNPASPTQQRNQSAPSVYDIL 339
QY 297 DDFHDQNIQVPSKSNDDPQVLTREDYTRSGCLTYGTVAGYVNFPCNTAVR 356
DB 340 GEFHNNALQVPCSKSNDDPQVLTREDYTRSGCLTYGTVAGYVNFPCNTAVR 399
QY 357 EATIQVIXKXGIIINPSNVLVLAASGIKETTLVQTLDTYTGCGMAGNDTAPREVTI 416
DB 400 EATIQVIXKXGIIINPSNVLVLAASGIKETTLVQTLDTYTGCGMAGNDTAPREVTI 459
QY 417 GRELQMSXKXSVVETCCSSQXNXXALYGDGSIIRKQNDQCLTGGRDSVSVIVIN 476
DB 460 GRELQMSXKXSVVETCCSSQXNXXALYGDGSIIRKQNDQCLTGGRDSVSVIVIN 518
QY 477 VSCSXKXQKWFTEKXALINLKKXXXDVYQAQNPFLRRITIIYPATGKFNQMWLPV 533
DB 519 VSCSXKXQKWFTEKXALINLKKXXXDVYQAQNPFLRRITIIYPATGKFNQMWLPV 575

RESULT 4
US-09-347-064-8
Sequence 8, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Beck, Jürgen
APPLICANT: Schmidt, Arno
APPLICANT: Schaefer, Jörg
TITLE OF INVENTION: Ribosome-Inactivating Proteins Based on
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
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Page 1

GenCore version 5.1.6  
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5	451	43.8	252	9	US-09-347-064-2
6	451	43.8	252	9	US-09-347-064-3
7	376	43.3	251	12	US-10-287-932-3
8	376	43.3	251	12	US-10-287-932-1
9	301	41.5	247	10	US-09-792-793A-39
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11	299	41.4	247	12	US-10-127-890-6
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13	287.5	40.8	263	12	US-10-127-890-4
14	287.5	40.8	263	12	US-10-127-890-11
15	286.5	40.7	251	12	US-10-127-890-102

16	278.5	40.6	247	10	US-09-792-793A-34	Sequence 34, App1
17	278.5	40.6	247	12	US-10-375-209A-34	Sequence 34, App1
18	275.5	40.5	251	12	US-10-127-890-101	Sequence 101, App
19	275.5	40.5	251	12	US-10-127-890-101	Sequence 101, App
20	272.5	40.5	332	9	US-09-765-527-253	Sequence 253, App
21	274.5	40.5	251	12	US-10-127-890-99	Sequence 99, App1
22	273.5	40.4	316	12	US-10-074-596-1	Sequence 1, App1
23	272.5	40.4	251	12	US-10-127-890-100	Sequence 100, App
24	272.5	40.4	251	12	US-10-127-890-105	Sequence 105, App
25	271.5	40.3	251	9	US-09-765-527-247	Sequence 247, App
26	271.5	40.3	251	12	US-10-127-890-2	Sequence 2, App1
27	271.5	40.3	251	12	US-10-127-890-103	Sequence 103, App
28	271.5	40.3	251	12	US-10-127-890-106	Sequence 106, App
29	271.5	40.3	251	12	US-10-127-890-108	Sequence 108, App
30	271.5	40.3	507	12	US-10-074-596-11	Sequence 11, App1
31	270.5	40.3	321	12	US-10-127-890-106	Sequence 106, App
32	268.5	40.2	293	9	US-09-765-527-253	Sequence 253, App
33	268.5	40.2	293	9	US-09-765-527-253	Sequence 253, App
34	268.5	40.2	309	9	US-09-765-527-253	Sequence 253, App
35	268.5	40.2	309	9	US-09-765-527-253	Sequence 253, App
36	263	40.0	198	12	US-10-083-336A-3	Sequence 3, App1
37	263	40.0	198	12	US-10-083-336A-7	Sequence 7, App1
38	263	40.0	199	12	US-10-083-336A-5	Sequence 5, App1
39	263	40.0	200	12	US-10-083-336A-10	Sequence 10, App1
40	249.5	9.7	263	12	US-10-127-890-7	Sequence 7, App1
41	249.5	9.5	185	12	US-10-083-336A-9	Sequence 9, App1
42	241	9.2	241	12	US-10-083-336A-8	Sequence 8, App1
43	241	9.2	188	12	US-10-083-336A-8	Sequence 8, App1
44	241	9.2	188	12	US-10-083-336A-8	Sequence 8, App1
45	241	9.2	190	12	US-10-083-336A-11	Sequence 11, App1

ALIGNMENTS

RESULT 1

US-09-347-064-10

Sequence 10, Application US/09347064A

Recent No.: US20010045208A1

APPLICANT: ECK, Jürgen

APPLICANT: Schmidt, Arno

APPLICANT: Zinke, Holger

TITLE OF INVENTION: Recombinant Fusion Proteins Based on

TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum

FILE REFERENCE: 09282-5

CURRENT APPLICATION NUMBER: US/09/347 064A

EARLIER FILING DATE: 1999-07-02

EARLIER APPLICATION NUMBER: PCT/EP98/00009

EARLIER FILING DATE: 1997-01-02

EARLIER APPLICATION NUMBER: EP 97 10 0012 0

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 10

LENGTH: 263

TYPE: PRT

ORGANISM: Viscum album

US-09-347-064-10

Query Match: 48.3%, Score 1267.5, DB 9, Length 263,

Best Match: 93.6%, Pct 48.3, e-132,

Matches 241, Conservative 1, Mismatches 20, Indels 1, Gaps 1,

DB 331

NGSCITTYGTAGYVYVIFDCNATAREKTIWQIKNGTINPRSNLVLAASGIGCTTT 390

61

NGSCITTYGTAGYVYVIFDCNATAREKTIWQIKNGTINPRSNLVLAASGIGCTTT 120

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us-09-601-667c-40.rat

Qy 240 ASLAIAMLVCGGERPS 255  
Db 250 PIALMYRCAPPSS 265

RESULT 15

US-08-425-336-1  
Sequence 1: US08425336  
Accession: 581083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studinka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: D30  
PRIORITY NUMBER: 123  
APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: 36,989  
PRACTICE NUMBER: 11354  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-1

Query Match 14.3% Score 376; DB 1; Length 267;  
Best Local Similarity 39.1%; Pred. No. 8, 2e-34;  
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

Qy 9 THGTTQKYEYFETLLIDYVSSG--FSNEIPL-ROSTIPVSDQRFVLVEITVQGXDSX 66  
Db 13 TGAATVOSYTNFIRAVKRLTADLVNHEIPLNVEGLPTN--QRFILVLSNHAELSV 70  
Qy 67 TAAIDNNKTYRQAGOSYTR-DAPRGA-THLFGTTRDSSLPFGOSYXDTERY 123  
Db 71 TLADYNNAYVGGKANKATFPHDQEDAAITLFT-DYGRYTFAGGVNDRLEQL 129  
Qy 124 AGF-RDQIPGIXOLIQSYAL---KFGSGSTRQASITLILQISEARFNIIMRXR 179  
Db 130 AGMLRENIENGPLERIASLYYSYGTQIPLARSPICIQIISDAPFOYIEGMR 189

Qy 180 QXINSGSEFDPDXMLELTSWGQSGTQVGHSTGVFNNPRLALIXGNEFTLXNRYVI 239  
Db 190 TRIRYRNSAPDPSPVITLNSWGRISTALQESNCAFSFTQLGRNKSKEFVYVSLII 249  
Qy 240 ASLAIAMLVCGGERPS 255  
Db 250 PIALMYRCAPPSS 265

Search completed: December 11, 2003, 14:11:38  
Job time : 19.4882 secs



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Page 7

Db 250 P11AMVRCAPPSS 265

RESULT 13

US-07-988-430-1

Sequence 1, Application US/07988430  
Patent No. 5416202  
GENERAL INFORMATION:  
APPLICANT: Bernhardt, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Lane, Julie A.  
APPLICANT: Lee, Charles  
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07988430  
FILING DATE: 19921209  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 1992-08-19  
PRIORITY DATE: 1992-08-19  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5416202and, Greer E.  
REGISTRATION NUMBER: 35302  
REFERENCE/DOCKET NUMBER: 31133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
FAX: 312-984-9740  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-07-988-430-1

Query Match 14.3%, Score 376, DB 1, Length 267,  
Best Local Similarity 39.1%, Pred. No. 8.2e-34,  
Matches 100, Conservative 43, Mismatches 101, Indels 12, Gaps 8,

Qy 9 THQTKGKRYFRFTLLADYVSSGS-FSNEIPL-RQSTIPVSDQRFVLTGNOGXDX 66  
Db 13 TGAATGQSYTNFIAVAGRLTGADVPHIIVLPNRVGLPIN-QRFLVLSNHAELSV 70  
Qy 67 TLAIDVTKRYVAVQAGQSYFLR-DAPRQAE--THLFTGTTPRQSLPFGXSIXDIEX 123  
Db 71 TLAIDVTKRYVAVQAGQSYFLR-DAPRQAE--THLFTGTTPRQSLPFGXSIXDIEX 123  
Qy 124 AGH-ROQIPGIXOLOSVAL--RXPQGSTXQARSIILIDMTSRAEFPILWPKR 179  
Db 130 AGHUNREIENGPILEHISALITVYSTGTOLPTLARSPTICQIMSEARFOYIEBMR 199

Db 250 P11AMVRCAPPSS 265

RESULT 14

US-08-218-303-16

Sequence 16, Application US/08218303  
Patent No. 5547867  
GENERAL INFORMATION:  
APPLICANT: Kato, Shunpandra V.  
APPLICANT: Hockney, Robert C.  
APPLICANT: Hockney, Robert C.  
TITLE OF INVENTION: FERMENTATION PROCESS  
TITLE OF INVENTION: FERMENTATION PROCESS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cushman, Darby & Cushman  
STREET: 1615 L Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036-5601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,303  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/841,533  
FILING DATE: 26-FEB-1992  
PRIORITY DATE: 1992-02-26  
APPLICATION NUMBER: 16,773  
ATTORNEY/AGENT INFORMATION:  
NAME: Kato, Shunpandra V.  
REGISTRATION NUMBER: 35302  
REFERENCE/DOCKET NUMBER: PRX/3893/94908/MX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-861-3000  
FAX: 202-861-3000  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-218-303-16

Query Match 14.3%, Score 376, DB 1, Length 267,  
Best Local Similarity 39.1%, Pred. No. 8.2e-34,  
Matches 100, Conservative 43, Mismatches 101, Indels 12, Gaps 8,

Qy 9 THQTKGKRYFRFTLLADYVSSGS-FSNEIPL-RQSTIPVSDQRFVLTGNOGXDX 66  
Db 13 TGAATGQSYTNFIAVAGRLTGADVPHIIVLPNRVGLPIN-QRFLVLSNHAELSV 70  
Qy 67 TLAIDVTKRYVAVQAGQSYFLR-DAPRQAE--THLFTGTTPRQSLPFGXSIXDIEX 123  
Db 71 TLAIDVTKRYVAVQAGQSYFLR-DAPRQAE--THLFTGTTPRQSLPFGXSIXDIEX 123  
Qy 124 AGH-ROQIPGIXOLOSVAL--RXPQGSTXQARSIILIDMTSRAEFPILWPKR 179  
Db 130 AGHUNREIENGPILEHISALITVYSTGTOLPTLARSPTICQIMSEARFOYIEBMR 199  
Qy 190 QXINSQKFLPDXYMLELFTSNQSGSTOVGHSTQVNNPXRATIXGNFVLKXNXYI 239  
Db 190 TRIRNRSSADPDSVLTLENMWRSLTAIGSNQCAFSPFQLORRNRSKFYSVDVSI 249

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us-09-601-667c-40.1a1

NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fletcher, Edmund R.  
REGISTRATION NUMBER: 17,829  
ADDRESS/DOCKET NUMBER: CRP-053  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-356-786-10

Query Match 15.3%; Score 403; DB 2; Length 534;  
Best Local Similarity 27.9%; Pred. No. 2,2e-36;  
Matches 143; Conservative 78; Mismatches 167; Indels 124; Gaps 23;

9 THQTGKXEPFRTLLRDVSSGS-FSNEIPL-ROSTIVSDAQFVLYEVTNQGXSK 66  
16 TAGATVOSTYFIRAVRGRLTTGADVHEIPVLPNVLGLPTN--ORFLVLSHMAELSV 73  
67 TAAIDVNTXVYAVAGDGYFLR-DAPGAE--THFTGTRDSSLFPKSGIXOLERY 123  
74 TLADVTNAVVGIRAGNSALFHHFDVQDAHAIHLF-DYQNYTFRFGANDLDEL 132  
124 AGH-RDQIPGLXKLOSYAL--RXPGRXKQASILLIOMISEARFNYLWEXR 179  
133 AGNLRENIELGMPLEFASLALYYSTGCTPLARSPFICIMISEARFOYIGEXR 192  
180 QXINSGSFLPDXVWLELETSMGQOSTVOGASTGVFNNPRLATIXGNFTLVNPKYI 239  
193 TRIRNRBSADPSPVITLNSMGRSLTAIOESNQGAFSPFOLGRNGSFVYDVSVI 252  
240 ASLAIMFVCGRRSSDVRWPLVTRVADDTGCASEFTRVIRYGMXMYVDNDDF 259  
253 FTLNRYVRCAPPSG---FSLIRVYVPMNADVQMDERGLV----- 264  
300 HDNGOQLMPSKSNNDPQLWTLIKRXTIRKSGSLCTYG----- 339  
235 QSGPEIK-----KFGK--TVK--ISCAAGTYFANQMMWKQAPGKJMWGINT 342  
340 YTA-GVYV-----NIFDNTAVEXTI-----WQIYNSTINP 372  
343 YTGSTVADDFKRRFASLETSATTAHQINNRNEDSATFCARRFPAWQGLIVSV 402  
373 RSNVLAASGICITLTITVQLDVTIQQMLANDTRPQVITYGPRDQMSNGSWIV 432  
403 SNTS---SSSGGSGS-----GGSSSGS-----GDSIDMGSPSGLA 437  
433 E-----TKSSQ--XNCKW-ALYGDGSR 454

DB 438 SICRVSITCRASODISLNTMISQBPGRGK 469

US-07-901-707-1  
Sequence 1, Application US/07901707  
Patent No. 5376546  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/901,707  
FILING DATE: 09/07/901,707  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5376546and, Greca E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 87129/30910  
TELEPHONE/CATLOG NUMBER: 346-5780  
TELEFAX: (312) 984-5750  
TREREX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-901-707-1

Query Match 14.3%; Score 376; DB 1; Length 267;  
Best Local Similarity 39.1%; Pred. No. 8,2e-34;  
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

9 THQTGKXEPFRTLLRDVSSGS-FSNEIPL-ROSTIVSDAQFVLYEVTNQGXSK 66  
13 TAGATVOSTYFIRAVRGRLTTGADVHEIPVLPNVLGLPTN--ORFLVLSHMAELSV 70  
67 TAAIDVNTXVYAVAGDGYFLR-DAPGAE--THFTGTRDSSLFPKSGIXOLERY 123  
71 TLADVTNAVVGIRAGNSALFHHFDVQDAHAIHLF-DYQNYTFRFGANDLDEL 129  
124 AGH-RDQIPGLXKLOSYAL--RXPGRXKQASILLIOMISEARFNYLWEXR 179  
130 AGNLRENIELGMPLEFASLALYYSTGCTPLARSPFICIMISEARFOYIGEXR 189  
180 QXINSGSFLPDXVWLELETSMGQOSTVOGASTGVFNNPRLATIXGNFTLVNPKYI 239  
190 TRIRNRBSADPSPVITLNSMGRSLTAIOESNQGAFSPFOLGRNGSFVYDVSVI 249



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us-09-601-667c-40.1a1

Page 4

STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-286-77

Query Match  
41.9%; Score 1101; DB 1; Length 540;  
Similarity 41.9%; Score 1101; DB 1; Length 540;  
Matches 242; Conservative 51; Mismatches 193; Indels 20; Gaps 11;

9 THOTGKXKREITLADYSSSS-FSEIPL-LRSTIVSDAQFVLELNOGXDSX 66  
13 TADATVSYNPIAVRSHLTGADVHEIPVLENEVGLIS--QRFILVLSNHAISV 70  
67 TADITNXYVAYQAGQSTYLR-DAPGAE--TETGTRDSLSPEYGSYDLEY 123  
71 TADITNXYVAYQAGQSTYLR-DAPGAE--TETGTRDSLSPEYGSYDLEY 123  
124 AGHROCPGLXOLIOSYXAL--XPGSTKXQASLILLOMTSPARFELIMXHQ 180  
130 GLEFRIELGTGLEDAISALVYSTGTCQIFLASFWICQWISSEAPQYIEZEW 189  
181 XINSKXSLPYXMLELTSWQSTVYCHSDGVNPNKXLAIXGNFVTLNPKYVA 240  
190 RIKYRSAPDESVITLMSKSLTAIOENQASAPFQIQRNSESFVYVLSILP 249  
241 STALPVCSPSSSVYVYHYPRIAD--DTCSASEPTATYKXGKQVYRD 297  
250 IIAVVRKAPPSG---PSLIRVYVNNADV-CQPEHIVRIYVBMGLCDVVB 304  
298 DFDGNCIQLWPSKNNPNLTKIKDYIISNGCLTYGVYVYMLPCQAVR 357  
305 RFDGNCIQLWPSKNNPNLTKIKDYIISNGCLTYGVYVYMLPCQAVR 357  
358 ATTQWKNCTINPESNVLAASSGKGLTYVTLDTLQGMAGNDTAPREYV 417  
365 RIKQWKNCTINPESNVLAASSGKGLTYVTLDTLQGMAGNDTAPREYV 417  
418 FRLCMESKXSVYVTCSSQXKXALYAGDSIRKQDQCLYXBSVYVYV 477  
425 LYMCLOANSGKWLBCPESKAEQ--QALYADDSIRKQDQCLYXBSVYVYV 483  
478 SCXKXKXQWVFTNEKALIMLXXXXXVDAQAPFLRRIIYPTAKQNMWLPV 533  
484 SCQKXKXQWVFTNEKALIMLXXXXXVDAQAPFLRRIIYPTAKQNMWLPV 539

US-08-776-059-39  
Sequence 39, Application US/08776059B  
Patent No. 6271368

GENERAL INFORMATION:  
APPLICANT: LEWIS, Hans  
APPLICANT: ECK, Jürgen  
APPLICANT: KUNZ, Jörg  
APPLICANT: KUNZ, Jörg  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 674503-2003  
CURRENT APPLICATION NUMBER: US/08/776, 059B  
EARLIER FILING DATE: 1999-06-19  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
EARLIER FILING DATE: 1996-06-25  
EARLIER APPLICATION NUMBER: 95109949.8  
NUMBER OF SEQ ID NOS: 56-26  
SEQUENCE: Patent Ver. 2.0  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Viscum album  
US-08-776-059-39

Query Match  
Best Local Similarity 40.9%; Score 1073; DB 3; Length 235;  
91.6%; Pred. No. 3, 6e-112;

Matches 217; Conservative 0; Mismatches 18; Indels 2; Gaps 1;  
18 FRIITLADYSSGFSNEIPLARQSTIVSDAQFVLELNOGXDSXTAIDVYXV 77  
1 FRIITLADYSSGFSNEIPLARQSTIVSDAQFVLELNOGXDSXTAIDVYXV 80  
78 VAYQAGQSTYLRAPRGAETHLFTGTRDSLSPEYGSYDLEZAGROQIGIXOL 137  
61 VAYQAGQSTYLRAPRGAETHLFTGTRDSLSPEYGSYDLEZAGROQIGIXOL 118  
138 IGVYALRPGSTKXQASLILLOMTSPARFELIMXHQXINSKXSLPYXMLEL 197  
119 IGVYALRPGSTKXQASLILLOMTSPARFELIMXHQXINSKXSLPYXMLEL 178  
198 FTSWQSTVYCHSDGVNPNKXLAIXGNFVTLNPKYVAIYVLSILPFCSE 254  
179 FTSWQSTVYCHSDGVNPNKXLAIXGNFVTLNPKYVAIYVLSILPFCSE 235

US-09-538-873-3  
Sequence 3, Application US/09538873  
Patent No. 6565500

GENERAL INFORMATION:  
APPLICANT: ELLIN, S  
APPLICANT: GIER, Victor F.  
APPLICANT: SMILSKAW, JON  
APPLICANT: BALDRA, ROXAN, G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK  
FILE REFERENCE: US/09/538, 873  
CURRENT APPLICATION NUMBER: US/09/538, 873  
EARLIER FILING DATE: 2000-03-30  
EARLIER APPLICATION NUMBER: 99/06426, 826  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 3  
LENGTH: 251  
TYPE: PRT  
ORGANISM: Abacus precatorius  
US-09-538-873-3

Query Match  
17.6%; Score 461; DB 4; Length 251;  
Similarity 17.6%; Score 461; DB 4; Length 251;  
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;

9 THOTGKXKREITLADYSSGFSNEIPLARQSTIVSDAQFVLELNOGXDSX 68  
9 TEGATSGYKQRIPLRRL-ROGHIDIVLPDP-TLQRRKRTIVLSSTISLV 66  
63 AIDTNYVAYQAGQSTYLRAPRGAETHLFTGTRDSLSPEYGSYDLEZAGROQIGIXOL 127  
67 GIDTNYVAYQAGQSTYLRAPRGAETHLFTGTRDSLSPEYGSYDLEZAGROQIGIXOL 124  
128 DCPGLXOLIOSYXALRPGSTKXQASLILLOMTSPARFELIMXHQXINSKXSLPYXMLEL 187  
125 QOIFDLOALHTGISFPGSGDNNEKARFLVILQVAAARAFYVLSRVASIGTGA 184  
188 FLPXVMELETSWQSTVYCHSDGVNPNKXLAIXGNFVTLNPKYVAIYVLSILPFCSE 237  
185 FLPXVMELETSWQSTVYCHSDGVNPNKXLAIXGNFVTLNPKYVAIYVLSILPFCSE 234  
238 -VISLAPFC 249  
235 FVAVLALMFC 247

US-08-378-761A-71  
Sequence 71, Application US/08378761A  
Patent No. 5633984  
GENERAL INFORMATION:

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us-09-601-667c-40.rat

Page 3

Db 2 YERIKLVHTQTESEYFRITLLADYVSSSPSENEILRQSTIPVSDAORPVLVETLN 61  
Qy 61 QGQSKXTALIDVTNXYVVAQAGDOSTFLRDAFPGATLHFTGTRDRSSLLPFGSYXDL 120  
Db 62 QGQSKXTALIDVTNXYVVAQAGDOSTFLRDAFPGATLHFTGTRDRSSLLPFGSYXDL 119  
Qy 121 ERYAGHRDOIPLGXOLQSVYALXPGSGTRGXARSTLLIOMISAPARFPIIMEXRQ 180  
Db 120 ERYAGHRDOIPLGXOLQSVYALXPGSGTRGXARSTLLIOMISAPARFPIIMEXRQ 179  
Qy 181 XINSKXSLPDXVMELESTMGQOSTGVSHSTGVNNPRLAIXXGNPVLTXNRYVIA 240  
Db 180 YINSKASFLPDVYMLESTMGQOSTGVSHSTGVNNPRLAIXXGNPVLTXNRYVIA 239  
Qy 241 SLATMFLVCGERS 254  
Db 240 SLATMFLVCGERS 253

RESULT 5

US-08-378-761A-77  
Sequence 77, Application US/08378761A  
Patent No. 5635384

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D

APPLICANT: KOSGMAN, ALICE ER  
TITLE OF INVENTION: INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN

COUNTRY: US  
ZIP: 46268

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651

REFERENCE/DOCKET NUMBER: 382728  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-378-761A-77

Query Match 41.9%, Score 1101, DB 1, Length 540;  
Best Local Similarity 45.1%, Pctd No 9, Seq-115

Matches 242; Conservative 81, Mismatches 193, Indels 20, Gaps 11;

Qy 9 THQITGKEYFRITLLADYVSSS-FSEIPL-ROSTIPYSDAORPVLVETLNQXSK 66  
Db 13 TADATVSTNPIAVRSHLTADAVHEHPVLRNNGVPIIS--GRFIVRSHLSHLSV 70  
Qy 67 TADIVTNXYVVAQAGDOSTFLR-DAFPGATLHFTGTRDRSSLLPFGSYXDLERY 123

Db 71 TLALDVNAYVVCAGNAGSYFFHPDNCDEAETHFT-DVONSFFPAFGNVDRELOL 129  
Qy 124 AGHRDOIPLGXOLQSVYAL--EXPGSGTRGXARSTLLIOMISAPARFPIIMEXRQ 180  
Db 130 GGLNENIELGHELEDAISLTYITSTGQIPLTAKSPVYCLQMSAPARFPIIMEXRQ 189  
Qy 181 XINSKXSLPDXVMELESTMGQOSTGVSHSTGVNNPRLAIXXGNPVLTXNRYVIA 240  
Db 180 ERYAGHRDOIPLGXOLQSVYALXPGSGTRGXARSTLLIOMISAPARFPIIMEXRQ 179  
Qy 190 RRYNRSAPDPSEVITLSENGRSLTAIOBNQAFAPFQLORRNGSKENVYDVSLILP 249  
Db 241 SLATMFLVCGERSDVRKMPVIRPVAD--DYCSASEPVRVIVGKXKXDVYRDO 297  
Qy 250 ILALMTYICAPPSQ---FSLIRPVVFNADV-CNDPEFVIRVIRGKLCVDVYGE 304  
Db 298 DPHNQIQLMPSKSNDDPNQNTTIRQXNTIRNSGLTITGTAGVYVIMPCNTANR 357  
Qy 305 EPPQNPQLMPSKSNDDPNQNTTIRQXNTIRNSGLTITGTAGVYVIMPCNTANR 364  
Db 358 ATIMQITNKGITINPRNMLYLAASGIGKTTLVQTDYTLGGQMLAGNDAPREYTVG 417  
Qy 365 ATRMQITNKGITINPRNMLYLAASGIGKTTLVQTDYTLGGQMLAGNDAPREYTVG 424  
Db 418 FPDLCNESKXSVYVETCSQXQXNAIYGDGSIIPKQNDQCTKGRDSVTVINIV 477  
Qy 425 IYVGMCLNNSKXSVYVETCSQXQXNAIYGDGSIIPKQNDQCTKGRDSVTVINIV 483  
Db 478 SCXSKXQXNVTNEKXALINIKXXXXDVQAQAPRLRIIYVARGKQNMVLY 533  
Qy 484 SCXSKXQXNVTNEKXALINIKXXXXDVQAQAPRLRIIYVARGKQNMVLY 539

RESULT 6

US-08-485-286-77  
Sequence 77, Application US/08485286  
Patent No. 5645026

GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D

APPLICANT: KOSGMAN, ALICE ER  
TITLE OF INVENTION: INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN

COUNTRY: US  
ZIP: 46268

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651

REFERENCE/DOCKET NUMBER: 382728  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid

Thu Dec 11 16:09:56 2003

us-09-601-667c-40.rat

Page 2

Db 332 DGNQIOLMPSKSNNDPNOJLWIKRQGTSSNSCLTTGTYAGVYWIIPDCTAVEATL 391  
QY 361 MOIWNGTIIINFRSNIVLAASGIGKTLTVQTLDTYLGQSMIAQNDTAPREVTIGFRD 420  
Db 392 MOIWNGTIIINFRSNIVLAASGIGKTLTVQTLDTYLGQSMIAQNDTAPREVTIGFRD 451  
QY 421 LCMESNGSVWTFKCSXQXWALYKDSIFRQWQOCLTKGDSYVTINIVGCS 460  
Db 452 LCMESNGSVWTFKCSXQXWALYKDSIFRQWQOCLTKGDSYVTINIVGCS 510  
QY 481 XXSXQWVFTNEXALINLXXXXXDDVAQANPKLRITIIYPATGKPNQWMLPV 533  
Db 511 AGSSQWVFTNEXALINLXXXXXDDVAQANPKLRITIIYPATGKPNQWMLPV 563

RESULT 2  
US-08-776-059-43  
Sequence 43; Application US/0876059B  
Patent No. 6271368  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: BAKR, Axel  
APPLICANT: ZINKE, Holger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 674503-2003  
CURRENT APPLICATION NUMBER: US/08/776, 059B  
CURRENT FILING DATE: 1999-06-19  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
EARLIER FILING DATE: 1996-06-25  
EARLIER PCT APPLICATION NUMBER: 95109949.8  
EARLIER FILING DATE: 1995-06-26  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 43  
LENGTH: 263  
TYPE: PRT  
ORGANISM: Viscum album  
US-08-776-059-43

Query Match 48.3%; Score 1267.5; DB 3; Length 263;  
Best Local Similarity 91.6%; Pctd. No. 6.3e-134;  
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;  
QY 271 DDTCSASEPTVRIYGRNGWCVDRDDPFDQNOJOLMPSKSNNDPNOJLWIKRQGTSS 60  
Db 1 DDTCSASEPTVRIYGRNGWCVDRDDPFDQNOJOLMPSKSNNDPNOJLWIKRQGTSS 60  
QY 331 NSCLTTGYAGVYWIIPDCTAVEATLWQIXNGTIIINFRSNIVLAASGIGKTLTV 390  
Db 61 NSCLTTGYAGVYWIIPDCTAVEATLWQIXNGTIIINFRSNIVLAASGIGKTLTV 120  
QY 391 VQTLDTYLGQSMIAQNDTAPREVTIGFRDLCMESNGSVWTFKCSXQXWALYKDS 450  
Db 121 VQTLDTYLGQSMIAQNDTAPREVTIGFRDLCMESNGSVWTFKCSXQXWALYKDS 179  
QY 451 GSIRPKQWQOCLTKGDSYVTINIVGCSXQXWALYKDSIFRQWQOCLTKGDSYVTINIVGCS 510  
Db 180 GSIRPKQWQOCLTKGDSYVTINIVGCSXQXWALYKDSIFRQWQOCLTKGDSYVTINIVGCS 239  
QY 511 NPKLRITIIYPATGKPNQWMLPV 533  
Db 240 NPKLRITIIYPATGKPNQWMLPV 262

RESULT 3  
US-08-776-059-33  
Sequence 33; Application US/0876059B  
Patent No. 6271368  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: BAKR, Jurgen

APPLICANT: BAKR, Axel  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 674503-2003  
CURRENT APPLICATION NUMBER: US/08/776, 059B  
CURRENT FILING DATE: 1999-06-19  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
EARLIER FILING DATE: 1996-06-25  
EARLIER PCT APPLICATION NUMBER: 95109949.8  
EARLIER FILING DATE: 1995-06-26  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 33  
LENGTH: 264  
TYPE: PRT  
ORGANISM: Viscum album  
US-08-776-059-33

Query Match 48.3%; Score 1267.5; DB 3; Length 264;  
Best Local Similarity 91.6%; Pctd. No. 6.3e-134;  
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;  
QY 271 DDTCSASEPTVRIYGRNGWCVDRDDPFDQNOJOLMPSKSNNDPNOJLWIKRQGTSS 61  
Db 2 DDTCSASEPTVRIYGRNGWCVDRDDPFDQNOJOLMPSKSNNDPNOJLWIKRQGTSS 61  
QY 331 NSCLTTGYAGVYWIIPDCTAVEATLWQIXNGTIIINFRSNIVLAASGIGKTLTV 390  
Db 62 NSCLTTGYAGVYWIIPDCTAVEATLWQIXNGTIIINFRSNIVLAASGIGKTLTV 121  
QY 391 VQTLDTYLGQSMIAQNDTAPREVTIGFRDLCMESNGSVWTFKCSXQXWALYKDS 450  
Db 122 VQTLDTYLGQSMIAQNDTAPREVTIGFRDLCMESNGSVWTFKCSXQXWALYKDS 180  
QY 451 GSIRPKQWQOCLTKGDSYVTINIVGCSXQXWALYKDSIFRQWQOCLTKGDSYVTINIVGCS 510  
Db 181 GSIRPKQWQOCLTKGDSYVTINIVGCSXQXWALYKDSIFRQWQOCLTKGDSYVTINIVGCS 240  
QY 511 NPKLRITIIYPATGKPNQWMLPV 533  
Db 241 NPKLRITIIYPATGKPNQWMLPV 263

RESULT 4  
US-08-776-059-31  
Sequence 31; Application US/0876059B  
Patent No. 6271368  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: BAKR, Jurgen  
APPLICANT: ZINKE, Holger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 674503-2003 US/08/776, 059B  
CURRENT APPLICATION NUMBER: US/08/776, 059B  
CURRENT FILING DATE: 1999-06-19  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
EARLIER FILING DATE: 1996-06-25  
EARLIER PCT APPLICATION NUMBER: 95109949.8  
EARLIER FILING DATE: 1995-06-26  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 31  
LENGTH: 253  
TYPE: PRT  
ORGANISM: Viscum album  
US-08-776-059-31

Query Match 44.0%; Score 1155; DB 3; Length 253;  
Best Local Similarity 91.3%; Pctd. No. 2.5e-121;  
Matches 223; Conservative 1; Mismatches 19; Indels 2; Gaps 1;  
QY 1 YRIARVHTQTKGEYFRFTLLADYVSGSFSNRPILKOSTIIPVSDQRFVAVELTN 60

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US-09-601-667C-40.rai

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: December 11, 2003, 13:53:19 ; Search time 18.4892 Seconds  
(without alignments) 1222.073 Million cell updates/sec

Title: US-09-601-667C-40  
Perfect score: 2626  
Sequence: 1 YERLARVHTGTGKEYRF.....RIIIPYATGKQWALPY 534  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310859 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: Issued Patents AA.\*
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- 3: /cgm2\_6/prodate/1/1aa/6A\_COMB.pep.\*
- 4: /cgm2\_6/prodate/1/1aa/6A\_COMB.pep.\*
- 5: /cgm2\_6/prodate/1/1aa/PCMS\_COMB.pep.\*
- 6: /cgm2\_6/prodate/1/1aa/backfill.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2504.5	95.4	564	3	US-08-776-059-35 Sequence 35, Appl
2	1267.5	48.3	263	3	US-08-776-059-43 Sequence 43, Appl
3	1267.5	48.3	264	3	US-08-776-059-33 Sequence 33, Appl
4	1155	44.0	253	3	US-08-776-059-31 Sequence 31, Appl
5	1101	41.9	540	1	US-08-378-761A-77 Sequence 77, Appl
6	1101	41.9	540	1	US-08-485-286-77 Sequence 77, Appl
7	1023	40.2	235	3	US-08-776-059-39 Sequence 39, Appl
8	1023	40.2	235	3	US-08-776-059-39 Sequence 39, Appl
9	453.5	17.5	250	1	US-08-378-761A-71 Sequence 71, Appl
10	453.5	17.5	250	1	US-08-378-761A-71 Sequence 71, Appl
11	403	15.3	534	2	US-08-485-286-10 Sequence 10, Appl
12	376	14.3	267	1	US-07-901-707-1 Sequence 1, Appl
13	376	14.3	267	1	US-07-988-430-1 Sequence 1, Appl
14	376	14.3	267	1	US-08-218-303-16 Sequence 16, Appl
15	376	14.3	267	1	US-08-425-336-1 Sequence 1, Appl
16	376	14.3	267	1	US-08-488-113B-1 Sequence 1, Appl
17	376	14.3	267	1	US-08-477-488B-1 Sequence 1, Appl
18	376	14.3	267	2	US-08-546-360-1 Sequence 21, Appl
19	376	14.3	267	2	US-08-546-360-1 Sequence 21, Appl
20	376	14.3	267	4	US-08-328-725D-61 Sequence 1, Appl
21	376	14.3	267	4	US-08-328-725D-61 Sequence 1, Appl
22	376	14.3	267	4	US-09-610-838-1 Sequence 1, Appl
23	376	14.3	267	4	US-09-610-838-1 Sequence 1, Appl
24	376	14.3	267	5	PCT-US92-09487-1 Sequence 1, Appl
25	376	14.3	268	5	US-08-356-786-8 Sequence 8, Appl
26	372	14.2	290	1	US-08-378-761A-27 Sequence 27, Appl
27	372	14.2	290	1	US-08-485-286-27 Sequence 27, Appl

28	372	14.2	290	6	US-08-324-301-15 Sequence 15, Appl
29	326	12.4	282	1	US-08-378-761A-74 Sequence 74, Appl
30	301	11.5	267	1	US-08-485-286-74 Sequence 74, Appl
31	301	11.5	267	1	US-08-485-286-74 Sequence 74, Appl
32	299	11.4	247	1	US-08-477-484B-6 Sequence 6, Appl
33	299	11.4	247	1	US-08-477-484B-6 Sequence 6, Appl
34	299	11.4	247	2	US-08-485-286-6 Sequence 6, Appl
35	299	11.4	247	2	US-08-485-286-6 Sequence 6, Appl
36	299	11.4	247	3	US-09-132F-185-6 Sequence 6, Appl
37	299	11.4	247	4	US-09-610-838-6 Sequence 6, Appl
38	294	11.2	289	1	US-08-184-237-4 Sequence 4, Appl
39	294	11.2	289	2	US-08-482-920-4 Sequence 4, Appl
40	294	11.2	289	3	US-08-484-341-4 Sequence 4, Appl
41	294	11.2	289	3	US-08-484-341-4 Sequence 4, Appl
42	294	11.2	289	3	US-08-483-502-4 Sequence 4, Appl
43	294	11.2	289	4	US-08-126-651A-4 Sequence 4, Appl
44	287.5	10.9	263	1	US-07-501-707-4 Sequence 4, Appl
45	287.5	10.9	263	1	US-07-588-430-4 Sequence 4, Appl

#### ALIGNMENTS

```
RESULT 1
US-08-776-059-35
Sequence 35, Application US/0877605B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: EXX, Jürgen
APPLICANT: ZINK, Axel
APPLICANT: ZINK, Axel
TITLE OR INVENTION: MISTLETOE LECTIN
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: patentin Ver. 2.0
SEQ ID NO 35
US-08-776-059-35
ORGANISM: Viscum album
Query Match 95.4%; Score 2504.5; DB 3; Length 564;
Best Local Similarity 51.7%; Pred. No. 2.5e-272;
Matches 489; Conservative 2; Mismatches 39; Indels 3; Gaps 2.
QY 1 YERLARVHTGTGKEYRFITLADYSSSSSNELPLRQSTIPYSDARFLYETRN 60
DB 61 GQXSTAIADYNNXYVAVAGQSGSFLAPRGAERHLFTGTRDRESLPXGXYXD 120
QY 34 YERLARVHTGTGDEIRITLADYSSSSSNELPLRQSTIPYSDARFLYETRN 93
DB 94 GQXSTAIADYNNXYVAVAGQSGSFLAPRGAERHLFTGTRDRESLPXGXYXD 151
QY 121 EYVAGRDQIDLIQLOSVAFKPGSTRQARSITLILQWISPAARFETLRRAR 180
DB 152 EYVAGRDQIDLIQLOSVAFKPGSTRQARSITLILQWISPAARFETLRRAR 211
QY 181 XNKGASRTPDYKWELEFSSQSGTQVSHDTCFNNPKALIXGNFTLXRVXTYA 240
DB 212 YNKGASRTPDYKWELEFSSQSGTQVSHDTCFNNPKALIXGNFTLXRVXTYA 271
QY 241 SLATMFVCGRRSSGVRKWLTPYADDTGASAEPTVATVYGKXVYVRDDPF 300
DB 272 SLATMFVCGRRSSGVRKWLTPYADDTGASAEPTVATVYGKXVYVRDDPF 331
QY 301 DQDQIUMPSKSNQDPMQJMTIKEDXTIRSNQSLCTTYGTAGYVWIPDNTAWEATI 360
```

DR N-PSDB; AA029120.  
XX  
PT Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure, Fig 18B; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
CC which have antitumor and immunostimulatory activity. The 286 subunit of  
CC the mistletoe lectin binds to and inactivates the 286 subunit of  
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
CC fragments are used to treat uncontrolled cell growth (particularly  
CC cancers) and if they lack cytotoxicity, to increase the strength of the  
CC immune response, particularly to a co-administered antigen  
CC (tumour-associated, bacterial or viral). The method allows production of  
CC mistletoe lectin, and its individual chains, in many different isoforms  
CC and on a large scale, at any time of the year. Recombinant products are  
CC free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a variant mistletoe lectin B5 protein.  
SQ Sequence 265 AA;  
  
Query Match 49.1%; Score 1290; DB 20; Length 265;  
Best Local Similarity 32.4%; Pred. No. 3,6e-134;  
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
  
QY 271 DDVTCASAEPTVRIKXKXKXVYRDDDPHDGNOQLWPKSKNDPQOLMTIKEDXTIR 330  
DB 1 DDVTCASAEPTVRIKXKXKXVYRDDDPHDGNOQLWPKSKNDPQOLMTIKEDXTIR 60  
QY 331 NSGCLTGYTACGYMTFPCNTNPRATQWQKNTINRSGNTLAAGGICKTTLF 390  
DB 61 NSGCLTGYTACGYMTFPCNTNPRATQWQKNTINRSGNTLAAGGICKTTLF 120  
QY 391 VQTLDTYTLGGWLAGNDTAPREVITYGFRDLCKESKXGSYWEFCSSOXNOXXNALYED 450  
DB 121 VQTLDTYTLGGWLAGNDTAPREVITYGFRDLCKESKXGSYWEFCSSOXNOXXNALYED 180  
QY 451 GSIRKXNODCLTKGRDSVTVINIVSCSXSKXQWFTNEXAILNKXXXXVDVAQN 510  
DB 181 GSIRKXNODCLTKGRDSVTVINIVSCSXSKXQWFTNEXAILNKXXXXVDVAQN 240  
QY 511 NPKLRRIITYPATGKNGMFLPV 533  
DB 241 NPKLRRIITYPATGKNGMFLPV 263

Search completed: December 11, 2003, 14:07:48  
Job time : 53.7657 secs



CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a mistletoe lectin B1 protein.  
 XX  
 SQ Sequence 264 AA;  
 Query Match 49.1%; Score 1290; DB 20; Length 264;  
 Best Local Similarity 92.4%; Pred. No. 3.5e-134;  
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 271 DDTGASAEPTVRIYGNKGNVYRDDDDPDGNGOILMPKSKNDNDQLTIRKDXITIS 330  
 DB 1 DDTGASAEPTVRIYGNKGNVYRDDDDPDGNGOILMPKSKNDNDQLTIRKDXITIS 60  
 QY 331 NSGCLITTYGTAGVYVWIPDCTAVRENTIWO:KXNGTINPNSNVLAASSGIGKTTLT 390  
 DB 61 NSGCLITTYGTAGVYVWIPDCTAVRENTIWO:KXNGTINPNSNVLAASSGIGKTTLT 120  
 QY 391 VQTLDTYTGQGNLGNMTAPRENTIYGFRLCMESSXSVWETCSQXQKXALYD 450  
 DB 121 VQTLDTYTGQGNLGNMTAPRENTIYGFRLCMESSXSVWETCSQXQKXALYD 180  
 QY 451 GSIRPKONODCLTSGRDSVSTVINIVSCSXGXQXWFTREXALINLXXXXXDVPAQA 510  
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCSXGXQXWFTREXALINLXXXXXDVPAQA 240  
 QY 511 NPKLRILITTPATGKNQMWLEPV 533  
 DB 241 NPKLRILITTPATGKNQMWLEPV 263  
 RESULT 14  
 ID AAY25996  
 XX AAY25996 standard; Protein: 264 AA.  
 XX  
 AC AAY25996;  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Mistletoe lectin B5 protein fragment.  
 XX  
 KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B5.  
 XX  
 OS Vascum album.  
 XX  
 PN DE19804210-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PP 03-FEB-1998; 98DE-1004210.  
 XX  
 PR 03-FEB-1998; 98DE-1004210.  
 XX  
 PX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 PI Morris P, Stiefel T, Voelter W, Welters P,  
 DR WPI; 1999-445335/38.  
 DR N-PSDB; AA209114.  
 XX  
 PT Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants

FS Claim 9; Fig 12b; 78pp; German.  
 XX  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a mistletoe lectin B5 protein.  
 XX  
 SQ Sequence 264 AA;  
 Query Match 49.1%; Score 1290; DB 20; Length 264;  
 Best Local Similarity 92.4%; Pred. No. 3.5e-134;  
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 271 DDTGASAEPTVRIYGNKGNVYRDDDDPDGNGOILMPKSKNDNDQLTIRKDXITIS 330  
 DB 1 DDTGASAEPTVRIYGNKGNVYRDDDDPDGNGOILMPKSKNDNDQLTIRKDXITIS 60  
 QY 331 NSGCLITTYGTAGVYVWIPDCTAVRENTIWO:KXNGTINPNSNVLAASSGIGKTTLT 390  
 DB 61 NSGCLITTYGTAGVYVWIPDCTAVRENTIWO:KXNGTINPNSNVLAASSGIGKTTLT 120  
 QY 391 VQTLDTYTGQGNLGNMTAPRENTIYGFRLCMESSXSVWETCSQXQKXALYD 450  
 DB 121 VQTLDTYTGQGNLGNMTAPRENTIYGFRLCMESSXSVWETCSQXQKXALYD 180  
 QY 451 GSIRPKONODCLTSGRDSVSTVINIVSCSXGXQXWFTREXALINLXXXXXDVPAQA 510  
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCSXGXQXWFTREXALINLXXXXXDVPAQA 240  
 QY 511 NPKLRILITTPATGKNQMWLEPV 533  
 DB 241 NPKLRILITTPATGKNQMWLEPV 263  
 RESULT 15  
 ID AAY25996  
 XX AAY25996 standard; Protein: 265 AA.  
 XX  
 AC AAY25996;  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Mistletoe lectin B5 variant protein fragment.  
 XX  
 KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B5.  
 XX  
 OS Vascum album.  
 XX  
 PN DE19804210-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PP 03-FEB-1998; 98DE-1004210.  
 XX  
 PR 03-FEB-1998; 98DE-1004210.  
 XX  
 PX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 PI Morris P, Stiefel T, Voelter W, Welters P,  
 DR WPI; 1999-445335/38.

XX Sequence 265 AA;  
 SQ Query Match 49.2%; Score 1291; DB 20; Length 265;  
 Best Local Similarity 92.4%; Pred. No. 2.8e-134;  
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 271 DDTCSASEPTVRIKSGKXGVVDVDDFDHNSQIQLPKSNNDPQMTIRKXTIRG 330  
 DB 1 DDTCSASEPTVRIKSGKXGVVDVDDFDHNSQIQLPKSNNDPQMTIRKXTIRG 60  
 QY 331 NSGCLTYGTAGYVMEFDQNTAVRPAITQIKXNGIIMPESNVLAAASGIGKTTLT 390  
 DB 61 NSGCLTYGTAGYVMEFDQNTAVRPAITQIKXNGIIMPESNVLAAASGIGKTTLT 120  
 QY 391 VQTLDTLGGQWLAGNDTAPREVTIYGFRLCMESKXSVWETCSQXQXKXVALYGD 450  
 DB 121 VQTLDTLGGQWLAGNDTAPREVTIYGFRLCMESKXSVWETCSQXQXKXVALYGD 180  
 QY 451 GSIRPKQNOQCLTGRDSVSTVINIVSGSXSKXQXQWFTNEZAIINLKXXXXXVDAQ 510  
 DB 181 GSIRPKQNOQCLTGRDSVSTVINIVSGSXSKXQXQWFTNEZAIINLKXXXXXVDAQ 240  
 QY 511 NPKLRRIITYPATGKPNQWMLPV 533  
 DB 241 NPKLRRIITYPATGKPNQWMLPV 263

RESULT 12  
 AA25993  
 ID AA25993 standard; Protein; 265 AA.  
 XX AA25993;  
 XX 18-OCT-1999 (first entry)  
 DB Mistletoe lectin B2 variant protein fragment.  
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B2.  
 XX Viscum album.  
 XX DB19804210-A1.  
 XX 12-AUG-1999.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX Morris P, Stiefel T, Voelker W, Welters P;  
 DR MPI; 1999-44535/38.  
 DR N-PDB; AA209117.  
 PT Preparation of mistletoe lectins in heterologous systems,  
 particularly for use as anticancer agents and immunostimulants  
 PS Disclosure; Fig 15B; 78pp; German.  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a variant mistletoe lectin B2 protein.  
 XX Sequence 265 AA;  
 SQ Query Match 49.2%; Score 1291; DB 20; Length 265;  
 Best Local Similarity 92.4%; Pred. No. 2.8e-134;  
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 271 DDTCSASEPTVRIKSGKXGVVDVDDFDHNSQIQLPKSNNDPQMTIRKXTIRG 330  
 DB 1 DDTCSASEPTVRIKSGKXGVVDVDDFDHNSQIQLPKSNNDPQMTIRKXTIRG 60  
 QY 331 NSGCLTYGTAGYVMEFDQNTAVRPAITQIKXNGIIMPESNVLAAASGIGKTTLT 390  
 DB 61 NSGCLTYGTAGYVMEFDQNTAVRPAITQIKXNGIIMPESNVLAAASGIGKTTLT 120  
 QY 391 VQTLDTLGGQWLAGNDTAPREVTIYGFRLCMESKXSVWETCSQXQXKXVALYGD 450  
 DB 121 VQTLDTLGGQWLAGNDTAPREVTIYGFRLCMESKXSVWETCSQXQXKXVALYGD 180  
 QY 451 GSIRPKQNOQCLTGRDSVSTVINIVSGSXSKXQXQWFTNEZAIINLKXXXXXVDAQ 510  
 DB 181 GSIRPKQNOQCLTGRDSVSTVINIVSGSXSKXQXQWFTNEZAIINLKXXXXXVDAQ 240  
 QY 511 NPKLRRIITYPATGKPNQWMLPV 533  
 DB 241 NPKLRRIITYPATGKPNQWMLPV 263

RESULT 13  
 AA25986  
 ID AA25986 standard; Protein; 264 AA.  
 XX AA25986;  
 XX 18-OCT-1999 (first entry)  
 DB Mistletoe lectin B1 protein fragment.  
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B1.  
 XX Viscum album.  
 XX DB19804210-A1.  
 XX 12-AUG-1999.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX Morris P, Stiefel T, Voelker W, Welters P;  
 DR MPI; 1999-44535/38.  
 DR N-PDB; AA209110.  
 PT Preparation of mistletoe lectins in heterologous systems,  
 particularly for use as anticancer agents and immunostimulants  
 PS Claim 9; Fig 8B; 78pp; German.  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of

QY 331 NSCLTITVYTGAGTWMIFECNTAVREATTMOIKWNGTIIINFSNITVLAASGIVKTTLT 390  
 DB 61 NSCLTITVYTGAGTWMIFECNTAVREATTMOIKWNGTIIINFSNITVLAASGIVKTTLT 120  
 QY 391 VQTLDTLTGGQWLAGNDTAPREATTYGFRLCMESNKGSVWETCSQXOXKXALYGD 450  
 DB 121 VQTLDTLTGGQWLAGNDTAPREATTYGFRLCMESNKGSVWETCSQXOXKXALYGD 180  
 QY 451 GSIRPKQNDQCLTYGSDVSFTVINTVSCGXSXKXQWVFTEKXALIMLXXXXXDVAAQ 510  
 DB 181 GSIRPKQNDQCLTYGSDVSFTVINTVSCGXSXKXQWVFTEKXALIMLXXXXXDVAAQ 240  
 QY 511 NPKLRRIITTPATGKQKQWMLPV 533  
 DB 241 NPKLRRIITTPATGKQKQWMLPV 263

## RESULT 10

AAV25988  
 ID AAV25988 standard; Protein; 264 AA.

AAV25988;

18-OCT-1999 (first entry)

Mistletoe lectin B3 protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

lymphokine-producing macrophage; uncontrolled cell growth; treatment;

cancer; cytotoxicity; antigen; isoform; lectin B3.

Viscum album.

DE19804210-AL.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Welters P;

WPI; 1999-445335/38.

N-PSDB; AA009112.

Preparation of mistletoe lectins in heterologous systems.

Particularly for use as anticancer agents and immunostimulants

Claim 9; Fig 10B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments

which have antitumour and immunostimulatory activity. The A-chain (MIA)

of the mistletoe lectin binds to, and inactivates, the 28S subunit of

ribosomes. Non-cytotoxic forms of (I) activate T-cell and its

lymphokine-producing macrophages, so stimulate immunity. (I) and its

fragments are used to treat uncontrolled cell growth (particularly

of tumour-associated bacterial or viral). The method allows production of the

immune response, particularly to a co-administered antigen

mistletoe lectin, and its individual chains, in many different isoforms

and on a large scale, at any time of the year. Recombinant products are

free from toxins present in natural mistletoe extracts. This sequence

represents a fragment of a mistletoe lectin B3 protein.

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 271 DVVTSASBPPTVTRKQKQVYVDDPFDQNOIQLPSSKSNPNQWLTKIDXTIRS 330  
 DB 1 DVVTSASBPPTVTRKQKQVYVDDPFDQNOIQLPSSKSNPNQWLTKIDXTIRS 60  
 QY 331 NSCLTITVYTGAGTWMIFECNTAVREATTMOIKWNGTIIINFSNITVLAASGIVKTTLT 390  
 DB 61 NSCLTITVYTGAGTWMIFECNTAVREATTMOIKWNGTIIINFSNITVLAASGIVKTTLT 120  
 QY 391 VQTLDTLTGGQWLAGNDTAPREATTYGFRLCMESNKGSVWETCSQXOXKXALYGD 450  
 DB 121 VQTLDTLTGGQWLAGNDTAPREATTYGFRLCMESNKGSVWETCSQXOXKXALYGD 180  
 QY 451 GSIRPKQNDQCLTYGSDVSFTVINTVSCGXSXKXQWVFTEKXALIMLXXXXXDVAAQ 510  
 DB 181 GSIRPKQNDQCLTYGSDVSFTVINTVSCGXSXKXQWVFTEKXALIMLXXXXXDVAAQ 240  
 QY 511 NPKLRRIITTPATGKQKQWMLPV 533  
 DB 241 NPKLRRIITTPATGKQKQWMLPV 263

## RESULT 11

AAV25994  
 ID AAV25994 standard; Protein; 265 AA.

AAV25994;

18-OCT-1999 (first entry)

Mistletoe lectin B3 variant protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

lymphokine-producing macrophage; uncontrolled cell growth; treatment;

cancer; cytotoxicity; antigen; isoform; lectin B3.

Viscum album.

DE19804210-AL.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Welters P;

WPI; 1999-445335/38.

N-PSDB; AA009118.

Preparation of mistletoe lectins in heterologous systems.

Particularly for use as anticancer agents and immunostimulants

Disclosure; Fig 16B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments

which have antitumour and immunostimulatory activity. The A-chain (MIA)

of the mistletoe lectin binds to, and inactivates, the 28S subunit of

ribosomes. Non-cytotoxic forms of (I) activate T-cell and its

lymphokine-producing macrophages, so stimulate immunity. (I) and its

fragments are used to treat uncontrolled cell growth (particularly

of tumour-associated bacterial or viral). The method allows production of the

immune response, particularly to a co-administered antigen

mistletoe lectin, and its individual chains, in many different isoforms

and on a large scale, at any time of the year. Recombinant products are

free from toxins present in natural mistletoe extracts. This sequence

represents a fragment of a variant mistletoe lectin B3 protein.

XV	Mistletoe; galactose-recognising mistletoe lectin; MLIII.
XX	Viscum album.
XS	Key
XT	Location/Qualifiers
XX	Misc-difference 223 /note= "Encoded by ATG"
FT	Misc-difference 251 /note= "Encoded by TTT"
FT	Misc-difference 314 /note= "Encoded by TCG"
FT	Misc-difference 380 /note= "Encoded by GCC"
FT	Misc-difference 448 /note= "Encoded by GTC"
XX	Misc-difference 498 /note= "Encoded by GTG"
XX	DE10044027.AL.
PN	14-NMR-2002.
PD	06-SEP-2000; 2000DB-1044027.
PE	06-SEP-2000; 2000DB-1044027.
PF	06-SEP-2000; 2000DB-1044027.
PG	(VISC-) VISCUM AG.
PA	Kieff S;
PI	WPI; 2002-316737/36.
DR	N-FSDB; AB556947.
DR	New nucleic acid encoding preprotein of mistletoe lectin, useful as diagnostic and therapeutic agents, also encodes polypeptide -
PT	diagnostic and therapeutic agents, also encodes polypeptide -
PS	Claim 1; Fig 1; 6pp; German.
XX	The invention relates to a nucleic acid molecule (AB556947) that encodes a preprotein (AB579450) which, after maturation, has the biological activity of the galactose-recognising mistletoe lectin (MLIII). The MLIII encodes nucleic acid molecule, primers specific to it or combination of them, a recombinant protein, polypeptides are useful as diagnostic and therapeutic agents.
XX	Sequence 551 AA:
SQ	83.3%; Score 2187; DB 23; Length 551; Best Local Similarity 83.6%; Pred. NO. 3,46-233; Matches 429; Conservative 14; Mismatches 62; Indels 8; Gaps 3
OY	1 YERLAVNHTOTCDIEPFIITLADVVSSGSFNEIPALRSTIPLSDQRFVELIN 50
DY	34 YERLAVNHTOTCDIEPFIITLADVVSSGSFNEIPALRSTIPLSDQRFVELIN 93
OY	61 QGGSDXTRALDVTMXYVAYVAGDQSYFLSDAPRGAEHLTQTTRRSSLEPYGSYDL 120
DY	94 QGGSDXTRALDVTMXYVAYVAGDQSYFLSDAPRGAEHLTQTTRRSSLEPYGSYDL 151
OY	121 ERKAGHDOIFGLXLTLSYSLAKXSGGTQASGITLIITOMSGRAAPILIRKXO 180
DY	152 ERKAGHDOIFGLXLTLSYSLAKXSGGTQASGITLIITOMSGRAAPILIRKXO 211
OY	181 XINSCKSFLEDVYMLELFTSWGQOSTVOQSSTDGVFNFRISLAISTGFVLSTNRDVA 240
DY	212 XINSCKSFLEDVYMLELFTSWGQOSTVOQSSTDGVFNFRISLAISTGFVLSTNRDVA 271
OY	241 SLALNFPGCSSESSSVNVEYLTPIT-----ADDTCAASPTVRVYGKXGWYXR 295
DY	272 SLALNFPGCSSESSSVNVEYLTPITRNSGADVDTCAASPTVALIGNDGLCYDR 331
OY	332 DDDFDNDQLOLMGSKANDPNQLMTIKEDXTIRSNGLCTTGTYTAQVWIMPKCIV 355
DY	356 DDDFDNDQLOLMGSKANDPNQLMTIKEDXTIRSNGLCTTGTYTAQVWIMPKCIV 391

Qy	356	RLATLMQIMXKXGILLINPSNMLVAASGIGKOTLLVLTGLVYLGAGLNGNDAPAEVTL	415
Dy	352	RLATLMQIMXGILLINPSNMLVAASGIGKOTLLVLTGLVYLGAGLNGNDAPAEVTL	451
Qy	416	YGFEDLDMESKXSVWETVCASQALXKXALVIGGSTRIRKNDQCLTKSRNSVSTYL	475
Dy	412	YGFEDLDMESKXSVWETVCASQALXKXALVIGGSTRIRKNDQCLTKSRNSVSTYL	510
Qy	476	IYSCSXKXKXORVVFEMEXKXILNIXXXXXXVLA 508	
Dy	511	IYSCSXKXKXORVVFEMEXKXILNIXXXXXXVLA 543	
RESULT 9			
AA125987	AA125987 standard; Protein: 264 AA.		
AA125987	AA125987		
DT	18-OCT-1999	(first entry)	
Dx	Mistletoe lectin B2 protein fragment.		
Kx	Mistletoe lectin; antitumor; immunostimulant; A-chain; WLA; immunity;		
Ky	lysozyme 28S subunit; non-cytotoxic; T-cell activation; immunostim;		
Kz	lymphokine-producing macrophages; T-cell activation; immunostim;		
Kx	cancer; cytotoxicity; antigen; isoform; lectin B2.		
Cs	Viscum album.		
Cx	DEJ9804210-A1.		
FD	12-AUG-1999.		
FE	03-FEB-1998; 98DE-1004210.		
FX	03-FEB-1998; 98DE-1004210.		
FX	(BIOS-) BIOSYN AKZHEMITTEL GMBH.		
PI	Morris P, Stiefel T, Voelter W, Welters P;		
DR	WPI; 1999-445335/38.		
DR	N-PSDB; AA209111.		
FX	Preparation of mistletoe lectins in heterologous systems.		
FX	particularly for use as anticancer agents and immunostimulants		
FX	Claim 9; Fig 9B; 78p; German.		
Cc	This invention describes a novel mistletoe lectin (1) and its fragments		
Cc	which have antitumor and immunostimulatory activity. The A-chain (WLA)		
Cc	of the mistletoe lectin binds to, and inactivates, the 28S subunit of		
Cc	ribosomes. Non-cytotoxic forms of (1) activate T-cell and its		
Cc	lymphokine-producing macrophages, so stimulate immunity. (1) and its		
Cc	fragments are used to treat uncontrolled cell growth. The strength of the		
Cc	fragments is determined primarily to a covalently administered antigen		
Cc	(immun-associated, bacterial or viral). The method allows production of		
Cc	mistletoe lectin, and its individual chains, in many different isoforms		
Cc	and on a large scale, at any time of the year. Recombinant products are		
Cc	free from toxins present in natural mistletoe extracts. This sequence		
Cc	represents a fragment of a mistletoe lectin B2 protein.		
SQ	Sequence 264 AA:		
Query Match	49.28;	Score 1291;	DB 20; Length 264;
Best Local Similarity	92.44;	Pred. No. 2.7e-134;	
Matches 243;	Conservative 0;	Mismatches 20;	Indels 0; Gaps 0
271	DVTYCSABEPTVYRKKKKVVDDEPDNDQIQAMPSSKNNPDNLTKRKYRYS 330		
1	DVTYCSABEPTVYRKKKKVVDDEPDNDQIQAMPSSKNNPDNLTKRKYRYS 60		

Query Match 95.4%; Score 2504.5; DB 18; Length 564;  
 Best Local Similarity 91.7%; Pred. No. 2.2e-268;  
 Matches 489; Conservative 2; Mismatches 39; Indels 3; Gaps 2;

DB 1 YERLALRTHTTCKRFRITTLADVTSSSSSSENFILRSGSTIPYDAQRVLYETN 60  
 34 YERLALRTHTTCKRFRITTLADVTSSSSSSENFILRSGSTIPYDAQRVLYETN 93  
 QY 61 QGSDXTALIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTRDRSSLPFGSYXDL 120  
 DB 94 QGSDXTALIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTRDRSSLPFGSYXDL 151  
 QY 121 ERYAGHDQIPLGIXQLQSYVALRXPQGSTKQARSLILLOMISAAENPILMRXQ 180  
 DB 152 ERYAGHDQIPLGIXQLQSYVALRXPQGSTKQARSLILLOMISAAENPILMRXQ 211  
 QY 181 XINGSGSLPQXVMELETSWQSGTQVGHSTIGVFNPFRLAIPQGVTLINVEDVIA 240  
 DB 212 YINGSGSLPQXVMELETSWQSGTQVGHSTIGVFNPFRLAIPQGVTLINVEDVIA 271  
 QY 241 SLALMFPVCGERSSSDVRYWPLVIRPVADVTCSASEPTVRIYGVKXKXVDVDDDFH 300  
 DB 272 SLALMFPVCGERSSSDVRYWPLVIRPVADVTCSASEPTVRIYGVKXKXVDVDDDFH 331  
 QY 301 DGNQOLMPSKSNNDPNQMLTRKDXTISNSGCLTTCGTAAGVYVLPDCTNAPRNT 360  
 DB 332 DGNQOLMPSKSNNDPNQMLTRKDXTISNSGCLTTCGTAAGVYVLPDCTNAPRNT 391  
 QY 361 MOIWKNGTINPRSNVLAASGDKGTLLVQGLDVTLAGQMLANDPAPREVTIYGRD 420  
 DB 392 MOIWKNGTINPRSNVLAASGDKGTLLVQGLDVTLAGQMLANDPAPREVTIYGRD 451  
 QY 421 LCHESNGSVWVETCSQXKXKXALYDGSIRPQNDQCLTXGDSVTVINIVSCS 480  
 DB 452 LCHESNGSVWVETCSQXKXKXALYDGSIRPQNDQCLTXGDSVTVINIVSCS 510  
 QY 481 XSGXGKRWFTNEXALITLXXXXXDDVAQANFKALRIIYPAKGRKMWLFV 533  
 DB 511 AGSGGQWVFTNEGALILNKGMLANDVAQANFKALRIIYPAKGRKMWLFV 563

RESULT 7  
 AAW90127 standard; Protein; 564 AA.  
 ID AAW90127;  
 XX AAW90127;  
 DT 20-MAR-2003 (updated)  
 DT 30-APR-1999 (first entry)  
 XX  
 XX Mistletoe lectin prepro-protein.  
 DE Mistletoe lectin; Mu; transgenic plant; glycosylation;  
 KM Mu; mistletoe; lectin; Mu; transgenic plant; glycosylation;  
 KM dimer; immunotoxin; large-scale production; diagnosis; therapeutic;  
 XX cancer.  
 XX Viscum album.  
 OS  
 XX  
 XX EP84386-AL.  
 XX  
 PD 16-DEC-1998.  
 XX  
 XX 26-JUN-1995; 98EP-0105660.  
 XX  
 XX 26-JUN-1995; 95EP-0109949.  
 XX  
 XX 26-JUN-1995; 98EP-0105660.  
 PA (MADU) MADUS KOEHL AG.  
 XX  
 XX Baur A, Eck J, Lentzen H, Zinke H;  
 PI  
 XX WFI; 1999-026582/03.  
 DR

DR N-PSDB; AAW74182.  
 XX New transgenic plant expressing mistletoe lectin - useful for  
 FT producing recombinant lectin in e.g. cancer diagnosis and therapy  
 XX  
 XX Claim 1a; Fig 4c; 30pp; German.  
 XX  
 CC This invention describes a novel transgenic plant transformed with a  
 CC vector capable of encoding a mistletoe (Viscum album) lectin  
 CC preproprotein or a biologically active fragment. The specification  
 CC also describes a polypeptide produced by a plant where the polypeptide  
 CC exhibits at least one enzymatic modification other than the glycosylation  
 CC that occurs in Viscum album or the polypeptide is a fusion protein, a  
 CC mistletoe lectin polypeptide dimer and an immunotoxin comprising the  
 CC polypeptide or the polypeptide dimer. The plants are used for large-scale  
 CC production of mistletoe lectin for diagnostic or therapeutic purposes  
 CC using the method of the invention.  
 CC (Updated on 20-MAR-2003 to correct PF field.)  
 CC  
 XX  
 50 Sequence 564 AA;  
 Query Match 95.4%; Score 2504.5; DB 20; Length 564;  
 Best Local Similarity 91.7%; Pred. No. 2.2e-268;  
 Matches 489; Conservative 2; Mismatches 39; Indels 3; Gaps 2;

DB 1 YERLALRTHTTCKRFRITTLADVTSSSSSSENFILRSGSTIPYDAQRVLYETN 60  
 34 YERLALRTHTTCKRFRITTLADVTSSSSSSENFILRSGSTIPYDAQRVLYETN 93  
 QY 61 QGSDXTALIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTRDRSSLPFGSYXDL 120  
 DB 94 QGSDXTALIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTRDRSSLPFGSYXDL 151  
 QY 94 QGSDXTALIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTRDRSSLPFGSYXDL 180  
 DB 121 ERYAGHDQIPLGIXQLQSYVALRXPQGSTKQARSLILLOMISAAENPILMRXQ 211  
 QY 152 ERYAGHDQIPLGIXQLQSYVALRXPQGSTKQARSLILLOMISAAENPILMRXQ 240  
 DB 181 XINGSGSLPQXVMELETSWQSGTQVGHSTIGVFNPFRLAIPQGVTLINVEDVIA 271  
 QY 212 YINGSGSLPQXVMELETSWQSGTQVGHSTIGVFNPFRLAIPQGVTLINVEDVIA 300  
 DB 241 SLALMFPVCGERSSSDVRYWPLVIRPVADVTCSASEPTVRIYGVKXKXVDVDDDFH 331  
 QY 272 SLALMFPVCGERSSSDVRYWPLVIRPVADVTCSASEPTVRIYGVKXKXVDVDDDFH 360  
 DB 301 DGNQOLMPSKSNNDPNQMLTRKDXTISNSGCLTTCGTAAGVYVLPDCTNAPRNT 391  
 QY 332 DGNQOLMPSKSNNDPNQMLTRKDXTISNSGCLTTCGTAAGVYVLPDCTNAPRNT 420  
 DB 361 MOIWKNGTINPRSNVLAASGDKGTLLVQGLDVTLAGQMLANDPAPREVTIYGRD 451  
 QY 392 MOIWKNGTINPRSNVLAASGDKGTLLVQGLDVTLAGQMLANDPAPREVTIYGRD 480  
 DB 421 LCHESNGSVWVETCSQXKXKXALYDGSIRPQNDQCLTXGDSVTVINIVSCS 510  
 QY 452 LCHESNGSVWVETCSQXKXKXALYDGSIRPQNDQCLTXGDSVTVINIVSCS 533  
 DB 481 XSGXGKRWFTNEXALITLXXXXXDDVAQANFKALRIIYPAKGRKMWLFV 563  
 QY 511 AGSGGQWVFTNEGALILNKGMLANDVAQANFKALRIIYPAKGRKMWLFV 563

RESULT 8  
 ABB79450 standard; Protein; 561 AA.  
 ID ABB79450;  
 XX ABB79450;  
 DT 08-JUL-2002 (first entry)  
 DT  
 XX Galactose-recognition mistletoe lectin.  
 XX  
 XX



XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX  
 PS Claim 40: Page 37-38; 78pp; German.  
 XX  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MEA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant isoforms  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a consensus sequence of the mistletoe lectin described in the  
 CC specification.  
 CC  
 XX  
 XX Sequence 533 AA:

Query Match 96.1%; Score 2524.5; DB 20; Length 533;  
 Best Local Similarity 99.6%; Pred. No. 1,2e-270;  
 Matches 531; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

1 YERLRIRVHTQTKKREYRFTLLRDYVSSGSFSNRIPLRSGTIVSDAKQRFVLELN 60  
 1 YERLRIRVHTQTKKREYRFTLLRDYVSSGSFSNRIPLRSGTIVSDAKQRFVLELN 60  
 61 QGXQSTALIDVNNXVVAQAGDSYFLAPAGAEHLFTGTRDRSSLPFGSYXDL 120  
 61 QGXQSTALIDVNNXVVAQAGDSYFLAPAGAEHLFTGTRDRSSLPFGSYXDL 119  
 121 ERYAGHRDQIFLGIXOLIOSVYALRPGSSTXQARSILLIOWISEAARFPIIMRXQ 180  
 120 ERYAGHRDQIFLGIXOLIOSVYALRPGSSTXQARSILLIOWISEAARFPIIMRXQ 179  
 181 XINSKSFPLPXWLETSWQSGSTOVQHSITGVNPFRLAIKXGNVTLNRYXIA 240  
 180 XINSKSFPLPXWLETSWQSGSTOVQHSITGVNPFRLAIKXGNVTLNRYXIA 239  
 241 SLATMLFVCGERSSSDVRYWLVIRPVJADVYCSAEPTVRIYGRXQGVURDDPH 300  
 240 SLATMLFVCGERSSSDVRYWLVIRPVJADVYCSAEPTVRIYGRXQGVURDDPH 299  
 301 DENOIQAMPKSNDDPQWLTTRDXTIRNSGCLTGYGYAAVYVMTDQNAVRENTI 360  
 300 DENOIQAMPKSNDDPQWLTTRDXTIRNSGCLTGYGYAAVYVMTDQNAVRENTI 359  
 361 MOIWKNGTIINPSNVLVAASGSKITTLVQTLDTLGGWLAGNDTAPREVTIYGRD 420  
 360 MOIWKNGTIINPSNVLVAASGSKITTLVQTLDTLGGWLAGNDTAPREVTIYGRD 419  
 421 LCMBSNKGSVWVETCKSSQONXQXWALYDGSIRPQONQOCLTXGRDSVSTVINVSCS 480  
 420 LCMBSNKGSVWVETCKSSQONXQXWALYDGSIRPQONQOCLTXGRDSVSTVINVSCS 479  
 481 XKSXKQWVFTNEKAILMKXXXXXXVQANPKRLRIITPATKPNQWMLPV 533  
 480 XKSXKQWVFTNEKAILMKXXXXXXVQANPKRLRIITPATKPNQWMLPV 532

RESULT 4  
 AA25979  
 ID AA25979 standard; Protein; 531 AA.  
 XX  
 AC AA25979;  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Mistletoe lectin I protein fragment.

XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MEA; immunity;  
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin I.  
 CC  
 CC Vascum album.  
 XX  
 XX DE19804210-21.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 XX Morris F. Stiefel T. Woeller W. Walters P;  
 XX  
 XX NFI: 1999-44535/38.  
 XX  
 XX N-PDB; AA209103.  
 XX  
 XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX  
 PS Claim 7; Fig 18; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MEA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a mistletoe lectin I protein fragment.

Query Match 95.9%; Score 2518.5; DB 20; Length 531;  
 Best Local Similarity 92.3%; Pred. No. 5.5e-270;  
 Matches 492; Conservative 0; Mismatches 38; Indels 3; Gaps 2;

1 YERLRIRVHTQTKKREYRFTLLRDYVSSGSFSNRIPLRSGTIVSDAKQRFVLELN 60  
 1 YERLRIRVHTQTKKREYRFTLLRDYVSSGSFSNRIPLRSGTIVSDAKQRFVLELN 60  
 61 QGXQSTALIDVNNXVVAQAGDSYFLAPAGAEHLFTGTRDRSSLPFGSYXDL 120  
 61 QGXQSTALIDVNNXVVAQAGDSYFLAPAGAEHLFTGTRDRSSLPFGSYXDL 118  
 121 ERYAGHRDQIFLGIXOLIOSVYALRPGSSTXQARSILLIOWISEAARFPIIMRXQ 180  
 120 ERYAGHRDQIFLGIXOLIOSVYALRPGSSTXQARSILLIOWISEAARFPIIMRXQ 178  
 181 XINSKSFPLPXWLETSWQSGSTOVQHSITGVNPFRLAIKXGNVTLNRYXIA 240  
 180 XINSKSFPLPXWLETSWQSGSTOVQHSITGVNPFRLAIKXGNVTLNRYXIA 238  
 241 SLATMLFVCGERSSSDVRYWLVIRPVJADVYCSAEPTVRIYGRXQGVURDDPH 300  
 240 SLATMLFVCGERSSSDVRYWLVIRPVJADVYCSAEPTVRIYGRXQGVURDDPH 298  
 301 DENOIQAMPKSNDDPQWLTTRDXTIRNSGCLTGYGYAAVYVMTDQNAVRENTI 360  
 300 DENOIQAMPKSNDDPQWLTTRDXTIRNSGCLTGYGYAAVYVMTDQNAVRENTI 358  
 361 MOIWKNGTIINPSNVLVAASGSKITTLVQTLDTLGGWLAGNDTAPREVTIYGRD 420

Db 61 GQXSNKALDVTNXXVYVAKQGGQSYFLADPRAGATHLFGTTR-XESLFFKSGSYDL 119  
Qy 121 ERYAGHRDIPILGIXOLIOSVAKLXPGSGTRKQASILLIOMISEAARPNFILMEXQ 180  
Db 120 ERYAGHRDIPILGIXOLIOSVAKLXPGSGTRKQASILLIOMISEAARPNFILMEXQ 179  
Qy 181 XINSKXSLPDXWLELETSNQSQSTQVQSHSTGVFNPRLALIKXNPVTIANVXYIA 240  
Db 180 XINSKXSLPDXWLELETSNQSQSTQVQSHSTGVFNPRLALIKXNPVTIANVXYIA 239  
Qy 241 SLATMLFVCGRRPSSSDVRWPLVRPVIADVTCSASEPTVRIYVXKCMQVDRDDPF 299  
Db 240 SLATMLFVCGRRPSSSDVRWPLVRPVIADVTCSASEPTVRIYVXKCMQVDRDDPF 299  
Qy 301 DGNQIOLMPSKSNNDPQIWTIKRDXIRKNGSLCTVYTGAGVYVAFEDCNVREXAT 360  
Db 300 DGNQIOLMPSKSNNDPQIWTIKRDXIRKNGSLCTVYTGAGVYVAFEDCNVREXAT 359  
Qy 361 WQWNGTINRSNLVLAASGKGTLYVQTLDTTGGMLAGNDVAPREPTIYGRD 420  
Db 360 WQWNGTINRSNLVLAASGKGTLYVQTLDTTGGMLAGNDVAPREPTIYGRD 419  
Qy 421 LCMENKGSWVETWCSSQXQXWALYQPSIPKQNOQCLITGRDSTVNTIVSCS 480  
Db 420 LCMENKGSWVETWCSSQXQXWALYQPSIPKQNOQCLITGRDSTVNTIVSCS 479  
Qy 481 XSGXQXWVETEXALINLKKXXXDVAQANPKLRILITYPATGKQWMLPV 533  
Db 480 XSGXQXWVETEXALINLKKXXXDVAQANPKLRILITYPATGKQWMLPV 532

## RESULT 2

XN125976  
XN125976 standard; protein; 533 AA.XN125976;  
AA125976;

18-OCT-1999 (first entry)

DE Mistletoe lectin protein consensus sequence 3.

XX Mistletoe, lectin; antitumor; immunostimulant; A-chain; MHA; immunity;  
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isotoxin.  
XX  
XX  
OS Viscum album.

FH Key Location/Qualifiers

FT Misc-difference 15 /label= Asp, Gln  
FT Misc-difference 63 /label= Gly, Gln  
FT Misc-difference 66 /label= Ile, Val  
FT Misc-difference 7 /label= Leu, Ala  
FT Misc-difference 107 /label= Asp, none  
FT Misc-difference 113 /label= Aen, Thr  
FT Misc-difference 117 /label= Pro, Thr  
FT Misc-difference 134 /label= Asp, Gln  
FT Misc-difference 141 /label= Ser, Thr  
FT Misc-difference 145 /label= Phe, Tyr  
FT Misc-difference 152 /label= Thr, Ala  
FT Misc-difference 177

FT /label= Ala, Tyr  
FT Misc-difference 180 /label= Tyr, Asp  
FT Misc-difference 185 /label= Ala, Gln  
FT Misc-difference 191 /label= Val, Met  
FT Misc-difference 218 /label= Ile, Phe  
FT Misc-difference 224 /label= Pro, Ser  
FT Misc-difference 225 /label= Pro, Thr  
FT Misc-difference 232 /label= Thr, Ser  
FT Misc-difference 236 /label= Asp, Ser  
FT Misc-difference 287 /label= Aen, Ser  
FT Misc-difference 290 /label= Cys, Arg  
FT Misc-difference 325 /label= Gly, Aen  
FT Misc-difference 364 /label= Gly, Asp  
FT Misc-difference 426 /label= Gly, Gln  
FT Misc-difference 435 /label= Val, Asp  
FT Misc-difference 439 /label= Gln, Lys  
FT Misc-difference 442 /label= Gly, none  
FT Misc-difference 443 /label= Arg, Lys  
FT Misc-difference 464 /label= Cys, Ser, Val  
FT Misc-difference 480 /label= Ala, Gly  
FT Misc-difference 481 /label= Gly, Ala  
FT Misc-difference 483 /label= Ser, Gly  
FT Misc-difference 484 /label= Gly, Ser  
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FT Misc-difference 500 /label= Asp, Ser, Thr, Lys  
FT Misc-difference 501 /label= Ser, Gly  
FT Misc-difference 502 /label= Leu, Pro  
FT Misc-difference 503 /label= Ala, Met  
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XX DB19804210-A1.  
XX 12-AUG-1999.  
XX 03-FEB-1998; 98DE-1004210.  
XX 03-FEB-1998; 98DE-1004210.  
XX (BIOG-) BIOSYN ARZENIMITTEL CMRH.  
XX Morris P, Stiefel T, Voelker W, Welters P,  
XX MPI; 1999-44535/38.  
XX DR



RESULT 2  
 AA125973 standard; protein; 533 AA.  
 AA125973;  
 AA125973;  
 18-OCT-1999 (first entry)  
 Mistletoe lectin protein consensus sequence 2.  
 Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;  
 ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 cancer; cytotoxicity; antigen; isoform.  
 Viscum album.  
 Key Location/Qualifiers  
 Misc-difference 15 /label= Asp, Glu  
 Misc-difference 63 /label= Gly, Glu  
 Misc-difference 66 /label= Ile, Val  
 Misc-difference 75 /label= Leu, Ala  
 Misc-difference 107 /label= Asp, Arg, none  
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 Misc-difference 134 /label= Asp, Glu  
 Misc-difference 141 /label= Ser, Thr  
 Misc-difference 145 /label= Phe, Tyr  
 Misc-difference 152 /label= Thr, Ala  
 Misc-difference 177 /label= Ala, Tyr  
 Misc-difference 180 /label= Tyr, Asp  
 Misc-difference 185 /label= Ala, Glu  
 Misc-difference 191 /label= Val, Met  
 Misc-difference 219 /label= Ile, Phe  
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 FT Misc-difference 464 /label= Arg, Lys  
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 FT Misc-difference 502 /label= Ser, Gly  
 FT Misc-difference 502 /label= Leu, Pro  
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 FT Misc-difference 504 /label= Met, Val  
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 FT DE19804210-AL.  
 FT 12-AUG-1999.  
 FT 03-FEB-1998; 98DE-1004210.  
 FT 03-FEB-1998; 98DE-1004210.  
 FT 03-FEB-1998; 98DE-1004210.  
 FT (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 FT Morris P, Stiefel T, Voelker W, Wellers P;  
 FT WPT; 1999-44535/38.  
 FT Preparation of mistletoe lectins in heterologous systems,  
 FT particularly for use as anticancer agents and immunostimulants  
 FT Claim 4; Page 28-29; 78bp; German.  
 PS This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumor and immunostimulatory activity. The A-chain (MA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a consensus sequence of the mistletoe lectin described in the  
 CC specification.  
 XX Sequence 533 AA;  
 SQ  
 Query Match 96.1%; Score 2524.5; DB 20; Length 533;  
 Best Local Similarity 99.6%; Pwd No. 12e-270;  
 Matches 531; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 YERLRARPTQGTGKEFFFTLLRDYVSSGSPNRPILRQSTIPVSDAQRVAVELTN 60  
 DB 1 YERLRARPTQGTGKEFFFTLLRDYVSSGSPNRPILRQSTIPVSDAQRVAVELTN 60  
 QY 61 QGMDXTRALDVMNVVAVYQAGDSYFLDAPRQGRGTHLFGTTRDSLPFXGSYXDL 120

Thu Dec 11 16:09:55 2003

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FT	Misc-difference	141	/label= Ser, Thr
FT	Misc-difference	145	/label= Phe, Tyr
FT	Misc-difference	154a	/label= Thr, Ala
FT	Misc-difference	177	/label= Ala, Tyr
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FT	Misc-difference	191	/label= Val, Met
FT	Misc-difference	219	/label= Ile, Phe
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FT	Misc-difference	439	/label= Glu, Lys
FT	Misc-difference	442	/label= Gly or none
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FT	Misc-difference	500	/label= Asn, Ser, Thr, Lys
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FT	Misc-difference	503	/label= Ala, Met
FT	Misc-difference	504	/label= Met, Val
FT	Misc-difference	533	/label= Pro, Phe
XX	DE:9804210-AL1		
XX	12-ANG-1999.		
XX			

GenCore version 5.1.6  
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OM protein - protein search, using fw model

Run on: December 11, 2003, 13:53:18 : Search time 52.7657 Seconds

[without alignments]  
1606.345 Million cell updates/sec

Title: US-09-601-667c-40

Perfect score: 2626

Sequence: 1 YERLRNRYHTGTXEYFRF.....RRILYPAKRNQMLPVX 534

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the hit being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2624.5	96.1	533	20	AA192970
2	2624.5	96.1	533	20	AA192972
3	2624.5	95.9	531	20	AA192973
4	2618.5	95.9	531	20	AA192982
5	2618.5	95.9	532	20	AA192982
6	2604.5	95.4	564	18	AA191021
7	2604.5	95.4	564	20	AA191027
8	2187	83.3	551	23	AA1979450
9	1291	49.2	264	20	AA192997

10	1291	49.2	264	20	AA192998	Mistletoe lectin B
11	1291	49.2	265	20	AA192994	Mistletoe lectin B
12	1291	49.2	265	20	AA192993	Mistletoe lectin B
13	1290	49.1	264	20	AA192986	Mistletoe lectin B
14	1290	49.1	264	20	AA192990	Mistletoe lectin B
15	1290	49.1	265	20	AA192996	Mistletoe lectin B
16	1290	49.1	265	20	AA192992	Mistletoe lectin B
17	1289	49.1	264	20	AA192992	Mistletoe lectin B
18	1289	49.1	264	20	AA192992	Mistletoe lectin B
19	1286	48.0	264	20	AA192978	Mistletoe lectin B
20	1286	48.0	264	20	AA192972	Mistletoe lectin B
21	1286	48.0	264	20	AA192975	Mistletoe lectin B
22	1277.5	48.6	264	20	AA192985	Mistletoe lectin B
23	1277.5	48.6	264	20	AA192991	Mistletoe lectin B
24	1267.5	48.3	263	19	AA196462	Mistletoe RMB var
25	1267.5	48.3	264	18	AA191023	Prepro mistletoe I
26	1267.5	48.3	264	19	AA190126	Mistletoe Wt B-cha
27	1267.5	48.3	267	19	AA196460	Mistletoe RMB pro
28	1229.5	46.8	576	18	AA192987	Castrolean lectin
29	1229.5	46.8	576	21	AA195892	Castrolean lectin
30	1229.5	46.8	576	21	AA195892	Castrolean lectin
31	1229.5	46.8	576	21	AA195892	Castrolean lectin
32	1229.5	46.8	576	22	AA1978301	Castrolean lectin
33	1229.5	46.8	576	22	AA1978302	Castrolean lectin
34	1228.5	46.8	565	6	AA190166	Sequence of prepro
35	1228.5	46.8	565	22	AA1978300	Sequence of prepro
36	1222.5	46.6	574	9	AA197025	Sequence of Ricin
37	1222.5	46.6	574	9	AA197025	Sequence of Ricin
38	1219.5	46.5	563	22	AA1978304	Sequence of Ricin
39	1213.5	46.2	576	8	AA190326	Sequence of Ricin
40	1194	45.5	256	20	AA192981	Mistletoe lectin A
41	1194	45.5	256	20	AA192984	Mistletoe lectin A
42	1193.5	45.4	267	19	AA196467	Mistletoe RMB pro
43	1180.5	45.0	562	10	AA199079	Ricin D, Ricinus
44	1165	44.4	254	20	AA192980	Mistletoe lectin A
45	1165	44.4	254	20	AA192983	Mistletoe lectin A

#### ALIGNMENTS

RESULT 1  
ID: AA192970 standard; protein; 533 AA.  
AA192970:

19-OCT-1999 (first entry)

Mistletoe lectin protein consensus sequence 1.

Mistletoe lectin; antitumor; immunostimulant; A-chain; MAb; immunity;  
ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
cancer; cytotoxicity; antigen; isoform.

viscum album.

viscum album.

viscum album.

viscum album.

viscum album.

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viscum album.

viscum album.

viscum album.

viscum album.

Query Match		37.2%	Score 977	DB 10	Length 251
Best Local Similarity		80.6%	Pred. No. 1, 35-91		
Matches 203		Conservative 7	Mismatches 36	Indels 6	Gaps 3
QY	1	YERLRVYHCTGKXEFRRPTLLADYSSGSPFNEIFLRQSTIPVSDAORFYLVELTN	60		
DB	1	YERLRVYHCTGDEYERFPKILRDSVSSGSPFNDIDILPFS-IPVSSAORFYLVELTN	59		
QY	61	Q---GDVXKALDVTNKYVAYOXGDSYFLRDAPRGATLHFTGTRDSSSLPFXSY	117		
DB	60	QGRKEDSTIKADIVNDFVVAIQGDSIFLRDAPDGRSHLFTGTT--RSSLPNSSY	117		
QY	118	XDLERYAGHRQIFLGIXQLIQSVALKXPGSTRXQARSLILQWISGARPNPILMR	177		
DB	118	ADLERVAGHRRIPLAREPLIRSVNLDYFGSTRQAQSSIIIVQWISGARPNPILMR	177		
QY	178	XROXINGXSEFDPDXMLELETSMGQOSTQVGHSTQGVFNNPYRLATXXGNFTLLANRX	237		
DB	178	ARQYINGGVSYLPDYVMLELMSMGQOSTQVQSTQGVFNNPRLGISTGNFWLSNTRD	237		
QY	238	VIASIATMLEFVC	249		
DB	238	VIASGIMVFC	249		

Search Completed: December 11, 2003, 14:01:06  
Job Time : 42.16 secs

RX MEDLINE-2156752; PubMed-11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RL Mol. Cells 13:215-220(2001).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.; to the EMBL/GenBank/DBJ databases.  
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADPOSOME ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: AF508915; AA046933.1; .  
 DR InterPro: IPR001574; RIF.  
 DR Pfam: PF00161; RIF; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 KW Hydrolase; Toxin.  
 FT NON\_TER 1  
 FT NON\_TER 249 1  
 SQ SEQUENCE 249 AA; 27821 MW; 3C5670F839BDAB5 CRC64;  
 Query Match 40.1%; Score 1054; DB 10; Length 249;  
 Best Local Similarity 83.9%; Pred No. 1.7e-99;  
 Matches 209; Conservative 13; Mismatches 25; Indels 2; Gaps 1;

QY 1 YERLRATVHTQCKEYFRITLLRDYSSSSSSNEFEELRQSTIPVSDAQRPVLYELRN 60  
 DB 1 YERLRATVHTQCKEYFRITLLRDYSSSSSSNEFEELRQSTIPVSDAQRPVLYELRN 60  
 QY 61 QGDSXTAIDVNTNYYAVAKGDSYFLRDAPRGAETHLFTGTDRSSSLPFGSYXDL 120  
 DB 61 QGDSXTAIDVNTNYYAVAKGDSYFLRDAPRGAETHLFTGTDRSSSLPFGSYXDL 120  
 QY 121 ERYAGROQELGICOLIOSVAPRPGSTYKQASIIILICWISGAAPNITMEXQ 180  
 DB 121 ERYAGROQELGICOLIOSVAPRPGSTYKQASIIILICWISGAAPNITMEXQ 180  
 QY 181 XINGSGSPDPXYMLETSSWQOQSTOVGSHSTGVFNNPRLATXXGNPTLLANRYA 240  
 DB 179 YISSGSPDPXYMLETSSWQOQSTOVGSHSTGVFNNPRLATXXGNPTLLANRYA 238  
 QY 241 SHATLFPVC 249  
 DB 239 SHATLFPVC 247

RESULT 14  
 OBLKO1 PRELIMINARY; PRT; 263 AA.  
 AC OBLKO1;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Lectin chain B isoform 3 (Fragment).  
 OS Viscum album subsp. coloratum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC NCBI\_TaxID=159976; Viscum.  
 RX MEDLINE-2156752; PubMed-11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RL Mol. Cells 13:215-220(2001).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RA EMBL: AF508915; AA046933.1; .  
 RA InterPro: IPR000772; Ricin B lectin.  
 DR Pfam: PF00652; Ricin B lectin, 6.  
 DR SMART: SM00458; RICIN; 2.  
 DR PROSITE: PS50231; RICIN\_B\_LECTIN; 2.  
 FT NON\_TER 1  
 FT NON\_TER 263 1  
 SQ SEQUENCE 263 AA; 29071 MW; 3F9C4AD860F051D CRC64;  
 Query Match 39.2%; Score 1029.5; DB 10; Length 263;  
 Best Local Similarity 21.5%; Pred No. 5.3e-97;  
 Matches 196; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

QY 271 DVTGASSEPTVIRYGRKXGVYDDPHDQIQCLPSSKNNDPQMLTKEDXTIRS 330  
 DB 1 DDTCTSEPTVIRYVGLNGLCVVHAKPHDGNPQLPCKSSTDRQMLTIRADGIRS 60  
 QY 331 NSGCLTYGTAVGYVMI FDCNANREANIIMQWNGIIPRSMVLAASSGKGTTLT 390  
 DB 61 NSGCLTYGTAVGYVMI FDCNANREANIIMQWNGIIPRSMVLAASSGKGTTLT 120  
 QY 391 VQTLDTYLQGMALNDTPRRTTYGFRDLCHNSKGSWVETTXSQXNXXALLYD 450  
 DB 121 VQGMALNDTPRRTTYGFRDLCHNSKGSWVETTXSQXNXXALLYD 179  
 QY 451 GSIRKQNDQCLNKRDSVTVIVYSCSXKXQRPVFTNKAIIILKXXXXXVQA 510  
 DB 180 GSIRKQNDQCLNKRDSVTVIVYSCSXKXQRPVFTNKAIIILKXXXXXVQA 239  
 QY 511 NPLRLRIIYPATGKPNMMLPV 533  
 DB 240 NPLRLRIIYPATGKPNMMLPV 262

RESULT 15  
 OBLKO1 PRELIMINARY; PRT; 251 AA.  
 AC OBLKO1;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Lectin chain A isoform 3 (EC 3.2.2.22) (RNA N-glycosidase)  
 OS Viscum album subsp. coloratum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC NCBI\_TaxID=159976; Viscum.  
 RX MEDLINE-2156752; PubMed-11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RL Mol. Cells 13:215-220(2001).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RL Mol. Cells 13:215-220(2001).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RL Mol. Cells 13:215-220(2001).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Papaverales; Fabaceae; Papilionoideae; Abreae; Abrus.  
 OC NCBI\_TaxID:3816;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=202902; PubMed=10636890;  
 RA Lin J.Y., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,  
 RT "Primary Structure and Function Analysis of the Abrus precipatoris  
 RT Agglutinin A Chain by Site-directed Mutagenesis: Prolyl of Amphiphilic  
 RT alpha-Helix H Impacts Protein Synthesis Inhibitory Activity.";  
 RL J. Biol. Chem. 275:1897-1901(2000).  
 CC -1- CATALYTIC ACTIVITY: ENDOPOLYMERASE OF THE N-GLYCOSIDIC BOND AT ONE  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC MEDLINE=210273; PubMed=828309.1;  
 DR HSB2; S1102; IPR000772; R1CIN\_B\_lectin.  
 DR Interpro: IPR000772; R1CIN\_B\_lectin.  
 DR Pfam: PF00652; R1CIN\_B\_lectin; 6.  
 DR Pfam: PF00652; R1CIN\_B\_lectin; 6.  
 DR PRINTS: PR00396; SHGARICIN.  
 DR SMART: SM00458; R1CIN\_2.  
 DR PROSITE: PS0231; R1CIN\_B\_lectin; 2.  
 DR PROSITE: PS0275; SHGA\_R1CIN; 1.  
 DR R1CINase; TcXan.  
 SQ SEQUENCE 547 AA; 61248 MW; 355A325C35A41BD CRC64;

Query Match 41.1%; Score 1079; DB 10; Length 547;  
 Best Local Similarity 43.7%; Pred. No. 1,4e-101;  
 Matches 234; Conservative 79; Mismatches 190; Indels 32; Gaps 10;

QY THGTGKRYFFITLLADYSSGSFSEPIPLRQSTIPYSDAKRFVLYELTNGKDXTA 68  
 DB TGSATPSYNOFTDLARKRTIGLALYQ-TPVLDPS-TVERKQYVYELSYDVSITOL 85  
 QY 69 AIDPTKRYVYAGAGSYETDAPGATFETCTTRKSLIPFGSYDLEKACH-R 127  
 DB 96 GIDLTNAVYVYRAGSSFFPKNPASSTYLTGCT--QQTSLPFGQVYDLEKMAQR 143  
 QY 128 DQIPGKXOLIGVYALAKXGSGTRKQASILLIQMISPAAREPILMKRQXINSQS 187  
 DB 144 ORISLGLAKNGIKETLRSQASDEDEIARTLVITQWVAARPRYVRKVLVISNRQA 203  
 QY 188 FLEPTKYLEETSMQOQSTVYHSTGCVFNNKELALIKKAFITLNNR- 237  
 DB 204 FQDPSLSEMTETEPISRYVHTVQCTF--PQN-----VLNTNAGERVYSSLSH 253  
 QY 238 -VIALSLALFPGCGRESSDTRWEVYRIVYADDTYCSAS-PPVYALVGRKXGQVDR 295  
 DB 254 PVSALALFPGCGRNATOS---PILIRSVYQSKTCSHYEPVYVIGRBLCYDVS 309  
 QY 296 DDEPHDNGIQLPFSKSNDDPQALITKDKTITRSNCSCTTYGTYAGYVMIPTCKTAV 355  
 DB 310 DVAHNNANFILLKACQDLQVAKLTLASDRTIRKSGCLTYGVAAGVYKLVYDSSAN 369  
 QY 356 REATITQWIKKGTINPNSVYLAASGIGKGTITVQCTDYLQCGALAGDPAAREVTI 415  
 DB 370 AATVYQITWDGTTINPESGLVLSNBSWGGLTIVQGDVYNNQGVATNDTSPVTSI 429  
 QY 416 YGFEDLQMSKXGVSWEYTCASQXQXWMLVYGSGTRKQNDQCTKGRSVSTVIN 475  
 DB 430 AGPFLQWAGHNSWMLDQVDTTTERD-QMAYVYPGSIRPVNTNNCLTGERKXGQVTV 488  
 QY 476 IYSCXKXKQKQRTFNEKALIANKXXXXVYQAMPEKRIIITPGRKQNM 530  
 DB 489 NMGSNNRMSQNRPRSGIINLMDWYNDYSSRSLQILNMYTIRNRM 543

RESULT 12  
 DBLMO2 PRELIMINARY; FRT; 263 AA.  
 ID QBLMO2

AC QBLMO2;  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Lactin chain B isoform 2 (fragment).  
 OS Lactum album subsp. coloratum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC NCBI\_TaxID:159976;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2156752; PubMed=1170524;  
 RA Park C.-H., Lee D.-W., Lee K.-H., Yoon T.-U., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mushroom (Lactum album coloratum).";  
 RL Mol. Cells 12:215-220(2001).  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Lee K.-H., Yoon T.-U., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF089318; AAM4636.1;  
 DR Interpro: IPR000772; R1CIN\_B\_lectin.  
 DR Pfam: PF00652; R1CIN\_B\_lectin; 5.  
 DR SMART: SM00458; R1CIN\_2.  
 DR PROSITE: PS0231; R1CIN\_B\_lectin; 2.  
 DR NON\_TER 263  
 FT NON\_TER 263  
 SQ SEQUENCE 263 AA; 23150 MW; B658C7C9C8D1F CRC64;

Query Match 40.4%; Score 1060.5; DB 10; Length 263;  
 Best Local Similarity 76.0%; Pred. No. 3.9e-100;  
 Matches 200; Conservative 19; Mismatches 43; Indels 1; Gaps 1;  
 QY 271 DPTVCSAPPTVTVGKXKXVYRDDPHFQNLQMLPESKSNDDPQALITKRXITRS 330  
 DB 1 DPTVCSAPPTVTVGKXKXVYRDDPHFQNLQMLPESKSNDDPQALITKRXITRS 330  
 QY 331 NSCLITVYAGVYVMIPTCKTAVREATTIQTQKNGTINPNSVYLAASGIGKGTIT 390  
 DB 61 NSCLITVYAGVYVMIPTCKTAVREATTIQTQKNGTINPNSVYLAASGIGKGTIT 390  
 QY 391 VQDTYTLQGLASNDPAAREVTIYGFEDLQMSKXGVSWEYTCASQXQXWMLVYGSG 450  
 DB 121 VQDTYTLQGLASNDPAAREVTIYGFEDLQMSKXGVSWEYTCASQXQXWMLVYGSG 450  
 QY 451 GSIRKQNDQCTKGRSVSTVINIYSCXKXKQKQRTFNEKALIANKXXXXVYQAM 510  
 DB 180 GSIRKQNDQCTKGRSVSTVINIYSCXKXKQKQRTFNEKALIANKXXXXVYQAM 510  
 QY 511 NPELSRIIITPGRKQNMILEV 533  
 DB 240 NPELSRIIITPGRKQNMILEV 262

RESULT 13  
 DBLMO5 PRELIMINARY; FRT; 249 AA.  
 AC QBLMO5;  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Lactin chain A isoform 2 (BC 3.2.2.22) (RNA N-glycosidase)  
 OS Lactum album subsp. coloratum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC NCBI\_TaxID:159976;  
 RN (1)  
 RP SEQUENCE FROM N.A.



RESULT 7  
 Q94BM5 PRELIMINARY; PRT; 581 AA.  
 ID Q94BM5, 2001 (TrEMBL), 19, Created  
 DT 01-DEC-2001 (TrEMBL), 19, Last annotation update  
 DT 01-MAR-2003 (TrEMBL), 23, Last annotation update  
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor  
 (EC 3.2.2.22) (RNA N-glycosidase).  
 OS Cinnamomum camphora (Camphor tree).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 NCBI\_TaxID=13429;  
 RX SOURCE FROM N.A.  
 RA Yang O, Gong Z Z, Liu W Y;  
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)  
 RT genes encoding cinnamomin proteins and study of their expression  
 RT patterns";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC EMBL: A039801; AA042458.1;  
 CC InterPro: IPR000777; R1CIN\_B\_lectin.  
 CC TrEMBL: A039801; R1CIN\_B\_lectin.  
 DR Pfam: PF00652; R1CIN\_B\_lectin, 5.  
 DR PRINTS: PR00161; R1P\_1.  
 DR SMART: SM00458; R1CIN, 2.  
 DR PROSITE: PS00231; R1CIN\_B\_lectin, 2.  
 DR Hydrolase; Signal; Toxin.  
 KW SIGNAL  
 FT CHAIN 1..581  
 FT POTENTIAL  
 FT CINNOMIN  
 FT CDS 1..581  
 SEQUENCE 581 AA; 64215 MW; 628242P0876078 CRCC4;  
 Query Match 45.5%; Score 1195; DB 10; Length 581;  
 Best Local Similarity 48.7%; Pred. No. 1.9e-113;  
 Matches 266; Conservative 70; Mismatches 184; Indels 26; Gaps 13;  
 QY 9 THQYTKAEYRFTLLADYVSSGSSSENPILRQSTTVSDNQPVYVETLNQKDS-X 66  
 DB 40 TKAKTKSYQTEILNAGLQSGSEHGLVFRERSTV--DKRFILVELSNMAHSEV 97  
 QY 67 TAAIVWYVYVAVAGQOSYPR-DAPKATHTLGTCTPSSGSPKSYGVYKARAG 125  
 DB 98 TLAVDTMAVVAVYKSGSFFRINDPDALEMLDPT--KYPFGSGYTLDEGTVG 155  
 QY 126 -HDDCPGLKICQSYALXRG-GSTRQAFSILILQWISSEAFNPILMXKQXIN 183  
 DB 156 EREBELILGMDPLEMALSILNINQOAPALSLIVYQWABVAFEFIEKRVAGSIS 215  
 QY 184 SGKSLPDXVLETSWGQSTQVQSTG-GVNPKKLAIXKQNTLVKNA-VYIAS 241  
 DB 216 PAKRFPDPNLSLEKMSALSNVQSGGVSSEVSLSTKPYVSGSDSTVSG 275  
 QY 242 LAIMLFVC--GSPSSDVYKWEIVRVLAD-----DYCSASEPTVAVYKXG 289  
 DB 276 LAIMLFICRSTRASSDQFIHMLMIRFIVVAVETADNDNDCCADDEPTVVISGNG 335  
 QY 290 MKIVVDPPDQNGQILWPKSKNDPQMLIKEDKTRNSGCLTVGTAGVYVIF 349  
 DB 336 LCVYVDEKNNNGPQLWPKCKNDPQMLIKEDKTRNSGCLTVGTAGVYVIF 385  
 QY 350 DQETANRATQIQWKTINRNSVYIAASGQKTLTVQDTLQGGNLAQNTA 409  
 DB 396 DQETPTASIQFMANGILINQSLVLSASGKPTLLVQNTIVASQGLAANTE 455  
 QY 410 PRVTVYGFRLCVESKSGSYWECKSSQXQKVALYKSGIRPKQND--CLTIGR 467  
 DB 456 PVTYSIVGFNDLCWQNGEDAMWVECESSKAO-KNALYPSGSIHPPQDGPACELDN 514

QY 468 DSVSTVNIWVSCXXKQRFVETKALINLKKXXXXVQAQNFKRLIIVYATQKN 527  
 DB 515 HPGSILITSSCSGSEBGRWVEMNDGTVLNGLWMDVKSNSPILHQLIHWATQKN 574  
 QY 528 QMILEY 533  
 DB 575 HEMLE 580  
 RESULT 8  
 ID Q06076 PRELIMINARY; PRT; 528 AA.  
 NC Q06076, 1996 (TrEMBL), 01, Created  
 DT 01-NOV-1996 (TrEMBL), 01, Last annotation update  
 DT 01-MAR-2003 (TrEMBL), 23, Last annotation update  
 DE Abtin-d (EC 3.2.2.22) (RNA N-glycosidase) (Fragment).  
 OS Abus precacorus (Indian licorice) (Fabaceae).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosida I; Fabales; Fabaceae; Papilionoideae; Abreae; Abus.  
 NCBI\_TaxID=3816;  
 RX SOURCE FROM N.A.  
 RA MEDLINE=911278; PubMed=642112; IAN J -Y;  
 RT "Structure of 'three distinct' isoforms determined by cDNA  
 RT sequencing: conservation and significance";  
 RL J. Mol. Biol. 229:263-267(1993).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC EMBL: M8346; AA03626.1;  
 CC HSP; P11140; IABR; R1CIN\_B\_lectin.  
 CC InterPro: IPR001574; R1CIN\_B\_lectin.  
 CC TrEMBL: M8346; R1CIN\_B\_lectin.  
 DR Pfam: PF00652; R1CIN\_B\_lectin, 6.  
 DR PRINTS: PR00161; R1P\_1.  
 DR SMART: SM00458; R1CIN, 2.  
 DR PROSITE: PS00231; R1CIN\_B\_lectin, 2.  
 DR PROSITE: PS00231; SHIGA\_R1CIN, 1.  
 DR Hydrolase; Toxin.  
 KW NON-TER  
 FT CHAIN 1..528  
 FT NON-TER  
 SEQUENCE 528 AA; 58870 MW; 628242P0876078 CRCC4;  
 Query Match 43.3%; Score 1137; DB 10; Length 528;  
 Best Local Similarity 46.0%; Pred. No. 1.5e-107;  
 Matches 242; Conservative 83; Mismatches 189; Indels 12; Gaps 9;  
 QY 9 THQYTKAEYRFTLLADYVSSGSSSENPILRQSTTVSDNQPVYVETLNQKDS-X 66  
 DB 9 TGAQSGYQTEFLNGLQSLTGLHDLVLPDT--TEERRRITVELSRSRSISV 66  
 QY 69 AIDVWYVYVAVAGQOSYPR-DAPKATHTLGTCTPSSGSPKSYGVYKARAG 127  
 DB 67 GIDVTVMAVVAVYKSGSFFRINDPDALEMLDPT--QVSLRDSYDLEEMAHQTR 124  
 QY 126 DQETLQKICQSYALXRG-GSTRQAFSILILQWISSEAFNPILMXKQXIN 184  
 DB 125 ERLSILQALTAISFREGSNDKARFLVLIQWSEAAVYCIENSVGSIKRTGA 184  
 QY 188 PLDPXVLETSWGQSTQVQSTGVPNPKRLAIXKQNTLVKNA-RVYIASLALNL 246  
 DB 185 PGPSPSSDVYKWEIVRVLADYVQVAFVYVLSINRQPVYDLSHPTVYVLEML 244  
 QY 247 PGPSPSSDVYKWEIVRVLADYVQVAFVYVLSINRQPVYDLSHPTVYVLEML 244  
 DB 245 PGNP--PKNAS--PILRSIVESKICSSAYEPTVIRIGRQGMGVYDVGYNQNR 300  
 QY 306 QUNBSKNDPQMLIKEDKTRNSGCLTVGTAGVYVIFDQNTAVRATIQWIX 365



NCBI\_TaxID=3988;  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=9238377; PubMed=1633311;  
 RA Roberts L.M., Tregear J.W., Lord J.N.;  
 RA Molecular cloning of Ricin B lectin.  
 RA J Biol Chem 267:11923-11927 (1992)  
 CC Catalytic activity: EC 3.2.1.163  
 CC -1- SIMILARITY: BELONGS TO THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: S40366; AA02282.1; -  
 DR HSP: P02879; IPR6.  
 DR InterPro: IPR000772; Ricin\_B\_lectin.  
 DR InterPro: IPR001574; RLP.  
 DR InterPro: IPR001400; Somatotropin.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam: PF00481; RLP; 1.  
 DR SMART: SM00456; RIGCANICIN.  
 DR SMART: SM00456; RIGCANICIN.  
 DR PROSITE: PS00231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE: PS00275; SHIGH\_RICIN; 1.  
 DR PROSITE: PS00338; SOMATOTROPIN\_2; 1.  
 KW Hydrolase; Toxin.  
 FT NON TER  
 SO SEQUENCE 541 AA; 60281 MW; 28782CDEF2E9D3 CRC64;  
 Query Match 46.8%; Score 1228.5; DB 10; Length 541;  
 Best Local Similarity 49.0%; Pred. No. 6,56-117; Indels 21; Gaps 12;  
 Matches 263; Conservative 78; Mismatches 175;  
 QY 9 THQTTQKYEFRITLADYSSGSESENIPLR-KSTIVSDQRFVLELNQGDGK 66  
 DB 13 TAGATVOSTNFIKARIGRLITGADVHDIPLRKYGLIN-QNFIIVLESLNALSIV 70  
 QY 67 TLAIDVYKVVAVYAGDQSGYFEL-DAPRGAE--THLTGTRDSSSLPXSXYDLERY 123  
 DB 71 TLADVYKVVAVYAGDQSGYFEL-DAPRGAE--THLTGTRDSSSLPXSXYDLERY 129  
 QY 124 AGR-RDQIFLGIXQLIGSYAL--KXFGSSTKQANSLILQWISPAAREPILNMX 179  
 DB 130 AGRLENTELNGHLEENISALYVSTGDTPLTARSPFICICOMISEAAREPILNMX 189  
 QY 180 QKINSKGFELPKYMLELFTNSGQOSTVQNSTDGVFNKXKLAIXKPFLLKXKXVI 239  
 DB 190 TRIRNRKADPDSVITLNSKSTSLQSSNQKSTSLQSSNQKSTSLQSSNQKSTSL 249  
 QY 240 ASIALMFLVCGERSSDVYVWYLPVYAD--DYTCASAEPTVAYGXKXVYDRO 296  
 DB 250 PIIADVYKAPPESSQ---PSLIIPFVNNRADV-CMDEPVIYVANGICVDRD 304  
 QY 297 DDFDGNQIQLPKSKNDVQMLTIRKXTIRSNGLTYYGTAGYVWIDCVNFA 356  
 DB 305 GRFHNSAIQLPKSKNDVQMLTIRKXTIRSNGLTYYGTAGYVWIDCVNFA 364  
 QY 357 EATMOWKNGTINRNSNYLAASGICGTLTQVLTPTTGQMLANDVAREVTV 416  
 DB 365 DATMOWKNGTINRNSNYLAASGICGTLTQVLTPTTGQMLANDVAREVTV 424  
 QY 417 GFRDLCHESNGSVWETCCSNGXKXWALYGGSGIFPKQNGOCICLFGDSDVYVNI 476  
 DB 425 GLYGLCLCHESNGSVWETCCSNGXKXWALYGGSGIFPKQNGOCICLFGDSDVYVNI 483  
 QY 477 VSCXKXKXQAVFNEXALINLKXXXXVAVQANPKLEIITTPATGPNQMLPV 533  
 DB 484 LSCGPKSGCQKXKXQAVFNEXALINLKXXXXVAVQANPKLEIITTPATGPNQMLPV 540

01-OCT-2002 (TribMrel. 22, last annotation update)  
 DE Type II ribosome-inactivating protein cinmammun (BC 3.2.2.22) (RNA  
 DE N-glycosidase) (Fragment)  
 OS Cinmammun camphora (Camphor tree)  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinmammun.  
 NCBI\_TaxID=11429;  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=9238377; PubMed=1633311;  
 RA Roberts L.M., Tregear J.W., Lord J.N.;  
 RA Molecular cloning of Ricin B lectin.  
 RA J Biol Chem 267:11923-11927 (1992)  
 CC Catalytic activity: EC 3.2.1.163  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: S40366; AA02282.1; -  
 DR HSP: P02879; IPR6.  
 DR InterPro: IPR000772; Ricin\_B\_lectin.  
 DR InterPro: IPR001574; RLP.  
 DR InterPro: IPR001400; Somatotropin.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 5.  
 DR Pfam: PF00481; RLP; 1.  
 DR SMART: SM00456; RIGCANICIN.  
 DR SMART: SM00456; RIGCANICIN.  
 DR PROSITE: PS00231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE: PS00275; SHIGH\_RICIN; 1.  
 DR PROSITE: PS00338; SOMATOTROPIN\_2; 1.  
 KW Hydrolase; Toxin.  
 FT NON TER  
 SO SEQUENCE 549 AA; 60648 MW; 02607E607CA4B0 CRC64;  
 Query Match 45.5%; Score 1196; DB 10; Length 549;  
 Best Local Similarity 48.7%; Pred. No. 1,48-113; Indels 26; Gaps 13;  
 Matches 266; Conservative 71; Mismatches 183;  
 QY 9 THQTTQKYEFRITLADYSSGSESENIPLR-KSTIVSDQRFVLELNQGDGK 66  
 DB 8 TKGITSTYQIIBALQALSGEHOIIVKESIVD--DSKFIIVLESLNALSIV 65  
 QY 67 TLAIDVYKVVAVYAGDQSGYFEL-DAPRGAE--THLTGTRDSSSLPXSXYDLERY 125  
 DB 66 TLADVYKVVAVYAGDQSGYFEL-DAPRGAE--THLTGTRDSSSLPXSXYDLERY 123  
 QY 126 -HRDQIFLGIXQLIGSYAL--KXFGSSTKQANSLILQWISPAAREPILNMX 183  
 DB 124 AGRLENTELNGHLEENISALYVSTGDTPLTARSPFICICOMISEAAREPILNMX 183  
 QY 180 QKINSKGFELPKYMLELFTNSGQOSTVQNSTDGVFNKXKLAIXKPFLLKXKXVI 239  
 DB 184 TRIRNRKADPDSVITLNSKSTSLQSSNQKSTSLQSSNQKSTSLQSSNQKSTSL 249  
 QY 240 ASIALMFLVCGERSSDVYVWYLPVYAD--DYTCASAEPTVAYGXKXVYDRO 296  
 DB 242 LAILMFLVCGERSSDVYVWYLPVYAD--DYTCASAEPTVAYGXKXVYDRO 296  
 QY 297 DDFDGNQIQLPKSKNDVQMLTIRKXTIRSNGLTYYGTAGYVWIDCVNFA 356  
 DB 299 DDFDGNQIQLPKSKNDVQMLTIRKXTIRSNGLTYYGTAGYVWIDCVNFA 356  
 QY 357 EATMOWKNGTINRNSNYLAASGICGTLTQVLTPTTGQMLANDVAREVTV 416  
 DB 350 EATMOWKNGTINRNSNYLAASGICGTLTQVLTPTTGQMLANDVAREVTV 416  
 QY 417 GFRDLCHESNGSVWETCCSNGXKXWALYGGSGIFPKQNGOCICLFGDSDVYVNI 476  
 DB 364 DCRPTKASIVQPRANGITINQSLVLAASGICGTLTQVLTPTTGQMLANDVAREVTV 424  
 QY 477 VSCXKXKXQAVFNEXALINLKXXXXVAVQANPKLEIITTPATGPNQMLPV 533  
 DB 484 LSCGPKSGCQKXKXQAVFNEXALINLKXXXXVAVQANPKLEIITTPATGPNQMLPV 540

KM Hydroxylase; Signal; Toxin.  
 FT SIGNAL 1 32  
 FT CHAIN 33 580  
 SQ SEQUENCE 580 AA; 64265 MW; 37642896CCEGAPF CRC64;  
 Query Match 47.4%; Score 1244.5; DB 10; Length 580;  
 Best Local Similarity 50.3%; Pred. No. 1.6e-118;  
 Matches 274; Conservative 69; Mismatches 177; Indels 25; Gaps 13;

QY 9 THQTGKYEPRFTLLRDVSSGSFSENPILRO-STIPVSDAQRFVVELTNGQSDXT 67  
 DB 40 TKNAKTSYTFLELRQQLSGSEPRGELFVNGDSYVE--DSKRFILVELSNMAADSPV 97  
 QY 68 A-NIDVTXYYVAYAGDSYRFL-DAPRGAETHLFGTTDRSSLPFGSYDLERYAG 125  
 DB 98 ALAVDTNAYVAYRFGSGSFLFEDNPPALLENLPDT--KRTFFSGSYDLERYAG 155  
 QY 126 H-EDQIFPGIXQLISVXALRFG-GSTRXQASILLIQMSFAAPNPILRFXQYIN 183  
 DB 156 ELKEEILLGMDPLENLSALMTSNINQOPALASLIVYQVAVARFTEYRRESIT 215  
 QY 184 SGXSFLLPDXYMLELTSWQGSQTOYQSHTD-GVFNNEPKRLAIKXGNVTLNVR-XVIA 241  
 DB 216 RAEFRPDPAMLSLKNKMSALSNVQSNQGVSSPVELRSISNRYVVGSDVLSG 275  
 QY 242 LAIMEFVC--GEPSSSDVRYVYRPIVAD-----DVTGASEPTVAVGXG 289  
 DB 276 LAIMEFICSSDRTSSDQFIDMLKRLIVYVADVADADNDQCADPEPTVAVISGN 335  
 QY 290 KXVDVDDPDHGNQIQLPESKNNNDNQLMTIKEDXTIRSNVSCLTGYGTAGYVWIP 349  
 DB 336 LCVDYDQKXKNGPQLMPCKNSDYNQMLTRRGGITRSEKCLITNGYSAGDVYLY 395  
 QY 350 DONTAVREATINQIKXGNTIINRSNIVLAASGIGKTLTYQTLDTLQGGVLAQNTA 409  
 DB 396 DCRPTVPAASIVQFANGTILNPSALVLSASGNETTILVQAVIYASRQMLANNTE 455  
 QY 410 PREVTIYGRDLQMSNGSVWVETCSGXQXKXALVGDSSIRPKNOQCLT-XGRD 466  
 DB 456 PVTSLVGNMDCQANGDMWVVECSKAEQ-KMLYVPSLIPRODRCLISTDNH 514  
 QY 469 SVSTVIVSCSXKXQKQWFTNEXAIIIMLXXXXXVQANPKLRIIYPATGRNQ 528  
 DB 515 SGGSIILISSCSPOSGQRWVPMNDGITLMLKNGLVWVKSFPQLIIMPATGRNQ 574  
 QY 529 MWLKV 533  
 DB 575 QMLPL 579

RESULT 4  
 Q94BW3 PRELIMINARY; PRT; 580 AA.  
 ID Q94BW3  
 AC Q94BW3  
 DT 01-DEC-2001 (TRENDArel. 19; Created)  
 DT 01-DEC-2001 (TRENDArel. 19; Last sequence update)  
 DT 01-MAR-2003 (TRENDArel. 23; Last annotation update)  
 DE Type 2, Ribosome-inactivating protein cinnamomol III precursor  
 DE 193.3.2.22 (RNA N-glycosidase).  
 OS Cinnamomum (Cannaceae) (Streptocarpales).  
 OC Eukaryota; Viridiplantae; Streptocarpales; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliopsida; Laurales; Lauraceae; Cinnamomum.  
 OX NCBI\_TaxID:13429;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yang Q., Gong Z.Z., Liu W.Y.;  
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomol proteins and study of their expression patterns";  
 RI Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 SPECIFIC ADENOSINE ON THE 26S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: AY039803; AK02460.1; -;  
 DR Interpro: IPR000772; R1cin\_B\_lectin.  
 DR DR Interpro: IPR001574; R1P\_-lectin; 6.  
 DR Pfam: PF00652; R1cin\_B\_lectin; 6.  
 DR Pfam: PF00161; R1P; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00453; R1CININ\_2.  
 DR PROSITE: PS00453; R1CININ\_2.  
 DR Hydroxylase; Signal; Toxin.  
 FT SIGNAL 1 32  
 FT CHAIN 33 580  
 SQ SEQUENCE 580 AA; 64421 MW; 94010P0LEFBS58 CRC64;  
 Query Match 47.3%; Score 1241.5; DB 10; Length 580;  
 Best Local Similarity 50.3%; Pred. No. 3.3e-118;  
 Matches 274; Conservative 71; Mismatches 175; Indels 25; Gaps 13;

QY 9 THQTGKYEPRFTLLRDVSSGSFSENPILRO-STIPVSDAQRFVVELTNGQSDX 66  
 DB 40 TKNAKTSYTFLELRQQLSGSEPRGELFVNGDSYVE--DSKRFILVELSNMAADSPV 97  
 QY 67 TRADVTXKYYVAYAGDSYRFL-DAPRGAETHLFGTTDRSSLPFGSYDLERYAG 125  
 DB 98 TLAVDTNAYVAYRTSSGFLFEDNPPALLENLPDT--KRTFFSGSYDLERYAG 155  
 QY 126 -HEDQIFPGIXQLISVXALRFG-GSTRXQASILLIQMSFAAPNPILRFXQYIN 183  
 DB 156 ERRESEILLGMDPLENLSALMTSNINQOPALASLIVYQVAVARFTEYRRESIT 215  
 QY 184 SGXSFLLPDXYMLELTSWQGSQTOYQSHTD-GVFNNEPKRLAIKXGNVTLNVR-XVIA 241  
 DB 216 RAEFRPDPAMLSLKNKMSALSNVQSNQGVSSPVELRSISNRYVVGSDVLSG 275  
 QY 242 LAIMEFVC--GEPSSSDVRYVYRPIVAD-----DVTGASEPTVAVGXG 289  
 DB 276 LAIMEFICSSDRTSSDQFIDMLKRLIVYVADVADADNDQCADPEPTVAVISGN 335  
 QY 290 KXVDVDDPDHGNQIQLPESKNNNDNQLMTIKEDXTIRSNVSCLTGYGTAGYVWIP 349  
 DB 336 LCVDYDQKXKNGPQLMPCKNSDYNQMLTRRGGITRSEKCLITNGYSAGDVYLY 395  
 QY 350 DONTAVREATINQIKXGNTIINRSNIVLAASGIGKTLTYQTLDTLQGGVLAQNTA 409  
 DB 396 DCRPTVPAASIVQFANGTILNPSALVLSASGNETTILVQAVIYASRQMLANNTE 455  
 QY 410 PREVTIYGRDLQMSNGSVWVETCSGXQXKXALVGDSSIRPKNOQCLT-XGRD 466  
 DB 456 PVTSLVGNMDCQANGDMWVVECSKAEQ-KMLYVPSLIPRODRCLISTDNH 514  
 QY 469 SVSTVIVSCSXKXQKQWFTNEXAIIIMLXXXXXVQANPKLRIIYPATGRNQ 528  
 DB 515 SGGSIILISSCSPOSGQRWVPMNDGITLMLKNGLVWVKSFPQLIIMPATGRNQ 574  
 QY 529 MWLKV 533  
 DB 575 QMLPL 579

RESULT 5  
 Q41174 PRELIMINARY; PRT; 541 AA.  
 ID Q41174  
 AC Q41174  
 DT 01-NOV-1996 (TRENDArel. 01; Created)  
 DT 01-NOV-1996 (TRENDArel. 01; Last sequence update)  
 DT 01-MAR-2003 (TRENDArel. 23; Last annotation update)  
 DE Proctolin A chain (ec 3.2.2.22) (RNA N-glycosidase)  
 DE (Fragment).  
 OS Reticulus communis (Castor bean).  
 OC Eukaryota; Viridiplantae; Streptocarpales; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;  
 CC eutrosid; Malpighiales; Euphorbiaceae; Reticulus.

Matches 483; Conservative 5; Mismatches 42; Indels 3; Gaps 2;

QY 1 YERLRLVHTQTKXEVFRFTLLADYSSGSPNEILPRLQSTIPVSDAQRPVLELTN 60  
 DB 1 YERLRLVHTQTKXEVFRFTLLADYSSGSPNEILPRLQSTIPVSDAQRPVLELTN 60

QY 61 CGDSXTAIDVTNLYVAVQAGUGSTFLDAPGATLFTGTTRDSSGTPKSGYDL 120  
 DB 61 CGDSXTAIDVTNLYVAVQAGUGSTFLDAPGATLFTGTTRDSSGTPKSGYDL 120

QY 121 ERYAGHRDQIPGIGXOLIOSVXALXPQSGTRXQASLILILQMSAPRNPILMRXQ 180  
 DB 121 ERYAGHRDQIPGIGXOLIOSVXALXPQSGTRXQASLILILQMSAPRNPILMRXQ 180

QY 119 ERYAGHRDQIPGIGXOLIOSVXALXPQSGTRXQASLILILQMSAPRNPILMRXQ 178  
 DB 119 ERYAGHRDQIPGIGXOLIOSVXALXPQSGTRXQASLILILQMSAPRNPILMRXQ 178

QY 181 XINSKSEFLPDXYMLETSMGQSTOVQSHTDGVNPNRRLAXXGNFVLAVRYVIA 240  
 DB 179 YINSKSEFLPDXYMLETSMGQSTOVQSHTDGVNPNRRLAXXGNFVLAVRYVIA 238

QY 241 SLATLFCGSRPSSDVRWVPLVIRPVADVTCSASEPTVIRVGNKCTVDREDFH 300  
 DB 239 SLATLFCGSRPSSDVRWVPLVIRPVADVTCSASEPTVIRVGNKCTVDREDFH 298

QY 301 DSNQIOLMPKSNNDPNOJLTIKXDTIRNSGCLTGYTAGVYVIFDQNTVAZATI 360  
 DB 299 DSNQIOLMPKSNNDPNOJLTIKXDTIRNSGCLTGYTAGVYVIFDQNTVAZATI 358

QY 361 WQJWNGTINRSNLVLAASSGIGTTLTVOJLDTYLGQGMAGNDTAPREVTIYGRD 420  
 DB 359 WQJWNGTINRSNLVLAASSGIGTTLTVOJLDTYLGQGMAGNDTAPREVTIYGRD 418

QY 421 LCMESNGSWWETCKSSQXQXKXALYQDGSIPRQNOQCLTGKSDVSTVNIYSCS 480  
 DB 419 LCMESNGSWWETCKSSQXQXKXALYQDGSIPRQNOQCLTGKSDVSTVNIYSCS 477

QY 481 XKSXQXWFTENXALINLKKXXKXDVQANFKRLRIIYFATGKPNQMLPV 533  
 DB 478 AGSGQRWFTENXALINLKKXGLANDVKSXPKRLIITVATGKPNQMLPV 530

RESULT 2

Q8W243 PRELIMINARY; PRT; 565 AA.

AC Q8W243; 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
 DB VCA precursor (BC 3.2.2.22) (rRNA N-glycosidase).  
 OS Viscum album subsp. coloratum.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Santalales; Viscaceae; Viscum.  
 RN [1]\_taxid=15976;  
 RP SEQUENCE FROM N.A.  
 RA Park W.-B., Liu S.;  
 RT "Cloning of Viscum album subsp. coloratum (Korean mistletoe).";  
 RL Biochem. Biophys. Res. Commun. 0:0-0(2002).  
 CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC EMBL: AF369961; AL040417.1; -  
 DB EMBL: AF369961; AL040417.1; -  
 DB Interpro: IPRO01574; Ricin\_B\_lectin.  
 DB Pfam: PF00652; Ricin\_B\_lectin.6.  
 DB PRINTS: PRO0396; SHIGARICIN.  
 DB SMART: SM00458; RICIN.2.  
 DB PROSITE: PS50231; RICIN\_B\_LECTIN.2.  
 KW Hydrolase; signal; toxin.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 273 VCA ALPHA CHAIN.  
 FT CHAIN 309 565 VCA BETA CHAIN.  
 SQ SEQUENCE 565 AA; 62401 MW; 991E3994D005511 CRC64;

Query Match 84.7%; Score 2224; DB 10; Length 565;  
 Best Local Similarity 81.6%; Pred. No. 6.2e-219;  
 Matches 439; Conservative 18; Mismatches 69; Indels 12; Gaps 4;

QY 1 YERLRLVHTQTKXEVFRFTLLADYSSGSPNEILPRLQSTIPVSDAQRPVLELTN 60  
 DB 34 YERLRLVHTQTKXEVFRFTLLADYSSGSPNEILPRLQSTIPVSDAQRPVLELTN 93

QY 61 CGDSXTAIDVTNLYVAVQAGUGSTFLDAPGATLFTGTTRDSSGTPKSGYDL 120  
 DB 94 CGDSXTAIDVTNLYVAVQAGUGSTFLDAPGATLFTGTTRDSSGTPKSGYDL 151

QY 121 ERYAGHRDQIPGIGXOLIOSVXALXPQSGTRXQASLILILQMSAPRNPILMRXQ 180  
 DB 152 ERYAGHRDQIPGIGXOLIOSVXALXPQSGTRXQASLILILQMSAPRNPILMRXQ 211

QY 181 XINSKSEFLPDXYMLETSMGQSTOVQSHTDGVNPNRRLAXXGNFVLAVRYVIA 240  
 DB 212 YINSKSEFLPDXYMLETSMGQSTOVQSHTDGVNPNRRLAXXGNFVLAVRYVIA 271

QY 241 SLATLFCGSRPSSDVRWVPLVIRPVADVTCSASEPTVIRVGNKCTVDREDFH 300  
 DB 272 SLATLFCGSRPSSDVRWVPLVIRPVADVTCSASEPTVIRVGNKCTVDREDFH 331

QY 299 DSNQIOLMPKSNNDPNOJLTIKXDTIRNSGCLTGYTAGVYVIFDQNTVAZATI 360  
 DB 332 DSNQIOLMPKSNNDPNOJLTIKXDTIRNSGCLTGYTAGVYVIFDQNTVAZATI 387

QY 361 WQJWNGTINRSNLVLAASSGIGTTLTVOJLDTYLGQGMAGNDTAPREVTIYGRD 420  
 DB 356 WQJWNGTINRSNLVLAASSGIGTTLTVOJLDTYLGQGMAGNDTAPREVTIYGRD 415

QY 421 LCMESNGSWWETCKSSQXQXKXALYQDGSIPRQNOQCLTGKSDVSTVNIYSCS 480  
 DB 388 LCMESNGSWWETCKSSQXQXKXALYQDGSIPRQNOQCLTGKSDVSTVNIYSCS 447

QY 481 XKSXQXWFTENXALINLKKXXKXDVQANFKRLRIIYFATGKPNQMLPV 533  
 DB 448 YKSNLQWENAGSVEFCSSQXQXKXALYQDGSIPRQNOQCLTGKSDVSTVNIYSCS 506

QY 476 XKSXQXWFTENXALINLKKXXKXDVQANFKRLRIIYFATGKPNQMLPV 533  
 DB 507 IVSCSGSGQRWFTENXALINLKKXGLANDVKSXPKRLIITVATGKPNQMLPV 564

RESULT 3

Q84B04 PRELIMINARY; PRT; 580 AA.

AC Q84B04; 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DB Type 2 ribosome-inactivating protein cinnamon II precursor  
 OS Cinnamomum camphora (Camphor tree).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 RN [1]\_taxid=19429;  
 RP SEQUENCE FROM N.A.  
 RA Yang Q., Gong Z.T., Liu W.Y.;  
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)  
 RT genes encoding cinnamon proteins and study of their expression  
 RT patterns.";  
 RT Submitted (JUN-2001) to the EMBL/Genbank/DDBJ databases.  
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC EMBL: AY039802; AA00458.1; -  
 DB EMBL: AY039802; AA00458.1; -  
 DB Interpro: IPRO01574; Ricin\_B\_lectin.  
 DB Pfam: PF00652; Ricin\_B\_lectin.6.  
 DB PRINTS: PRO0396; SHIGARICIN.  
 DB SMART: SM00458; RICIN.2.  
 DB PROSITE: PS50231; RICIN\_B\_LECTIN.2.



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Db 218 FIENOIRNNPQORIR-----PANNTISLEHKGKLSFOIRTSANGWSESEAVELEBRANG 271  
Qy 228 NPVTLXNVEXVYASLAIMLV 248  
Db 272 KRYVTADDOVEREIALKLV 292

Search completed: December 11, 2003, 14:09:09  
Job time : 10.26 secs

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CC
DR EMBL: AF055086; AAD02686.1; -.
DR HSSP: P33185; 1BRX.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIG_RICIN; FALSE NEG.
KW Ribosome/protein synthesis inhibitor; Hydrolase; Toxin;
KW Glycoprotein; signal.
FT SIGNAL 1 19
FT CHAIN 20 264
FT TYPE I RIBOSOME-INACTIVATING PROTEIN
FT TETRACHONUTIN.
FT PROPEP 265 294
FT ACT_SITE 177 177 BY SIMILARITY.
FT ACT_SITE 180 180 BY SIMILARITY.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (PROBALE).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (PROBALE).
FT CONFLICT 51 51 C -> Y (IN REF. 2).
FT CONFLICT 65 65 W -> R (IN REF. 2).
FT CONFLICT 85 85 A -> D (IN REF. 2).
FT CONFLICT 154 154 A -> S (IN REF. 2).
FT CONFLICT 174 174 A -> H (IN REF. 2).
FT CONFLICT 245 245 N -> H (IN REF. 2).
SQ SEQUENCE 294 AA; 32234 MW; DA4F8D7C3250994 CRC64;
Query Match 10.6%; Score 278.5; DB 1; Length 294;
Best Local Similarity 32.5%; Pred. No. 1e-19;
Matches 82; Conservative 40; Mismatches 115; Indels 15; Gaps 7;
QY 13 TXKXYPFTLLADYVSSGSFSENEIPLRQSTIFVSDAGFVLVELNQGQSKXPAIDV 72
DB 29 TKKSSSFTQARALPTQCTGCPILPST--ASSQMFERRFLNINDETVAVANNV 85
QY 73 TXKYVAYOGADQSYELADPAGGFTLCTRTDSSTLFPQSYKLERAG-ERQCLP 131
DB 86 TWYIVAYADAVSYFEDTPPAFAFLIPACTIKY--LYSQNYDKLASYVQKRWIE 143
QY 132 LGIQLQISYALRXKSGSTRKQARSLILQIMISFARFNPILMRKQXINSQSPED 191
DB 144 LGIPALSSAITNMWY--VDYSTALALVLQCTEMAFKYLIDQVSSHSS--NFPYD 199
QY 192 XTMLELEFWSQOSTQVQ--HSTDGVFNNKELAXKXNPVLXWRX-VTASLALM 246
DB 200 QAVTSJNNKGLSKQIDINRTGQFENEVELINPDGRFSYVTSAGVAKNIKLL 259
QY 247 FVCGERSSSDV 258
DB 260 YKKAQVGSSEYDI 271
RESULF 15
RIPG_GELNUT
AC P33186;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein gelonin precursor (cDNA N-glycosidase)
DE (EC 3.2.2.22).
GN GEL.
OS Gelonium multiflorum (Euphorbiaceae himalayana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Rosales; Malpighiales; Euphorbiaceae; Gelonium.
NCBI_taxonomy:3979;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:94085781; PubMed:7916721;
RA Nolan P.A., Garrison D.A., Better M.;
RT "Cloning and expression of a gene encoding gelonin, a ribosome-
RT inactivating protein from Gelonium multiflorum."
RL Gene 134:223-227(1993).
RN [2]
RP SEQUENCE OF 47-93.
RX MEDLINE:85326591; PubMed:2753586;
RA Monneveux P.C., Lazzarini A.M., Barbieri L., Soria M.,
RA Lappi D.;
RT "N-terminal sequence of some ribosome-inactivating proteins."
RL Int. J. Pept. Protein Res. 33:263-267(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE:9533189; PubMed:7608981;
RA Hsuar M.V., Nair B., Sanyamurthy P., Masguth S., Sitrolia A.,
RA Kachar R.K.;
RT "X-ray structure of gelonin at 1.8-A resolution."
RL J. Mol. Biol. 250:363-379(1995).
CC -1- CONFLICT: Activity of hydrolysis of the N-glycosidic bond at one
CC -1- specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Homodimer.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: L12243; AAL16312.1; -.
DR PIR: J70753; J70753.
DR HSSP: P09899; 1MBJ.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00151; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIG_RICIN; FALSE NEG.
KW Ribosome/protein synthesis inhibitor; Hydrolase; Toxin; signal;
KW Glycoprotein; signal.
FT SIGNAL 1 26
FT PROPEP 27 46
FT CHAIN 47 297 POTENTIAL.
FT PROPEP 298 316 RIBOSOME-INACTIVATING PROTEIN GELONIN.
FT DISULFID 90 96 MISSING IN MATURE PROTEIN.
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .).
FT ACT_SITE 212 212
FT CONFLICT 90 90
FT CONFLICT 93 93 C -> R (IN REF. 2).
FT CONFLICT 99 99 P -> D (IN REF. 2).
SQ SEQUENCE 316 AA; 35418 MW; 1252F3E710901B85 CRC64;
Query Match 10.4%; Score 273.5; DB 1; Length 316;
Best Local Similarity 33.3%; Pred. No. 3.4e-19;
Matches 87; Conservative 33; Mismatches 110; Indels 31; Gaps 7;
QY 9 TQGTGXYPFTLLADYVSSGSFSENEIPLRQSTIFVSDAGFVLVELNQGQSKXPAIDV 55
DB 42 TSKTADLPVSSPTKAGVITTYVNLKRLVYLKPRNSHDIILKKK--DQKQFVL 99
QY 56 VELNMQGSKXPAIDVNTXKYVAYOGADQSYELADPAGGFTLCTRTDSSTLFPQSYK 115
DB 100 VALSNNQALALADVTSVAVNGVRKNSFTQHPALVAGSLGKNTIKR-LHFGS 157
QY 116 SYXDLEKAGHROIPLGIXOT---TQSYALRXKSGSTRKQARSLILQIMISFARFNP 171
DB 158 SYSLBGRKXVETTLGIPRLDITKKDENDALIDVYKREILASLVLVAVQVBSKRT 217
QY 172 ---NLLMRKQXINSQSPEDXMTLEFWSQOSTQVQHS-TDGVFNNKELAXKXNPVLX 227

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OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.  
 OX Kcal\_Taxid=4202;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Bark;  
 RK MEDLINE=96215449; PubMed=8647092;  
 RL Van Damme E.J., Barts A., Rojce F., Van Leuven F., Penmans W.J.,  
 RT Characterization and molecular cloning of Sambucus nigra agglutinin V  
 RT (a ribosome-inactivating protein) from the bark of elderberry (Sambucus nigra).  
 RL Eur. J. Biochem. 237:505-513 (1996).  
 RN (2)  
 RP SEQUENCE OF 26-49 AND 298-321.  
 RC TISSUE-Bark;  
 RK MEDLINE=94003077; PubMed=8400135;  
 RL Githes T., Clottes L., Ferreira J.M., Rojo W.A., Iglesias E.,  
 RT Molecular cloning and characterization of a novel type 2 ribosome-inactivating protein  
 RT from the bark of elderberry (Sambucus nigra).  
 RL Plant Mol. Biol. 22:1181-1186 (1993).  
 CC -1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN  
 CC PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN  
 CC SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN  
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL  
 CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE  
 CC B CHAIN IS RESPONSIBLE FOR BINDING OF THE TOXIC TYPE 2 RIBOSOME-  
 CC BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES  
 CC ENDOCYTOSIS.  
 CC -1- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC EMBL accession: S71382.1;  
 CC EMBL accession: S71382.1;  
 DR Interpro: IPR000772; Ricin\_B\_lectin.  
 DR Interpro: IPR001574; RIP.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR SMART: SM00458; RICIN; 2.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 2.  
 RK plant defense; Ricin B-lectin; 2.  
 KW glycoprotein; lectin; signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 297  
 FT CHAIN 298 563  
 FT DOMAIN 305 431  
 FT DOMAIN 434 559  
 FT REPEAT 316 356  
 FT REPEAT 357 397  
 FT REPEAT 398 438  
 FT REPEAT 439 482  
 FT REPEAT 483 524  
 FT REPEAT 525 564  
 FT ACT\_SITE 188 189  
 FT ACT\_SITE 302 302  
 FT DISULFID 274 319  
 FT DISULFID 319 338  
 FT DISULFID 360 377  
 FT DISULFID 463 463  
 FT DISULFID 489 506  
 FT NIGRIN B A CHAIN.  
 FT NIGRIN B B CHAIN.  
 FT RICIN B-TYPE LECTIN 1.  
 FT RICIN B-TYPE LECTIN 2.  
 FT 1-ALPHA.  
 FT 1-BETA.  
 FT 2-ALPHA.  
 FT 2-BETA.  
 FT 2-GAMMA.  
 FT BY SIMILARITY.  
 FT INTERCHAIN (BY SIMILARITY).  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.

FT CARBOHYD 221 221 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 376 376 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CONFLICT 39 39 K -> V (IN REF. 2).  
 SO SEQUENCE 563 AA; 62300 MW; F250CB24621B14 CRC64;  
 Query Match 31.2% Score 819 DB 1; Length 563;  
 Matches 197; Conservative 88; Identical 211; Indels 38; Gaps 16;  
 17 YFPTLLADYVSSGSPS-NEIFLLRQSTIVSDQRFVVELINQGXSTADLVNXX 75  
 43 YRPTSLKTKTAVGVVGVNGLPLRRES-EVQVSRPVVPLTNVGNATVLAADVNL 101  
 76 YVVAQAGQSPFLKADPRASTHLEFCTDRSSLPXQSTKLELVAG-HNOQPLGT 134  
 102 YVNSGNANSTFNDATVQKSNFVGT-KNTLSFQNDVLEFANRSEIDLP 159  
 135 XOLISYXALXPGSGSTXQASILLILQMSAPNPLKPKXKINSXGFLPDVX 194  
 160 SPLDQATLS-YHQDSV--ASLLVIVQMSAPRPFVEQVRSLSQATSTPMALX 215  
 195 LELETWQCGOSTVOVHSTDEV--FNPKRLAIXNPFVIANVXVYASIA 243  
 216 LSNRNNSNSLSLEIQANNSNPFQVQLANTHRLV--DREELIXV---TGLA 268  
 244 IMFLGSGSPSSDPVWPLVIR--FVLADYTCASDEPTV-IVGXKXVDDDDP 299  
 269 ILFLFCS-PSNDVALRPLDLAGEDKNDGFTCTLRSTFRNIVGSDGCDVRNGV 327  
 300 HDNGQIDLPSPKSNNDPVQMLTIRKXITRNSGCLTYGYTAGVYVLPDNTVREAT 359  
 328 TDSTFLWPCSTOR-KQMTFTSDTTLFENKRCWLNKNSNIVLFGCTALENAI 385  
 360 INQKXGNTINPSNUTVLAASGCKTTLTVQTLDTLQOALAGNDARREVTGFR 419  
 386 MEVPIGGLINPSSGLTWRPAASTLILLDNRYAAGQVTVNVAIGVGVX 445  
 420 DLQNSN-XGSAVETKSSQXQXKMLVGGSIKPKNDQGLTKGRDSVGVIVY 477  
 446 EWLQSGENGVWMDKERTSLQ-QMLVGRITRVNLTGLCTVNGYNSDILLI 504  
 478 CSXKXKQGVFWFNKXLLNLTXXXXXVQVQANPELRILLTPATKRNQMT 531  
 505 KCGQLP-SGVWFTVSGALVWRKSHVYVANSAGNLEILLFPHQNKQW 557  
 RESULT 9  
 RIP2 BRVDI STANDARD; FRT; 282 AA.  
 ID P98184; G8890;  
 DT 16-OCT-2001 (Ref. 40; Created)  
 UT 26-SEP-2003 (Ref. 40; Last sequence update)  
 DE 26-SEP-2003 (Ref. 40; Last sequence update)  
 DE Ribosome-inactivating protein bryodin II precursor (RIN N-  
 DE glycosidase) (EC 3.2.2.22) (BD2).  
 OC Bryonia dioica (Red bryony).  
 CC Eurytomidae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;  
 CC eucotsid 1; Cucurbitales; Cucurbitaceae; Bryonia.  
 OX NCBI\_Taxid=5652;  
 RK SEQUENCE FROM N.A.  
 RL Sigall C.B., Gawlak S.L., Margard H.;  
 RT Bryodin 2 a ribosome-inactivating protein isolated from the plant  
 RL Bryonia dioica.\*;  
 RL Patent number US5597569, 28-JAN-1997.  
 RN (2)  
 RP SEQUENCE OF 22-42.  
 RC TISSUE-Root;  
 RK MEDLINE=95151812; PubMed=7849072;

RESULT 7  
AGGL\_RICCO STANDARD; PRT: 564 AA.  
AC P06750;  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Agglutinin precursor (RCA) [contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].  
OS Ricinus communis (Castor bean).  
OC Stereophyllaceae; Euphorbiaceae; Stereophyllaceae; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicotyledons; Core eudicotyledons; Rosidae; Euphorbiales; Malpighiales; Euphorbiaceae; Ricinus.  
NCBI\_TaxID=3989;  
CX [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=6059449; PubMed=299130;  
RA Roberts L.M., Lamb F.I., Peppin D.J.C., Lord J.M.;  
RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin.";  
RL U. Biol. Chem. 260:15682-15686(1985).  
RL SEQUENCE OF 303-564.  
RC Trisup-Sect.  
RA Araki T., Yoshida Y., Funatsu G.;  
RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds.";  
RL Biochim. Biophys. Acta 872:277-285(1986).  
RN [3]  
RP SEQUENCE OF 303-337.  
RX MEDLINE=60178723; PubMed=6768555;  
RA Lin T.T.-S., Li S.S.-L.;  
RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis.";  
RL Eur. J. Biochem. 105:453-459(1990).  
CC -1- Specific activity: Embryocytotoxicity of the N-glycosidic bond at one specific amino acid residue.  
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYR2 R1P SUBFAMILY.  
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.  
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CC -----  
DR EMBL: M12089; AAA33869.1; -  
DR EMBL: S40366; AAB22564.1; -  
DR PIR: A24261; RLCASG.  
DR HSSP: P02879; IBR6.  
DR GlycoSiteDB; P06750; -  
DR InterPro; IPR001574; Ricin\_B\_lectin.  
DR Pfam; PF00682; Ricin\_B\_lectin; 6.  
DR SMART; SM00456; RCTN2.  
DR SMART; SM00456; RCTN2.  
DR PROSITE; PS00231; Ricin B LECTIN; 1.  
DR PROSITE; PS00275; SHIGA\_RICIN; 2.  
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
KW Glycoprotein; Lectin; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 290 AGGLUTININ A CHAIN.  
FT PROPEP 291 302 LINKER PEPTIDE.  
FT CHAIN 303 564 AGGLUTININ B CHAIN.  
FT DOMAIN 309 453 RICIN B-TYPE LECTIN 1.  
FT DOMAIN 454 564 RICIN B-TYPE LECTIN 2.  
FT REPEAT 312 401 1 REPT.  
FT REPEAT 362 401 1 REPT.  
FT REPEAT 405 437 1-GNMA.

FT REPEAT 450 485 2-ALPHA.  
FT REPEAT 486 532 2-BETA.  
FT REPEAT 533 564 2-SIMILARITY.  
FT ACT SITE 200 200 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 282 306 BY SIMILARITY.  
FT DISULFID 322 341 BY SIMILARITY.  
FT DISULFID 365 382 BY SIMILARITY.  
FT DISULFID 453 466 BY SIMILARITY.  
FT CYSBOHD 492 509 BY SIMILARITY.  
FT CYSBOHD 34 34 N-LINKED (GLCNAc... ) (POTENTIAL).  
FT CYSBOHD 259 259 N-LINKED (GLCNAc... ) (POTENTIAL).  
FT CYSBOHD 357 357 N-LINKED (GLCNAc... ) (POTENTIAL).  
FT CYSBOHD 437 437 N-LINKED (GLCNAc... ) (POTENTIAL).  
FT CYSBOHD 437 437 N-LINKED (GLCNAc... ) (POTENTIAL).  
FT CONFLICT 362 362 R -> D (IN REF. 2).  
FT CONFLICT 374 374 R -> G (IN REF. 2).  
FT CONFLICT 404 404 R -> T (IN REF. 2).  
FT CONFLICT 552 552 F -> V (IN REF. 2).  
SQ SEQUENCE 564 AA; 62851 MW; D455F2A72F609759 CRC64;  
Query Match 41.98; Score 1101; DB 1; Length 564;  
Best Local Similarity 45.14; Pred.No. 4.7e-100;  
Matches 242; Conservative 81; Mismatched 193; Indels 20; Gaps 11;  
QY 9 THOTTGKRYRITLLADYVSSGS-FSETRPL-RGSTFVSDAQRFTVTLNQSKQX 66  
DB 37 TDAIVTXYNYNRYASHLTDVDRHIFVLRVGLRIS-QFTLHLSNRLALV 94  
QY 67 TDAIVTXYNYNRYASHLTDVDRHIFVLRVGLRIS-QFTLHLSNRLALV 123  
DB 95 TDAIVTXYNYNRYASHLTDVDRHIFVLRVGLRIS-QFTLHLSNRLALV 153  
QY 124 AGRHDIDPLGIVQLGCVYAL--RFGQSTKQARSLIILQWISFAFPNLTMRXQ 180  
DB 154 GRENITLTPSLLEDAIYVYSTCTDPTLAFSPVCIQWLEKARFQYIGEMRT 213  
QY 181 XINGKASTEDKWLLETSNGQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQV 240  
DB 214 KLRNRRBARDSTVTLNMRKSLTALQSNQAFSLQDQRNRSKNTVLSLIP 273  
QY 241 SLATMLFVCGEPSSDPVWYVLRPVIND--DYTCASEPTVAVGXGXVDRD 297  
DB 274 IIALVYECAPPESSO---FSLIFVFNRLNV-CHDEPVIIVGNNGLCVDTGSR 328  
QY 298 DFHDGNOQLMPKKNEDNQLATIRKXITTSNQSCLTGTGTAQVAVIPDCNTVAB 357  
DB 329 EEPNSNPQLMPKKNEDNQLATIRKXITTSNQSCLTGTGTAQVAVIPDCNTVAB 388  
QY 358 AITHTQVNGTINRNSNYLASSTGCTTTLTGTLDTLACGHLAANRPAPATYTG 417  
DB 389 ATRQVKNNTINRNSNYLASSTGCTTTLTGTLDTLACGHLAANRPAPATYTG 448  
QY 418 FPDICANNGSVWETCKSSQKQKXAAAYGQSIIPKQNOQDCLTGKSDSVYNTV 477  
DB 449 LYGMCICANGKWLDECTSEKAO-QMALVYDSIGIPQQRNDCLTDNRIKGVKLL 507  
QY 478 SCSSXSKQQRVFTNEXATLTKKXXDVAQANPKRLIITVPAQGEPMQWALPV 533  
DB 508 SCGPASSQQRVFTNEXATLTKKXXDVAQANPKRLIITVPAQGEPMQWALPV 563  
RESULT 8  
NIGB\_SAMMI STANDARD; PRT: 553 AA.  
AC P33183; P33184; P33542;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Nigra b precursor (Agglutinin V) (SNV) [contains: Nigra b A chain (rRNA N-glycosidase) (EC 3.2.2.22); Nigra b B chain].  
OS Samnucis nigra (European elder).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicotyledons; Magnoliophyta; Eudicotyledons; Core eudicotyledons; Rosidae; Euphorbiales; Malpighiales; Euphorbiaceae; Ricinus.





Query Match	46.3%;	Score 1190;	Ds 1;	Length 528;
Best Local Similarity	45.3%;	Pred. No. 86-109;		
Matches 248;	Conservative 79;	Mismatches 177;	Indels 32;	Gaps 10;
Dy	THQTTGXERFFITLRLPYVASGGSFNSRILPILRSGTIPVSDADREYVWEIYQXKXSTA	66		
Dy	9	LEQKQSVNACQALAREE-ROGLIHIDVLEDPF-TLQSRRIITVELSNSTSEI75	68	
Dy	63	AIDNNRYNVAACQAGQAFYLRPARAGETHPLFTGSDSLSPXQSYQLEKYAR-R	127	
Dy	67	GIDVYNNVYVIRAGQGYFLIRAPSSADPVLFTGR-DQMSIPYGTIDELHAKSR	124	
Dy	128	DQLEPQXKQLOSYXALXPQSGSTQKSHLIIQSLQSAAPFPIWEXKXSGKS	187	
Dy	125	QQLPQVQALMTGSSFFRSGQGNREKRAKTLVIVQWAEAPFYSINRWVSIOTGA	184	
Dy	168	FLEDDYMLREMGSGQSTVQSTGDFVFNKXLAIXXGNFTLVNXX-----	237	
Dy	185	FQDANNAISLENNNDLRSYGQSVQDPFNN-----ATLTNRREPVLSLSH	234	
Dy	238	-VIALSLMLPFGEEPSSTWELVIRPVADDTGCSAS-EPVYVIGKXKAYDR	295	
Dy	225	PYVATLMLPFCNP-PKNGS---PLHSIKSEKSIKSRFFPVAIGSDMCLVDY	290	
Dy	291	DNGYHNGRILIMKCDREBNOLWTLSKPTISAKKLTIVGACASVYVITDTSIV	350	
Dy	356	REKTIQIMYKNTIIPNSNLYVLAASGIGITVTLVQTLDTLTGGQKAGNTPREVTI	415	
Dy	351	AEATYWEIMDNITIPSAVLAESSSGVGLTVQVINEIMRGWRGNNTSPFVSI	410	
Dy	416	YGRNLCHEKSGSVWETCKSSQXQKXKALHIGDSIRPKQNDQCLTIGKSDSVYN	475	

Db	41158YSDYD.CMCAQGSVMAMCDCKSNKEQ-QMALVTQDSIRSVQNTNCLTSHDKROGSTL	469
Qy	476 IVYSCSSXXSXQWVFWETNEALINLXXXXXVQVQANPLKRIIRIIVPARGKNQNPVL	531
Db	470 LMGSGSMASQSMVFKNDISYSLVDNMWVDKSGDPSLKLIIIMPTGKNDIWL	525
RESULT 4		
MLA_VISUAL	STANDARD. FRT. 254 AA.	
ID	MLA_VISUAL	
AC	RS1446.	
DT	15-DEC-1998 (Rel. 17. Created)	
DR	15-DEC-1998 (Rel. 17. Last sequence update)	
DE	26-DEC-1998 (Rel. 17. Last sequence update)	
DE	Beta-galactosidase specific lectin I A chain (MLA) (ML-I A) (RNA N-glycosidase) (EC 3.2.2.22)	
OC	Vesum album (European mistletoe).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; euclidyales; core euclides; Gnematales; Santalaceae; Viscum.	
CC	1) Taxid:35172;	
RP	SEQUENCE.	
RP	STRAIN=Subsp. album;	
RC	MEDLINE=97134531; PubMed=890141;	
RA	Soler M.H., Stoeva S., Schwaborn C., Wilhelm S., Stiefel T., Voelker W.;	
RT	"Complete amino acid sequence of the A chain of mistletoe lectin I."	
RT	"The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits by removing adenine from position 4,324 of 28 S RNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN. B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLUTINATION (LECTIN ACTIVITY)."	
CC	-1- SPECIFIC DEPOSITION OF THE 28S RNA OF THE N-glycosidic bond at one	
CC	-1- SUBUNIT. Disulfide-linked dimer of A and B chains.	
CC	-1- PHARMACEUTICAL. Due to its immunomodulatory effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.	
CC	-1- MISCELLANEOUS. TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA	
CC	-1- SIMILARITY. BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
CC	-1- TYPES 2 RIP SUPERFAMILY.	
DR	PIR: PD018; P0018.	
DR	HSP8; P1140; IABR.	
DR	InterPro: IPR01574; RIP.	
DR	Profam: PF00163; RIP-1.	
DR	Prosite: PS00029; SH3-GRKIN.	
DR	Plant defense; Hydroxamate; Toxin; Repeat; Glycoprotein; Lectin.	
KW	ACT SITE	
FT	CARBOHYD	
FT	15	
FT	16	
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FT	18	
FT	19	
FT	20	
FT	21	
FT	22	
FT	23	
FT	24	
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FT	128	
FT		





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Page 3

CC	cell The B chain binds to cell receptors and facilitates the
CC	entry into the cell of the A chain. B chains are also responsible
CC	for cell agglutination (lectin activity). It binds to beta-D-
CC	-1 CARBOHYD. ACTIVITY. Endopolymerolysis of the N-glycosidic bond at one
CC	-1 specific asparagine on the 28S rRNA.
CC	-1 SUBUNIT: Disulfide-linked dimer of A and B chains.
CC	-1 DOMAIN: The B chain is composed of two domains, each domain
CC	consists of 3 homologous subdomains (alpha, beta, gamma).
CC	-1 THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE
CC	MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 277.
CC	-1 INACTIVATING PROTEIN FAMILY: TYPE 2 RNA DEPENDENT THE RIBOSOME-
CC	-1 SIMILARITY: Contains 2 alpha B-type lectin domains.
CC	-1 CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
CC	WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
CC	-1 DATABASE: NAME=Protein Spotlight;
CC	NOTE=Issue 31 of February 2003;
CC	URL="http://www.expasy.org/proteolitics/articles/spl031.html"
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC	CC The European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announcements">http://www.isb-sib.ch/announcements</a>
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).
CC	CC
DR	EMBL; X03179; CAA26329.1; -
DR	EMBL; X52908; CAA37095.1; -
DR	EMBL; X02380; CAA26230.1; -
DR	EMBL; A12892; CAA01058.1; -
DR	PIR; A24041; RELSD
DR	PDB; 2A41; 1-UNAN-84
DR	PDB; 2A42; 1-UNAN-84
DR	PDB; 1P5P; 31-OCT-93
DR	PDB; 1P5S; 14-JAN-98
DR	PDB; 1IEU; 14-JAN-98
DR	PDB; 1R7C; 31-OCT-93
DR	PDB; 1ORS; 16-JUN-97
DR	PDB; 1ORL; 05-JUN-98
DR	PDB; 1BR6; 02-SEP-98
DR	PDB; 1I13; 16-JAN-02
DR	PDB; 1I19; 16-JAN-02
DR	Glycosylated; P02879;
DR	Interpro: IPR000772; Ricin_B_lectin.
DR	Interpro: IPR001574; Ricin.
DR	RefSeq: P00012; Ricin_B_lectin; 6.
DR	RefSeq: P00012; Ricin_B_lectin; 6.
DR	PRINTS; P002396; SHICARICIN
DR	SMART; SMO0458; Ricin; 2.
DR	PROSITE; PS00231; Ricin_B_Lectin; 2.
DR	PROSITE; PS00275; SHIGA_RICIN; 1.
KM	Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
KM	Glycoprotein; Lectin; Signal; 3D-structure.
FT	CHAIN 1
FT	CHAIN 2
FT	PEPTIDE 36 302
FT	CHAIN 303 314
FT	CHAIN 315 576
FT	DOMAIN 321 448
FT	DOMAIN 451 575
FT	REPEAT 331 373
FT	REPEAT 374 448
FT	REPEAT 449 497
FT	REPEAT 501 540
FT	REPEAT 543 570
FT	ACT_SITE 212 212
FT	DISULFID 294 318
FT	DISULFID 334 353
FT	INTERCHAIN

[illegible]

FT VARIANT 231 231 N -> S OR T.  
 FT VARIANT 231 233 NGL-> KSP.  
 FT VARIANT 232 235 GRAM -> SLAV.  
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 Best Local Similarity 92.4%; Pred. No. 5e-119;  
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 DB 271 DDTGCSSEPTVRIYERKCKVYDTPDDPDRGQGLIPKSNNDPQVLTIRKDTIRG 330  
 1 DDTGCSSEPTVRIYERKCKVYDTPDDPDRGQGLIPKSNNDPQVLTIRKDTIRG 60  
 DB 331 NSGCLTYGTAGVYVNFPCNTAVREATTQIKXKGIINPRSNLYLAAGSGIKGTLT 390  
 61 NSGCLTYGTAGVYVNFPCNTAVREATTQIKXKGIINPRSNLYLAAGSGIKGTLT 120  
 DB 331 VQTLDTYTLQGMLAGNDTRAREVTVYGFQDLQWESNKGSSWVERCKSSQXQXVXALYGD 450  
 121 VQTLDTYTLQGMLAGNDTRAREVTVYGFQDLQWESNKGSSWVERCKSSQXQXVXALYGD 180  
 DB 451 GSIRKONQDQGLKGDSSGTYVIVSCSXKXGPPVTEKAIINIKXXXXVACH 510  
 161 GSIRKONQDQGLKGDSSGTYVIVSCSXKXGPPVTEKAIINIKXXXXVACH 240  
 DB 511 NPFLRRIITYPATKKNQMWLPV 533  
 241 NPFLRRIITYPATKKNQMWLPV 263  
 DB 241 NPFLRRIITYPATKKNQMWLPV 263  
 RESULT 2  
 RI RI  
 ID RI RI  
 AC P02879; P02880; STANDARD; PRT; 576 AA.  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ricin precursor [Contains: Ricin A chain (RNA N-glycosidase)]  
 EC 3.2.2.22; Ricin B chain)  
 OS Ricinus communis (Castor bean).  
 OC Eukaryota; Viridiplantae; Stereophyta; Embryophyta; Tracheophyta;  
 OC Euphorbiales; Euphorbiaceae; Sapotales; Core eudicots; Rosidae;  
 CC eudicotids; Malpighiales; Sapotales; Ricinus.  
 NX NCBI\_TaxID:3984;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86067214; PubMed=29997112;  
 RA Halling K.C., Halling A.C., Murray B.E., Ladin B.F., Houston L.T.,  
 RA Weaver R.F.;  
 RA Genomic cloning and characterization of a ricin gene from Ricinus  
 RA communis.  
 RL Nucleic Acids Res. 13:8019-8033(1985).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9163016; PubMed=1371405;  
 RA Tregear J.W., Roberts L.W.;  
 RT "The lectin gene family of Ricinus communis: cloning of a functional  
 RT ricin gene and three lectin pseudogenes."  
 RL Plant Mol. Biol. 18:515-525(1992).  
 RN [13]  
 RP SEQUENCE OF 12,576 FROM N.A.  
 RX MEDLINE=9172423; PubMed=1389723;  
 RA Lamb A., Roberts L.W.,  
 RA "Nucleotide sequence of cloned cDNA coding for preproricin."  
 RL Eur. J. Biochem. 148:265-270(1985).  
 RN [14]  
 RP SEQUENCE OF 36-302.  
 RA Yoshitake S., Funatsu G., Funatsu M.;  
 RT Isolation and sequences of peptic peptides, and the complete  
 RT sequence of the chain of ricin-B.  
 RL Agric. Biol. Chem. 42:1267-1274(1978).  
 RN [15]  
 RP SEQUENCE OF 315-576.  
 RA Funatsu G., Kimura M., Funatsu M.;  
 RT "Primary structure of Aa chain of ricin D."  
 RL Agric. Biol. Chem. 43:2221-2224(1979).  
 RN [16]  
 RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.  
 RX MEDLINE=9034423; PubMed=168517;  
 RA Kimura Y., Kimura H., Tada M., Takagi S., Funatsu G.;  
 RT "Structural analyses of sugar chains from ricin A-chain variant."  
 RL Agric. Biol. Chem. 54:157-162(1990).  
 RN [17]  
 RP RI  
 RX MEDLINE=21480122; PubMed=11595634;  
 RA Olivas S., Kozlov J.V.;  
 RT "Ricin."  
 RL Toxicol. 39:1723-1728(2001).  
 RN [18]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=87165983; PubMed=358397;  
 RA Montfort W., Vallerance J.E., Koningo A.F., Ernst S.R., Katzin B.,  
 RA Ruebner B., Xiong N.H., Hamlin R., Roberts J.D.;  
 RT "The three-dimensional structure of ricin at 2.8 A."  
 RL J. Biol. Chem. 262:15398-15403(1987).  
 RN [19]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE=91352004; PubMed=1681881;  
 RA Katzin B.J., Collins E.J., Roberts J.D.;  
 RT "Structure of ricin A-chain at 2.5 A."  
 RL Proteins 10:251-259(1991).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.  
 RX MEDLINE=91352005; PubMed=1681882;  
 RA Katzin B.J., Collins E.J., Roberts J.D.;  
 RT "Structure of ricin B-chain at 2.5 A resolution."  
 RL Proteins 10:260-269(1991).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE=95082010; PubMed=7990130;  
 RA Weston S.A., Tucker A.D., Thatcher D.R., Dedyshere D.J.,  
 RA Fawcett R.A.;  
 RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution."  
 RL J. Mol. Biol. 244:410-421(1994).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.  
 RX MEDLINE=96374222; PubMed=8760513;  
 RA Day P.V., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,  
 RA Molina-Svahn M.C., Robertus J.D.;  
 RT "Structure and activity of an active site substitution of ricin A  
 RT chain."  
 RL Biochemistry 35:11098-11103(1996).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE=97240820; PubMed=906680;  
 RA Yan X., Hollis T., Smith M., Day P., Monzingo A.F., Milne G.W.,  
 RA "Structure-based identification of a ricin inhibitor."  
 RL J. Mol. Biol. 266:1043-1049(1997).  
 RN [14]  
 RP MUTAGENESIS.  
 RX MEDLINE=93165632; PubMed=1287657;  
 RA Kim Y., Robertus J.D.;  
 RT "Analysis of several key active site residues of ricin A chain by  
 RT site-directed mutagenesis."  
 RL Biochemistry 37:775-779(1992).  
 RN [15]  
 RP FUNCTION.  
 CC "FUNCTION: Ricin is highly toxic to animal cells and to a less  
 CC extent to plant cells. The A chain is responsible for inhibiting  
 CC protein synthesis through the catalytic inactivation of 60S  
 CC ribosomal subunits. It acts as a glycosylase that removes a  
 CC specific adenine residue from an exposed loop of 28S ribosomal  
 CC RNA. As this loop is involved in the binding of elongation  
 CC factors, the modified ribosomes are unable to support protein  
 CC synthesis. The A chain can inactivate a few thousand ribosomes  
 CC per cell. The B chain is responsible for binding to cell surface  
 CC new ones. A single A-chain molecule can therefore kill an animal  
 CC cell."

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 9.17665 Seconds

Title: US-09-601-667C-40 (without alignments) 2736.539 Million cell updates/sec

Sequence: 1 TERNALRVHTQITKXETFR.....RRIITPATKRNQWLPVX 534

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

Searched: 127663 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127663

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1230.5	49.1	264	1	MIA_VISAL
2	1229.5	46.8	576	1	RICI_RICCO
3	1190	45.3	528	1	ABRA_ABRPR
4	1165	44.4	254	1	MLA_VISAL
5	1138	43.3	562	1	ABRG_ABRPR
6	1112.5	42.4	527	1	ABRG_ABRPR
7	1101	41.9	564	1	AGGL_RICCO
8	1101	41.9	564	1	AGGL_RICCO
9	326	11.2	262	1	NIGR_SAMNI
10	301	11.4	289	1	RIP2_RICCO
11	300	11.4	289	1	RIP2_RICCO
12	287.5	10.9	286	1	RIP2_RICCO
13	278.5	10.6	294	1	RIP1_RICCO
14	273.5	10.4	316	1	RIP1_RICCO
15	267.5	10.2	286	1	RIP1_RICCO
16	267.5	10.2	286	1	RIP1_RICCO
17	267.5	10.2	286	1	RIP1_RICCO
18	249.5	9.3	277	1	RIP1_RICCO
19	249.5	9.1	250	1	RIP1_RICCO
20	249.5	9.1	250	1	RIP1_RICCO
21	233.5	8.9	261	1	RIP1_RICCO
22	233.5	8.9	261	1	RIP1_RICCO
23	181	6.4	253	1	RIP1_RICCO
24	163.5	6.3	253	1	RIP1_RICCO
25	163.5	6.3	253	1	RIP1_RICCO
26	157	6.0	292	1	RIP1_RICCO
27	157	6.0	292	1	RIP1_RICCO
28	138.5	5.3	310	1	RIP1_RICCO
29	131	5.0	236	1	RIP1_RICCO
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31	131	5.0	236	1	RIP1_RICCO
32	114	4.6	280	1	RIP1_RICCO
33	114	4.6	280	1	RIP1_RICCO

# ALIGNMENTS

RESULT	ID	STANDARD	PFT	264 AA
1	MIA_VISAL			
2	RICI_RICCO			
3	ABRA_ABRPR			
4	MLA_VISAL			
5	ABRG_ABRPR			
6	ABRG_ABRPR			
7	AGGL_RICCO			
8	AGGL_RICCO			
9	NIGR_SAMNI			
10	RIP2_RICCO			
11	RIP2_RICCO			
12	RIP2_RICCO			
13	RIP1_RICCO			
14	RIP1_RICCO			
15	RIP1_RICCO			
16	RIP1_RICCO			
17	RIP1_RICCO			
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19	RIP1_RICCO			
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33	RIP1_RICCO			

A/Reference number: A36274; MUID:90256790; PMID:2341400  
A/Molecule type: DNA  
A/Residues: 1-233; 'T', 235-246; 'M', 248-289 <CHO>  
A/Cross-references: GB:J05434; MID:9170534; PIND:AAA34206.1; PID:9170535  
R:Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.  
A/Title: Cloning and sequencing of the gene encoding trichosanthin.  
A/Reference number: JCI093; MUID:94271611; PMID:8003348  
A/Accession: JCI093  
A/Molecule type: DNA  
A/Residues: 1-72; 'V', 74-90; 'S', 92-233; 'T', 235-267; 'D', 269-289 <ZHE>  
A/Cross-references: GB:S70176; MID:9547148; PIND:AB31048.1; PID:9547149  
R:Collins, E.J.; Robertus, J.D.; Lopresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwar  
J. Biol. Chem. 265, 8665-8669, 1990  
A/Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abor  
A/Reference number: A36273; MUID:90256789; PMID:2341399  
A/Accession: A36273  
A/Molecule type: protein  
A/Residues: 1-247 <TOY>  
R:Wang, Y.; Zhao, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z  
Pure Appl. Chem. 58, 789-798, 1986  
A/Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application  
A/Reference number: JF0003  
A/Accession: JF0003  
A/Molecule type: protein  
A/Residues: 24-56; 'L', 58-59; 'I', 61-71; 'T', 73-81; 85-86; 'L', 88-92; DAGEPRAWL, 93-142; 'GU'  
A/Experimental source: tuber  
R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
Submitted to the Brookhaven Protein Data Bank, July 1994  
A/Reference number: A67092; PBI:IRK047; PBI:IRK047  
R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
Submitted to the Brookhaven Protein Data Bank, July 1994  
A/Reference number: A67092; PBI:IRK047  
A/Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-  
R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
Submitted to the Brookhaven Protein Data Bank, December 1994  
A/Reference number: A6711; PBI:ITCS  
A/Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27  
R:Kiong, J.P.; Xia, Z.X.; Wang, Y.  
Nat. Struct. Biol. 1, 695-700, 1994  
A/Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstrom resolution re  
A/Reference number: A6711; PBI:ITCS  
A/Contents: annotation; X-ray crystallography, 1.7 angstroms  
A/Comment: Alpha-trichosanthin has been used to induce abortions.  
A/Genes: tcs  
C/Function:  
A/Description: Hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA then  
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C/Keywords: abortifacient; glycosidase; hydrolase; root; toxin  
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F:1-23/Domain: signal sequence #status predicted <SIG>  
F:27-267/Domain: rRNA N-glycosidase homology #status predicted <NMT>  
F:27-267/Domain: rRNA N-glycosidase homology #status predicted <NMT>  
F:271-289/Domain: carboxy-terminal homology #status predicted <CTP>  
F:93,183,186/Active site: Tyr, Glu, Arg #status predicted

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Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

QY 13 TXEXYFFITLLRDYVSGSFSNEIFLRQSTIPVSDQRFVLELITNQGXSXTAIVD 72  
DB 33 TSSSTGVFISNRKALPERKCDIPLRL-SLFGS-QRYALHLINVADETIVADIV 89  
QY 73 TXNYVYVAGQSGSYETADA-PRGATHTLTGTTTPRDSSTPEFGSXYLERNAGH-EDQI 130  
DB 90 TNYVYVAGQSGSYETADA-PRGATHTLTGTTTPRDSSTPEFGSXYLERNAGH-EDQI 148  
QY 131 PLGIXLOISVXALRPGSGSTRKQARSLILLOMISGAARFPIIMKXROKINSXSFPL 190  
DB 149 PLGIPALDSAITTLFTYVNNNS--AASALMWLIQSTSEARVYKFIQOIGKRVXK--TFLP 204

QY 191 DXYVLELFTSMQSGSTQVO--HSTQGVNPNPKRLAIXGNFTLXNVEX--VIASLAINL 246  
DB 205 SLATISLNSWMSALSROIOIASTNQGEPFVVLNKNQKQVITTVDAQVATSNIALLL 264  
RESID 15  
J00393  
Accession: J00393  
Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 12-Apr-1995  
C/Accession: J00393; PS0163  
R:Toyokawa, S.; Takeda, T.; Kato, Y.; Nakabayashi, K.; Ogihara, Y.  
Chem. Pharm. Bull. 39, 1244-1249, 1991  
A/Title: The complete amino acid sequence of an abortifacient protein, karasurin.  
A/Reference number: J00393; MUID:92005921; PMID:1914000  
A/Accession: J00393  
A/Molecule type: protein  
A/Residues: 1-247 <TOY>  
A/Note: a sequence which lacks Ala-247 is also shown in this publication  
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C/Keywords: abortifacient; glycosidase; hydrolase; root; toxin  
F:1-243/Domain: rRNA N-glycosidase homology <NMG>

Query Match 11.4%; Score 300; DB 2; Length 247;  
Best Local Similarity 35.4%; Pred. No. 2,4e-21;  
Matches 85; Conservative 46; Mismatches 95; Indels 14; Gaps 9;

QY 13 TXEXYFFITLLRDYVSGSFSNEIFLRQSTIPVSDQRFVLELITNQGXSXTAIVD 72  
DB 10 TSSSTGVFISNRKALPERKCDIPLRL-SLFGS-QRYALHLINVADETIVADIV 66  
QY 73 TXNYVYVAGQSGSYETADA-PRGATHTLTGTTTPRDSSTPEFGSXYLERNAGH-EDQI 130  
DB 67 TNYVYVAGQSGSYETADA-PRGATHTLTGTTTPRDSSTPEFGSXYLERNAGH-EDQI 125  
QY 131 PLGIXLOISVXALRPGSGSTRKQARSLILLOMISGAARFPIIMKXROKINSXSFPL 190  
DB 126 PLGIPALDSAITTLFTYVNNNS--AASALMWLIQSTSEARVYKFIQOIGKRVXK--TFLP 181  
QY 191 DXYVLELFTSMQSGSTQVO--HSTQGVNPNPKRLAIXGNFTLXNVEX--VIASLAINL 246  
DB 182 SLATISLNSWMSALSROIOIASTNQGEPFVVLNKNQKQVITTVDAQVATSNIALLL 241

Search completed: December 11, 2003, 13:55:47  
Job time: 16.5989 secs

A/Residues: 1-69, 'PS', 72-209, 'N', 211-241, 243-250, 'V', 252-263 <NA>  
 A/Experimental source: seed  
 C/Superfamily: ricin; rRNA N-glycosidase homology  
 C/Keywords: duplication; glycoprotein; glycosidase; hydrolase  
 F:1-263/Product: ricin B chain B #status experimental <CH>  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40 residue repeats  
 F:20-59, 63-80, 151-164, 190-207/Dissulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match  
 Best Local Similarity 59.2%; Pred. No. 4, 5a-72;  
 Matches 154; Conservative 32; Mismatches 72; Indels 2; Gaps 2;

OY 275 CSASPTVTRIVGRKXKXVDVDDPHDQIQIIMPESKNDPVOQMTIKEDYTRRSNQC 334  
 DB 4 GMPSEIVIVGNGACVDVADGRFHNGALQIMPCKSNIDNQLMTLEKQNTIRSNKC 63  
 OY 335 LTTGYTRGVYVYVFPQCTAPRATVQKXKXVTFNRSNVTAAASGISTTLTQCT 394  
 DB 64 LTTGYSPGVYVYVYDQNTATDAPRQVIMNGFTINRSSTVLAASNGSTTLVQCN 123  
 OY 395 DYLQAGNLAGNDTAPREVITYFPGDQCMESKXSVVETCKSSQXQXVALYDQGSIR 454  
 DB 124 IVASQGMLEPTNTPQPTVTVVGLVGCQNSKXVLEDCSTKRAQ-QVALYDQGSIR 182  
 OY 455 FKQNDQCTLRGRDSVSTVIVIVSGSKXKXKXKXVTEKALINIKKXKXQVDAQNF-R 513  
 DB 183 FQKRNQDLTPAKIKQTVILVIVSGVSSQKRNKNDGTILINIVGLVDPKNSDPS 242  
 OY 514 LRRIIVPATKQKQNMPLPV 533  
 DB 243 LKQIVHPFHGNLQIMLPL 262

## RESULT 12

OY 275 CSASPTVTRIVGRKXKXVDVDDPHDQIQIIMPESKNDPVOQMTIKEDYTRRSNQC 334  
 DB 4 GMPSEIVIVGNGACVDVADGRFHNGALQIMPCKSNIDNQLMTLEKQNTIRSNKC 63  
 N/Contains: rRNA N-glycosidase (IBC 3.2.2.22)  
 C/Species: Abrus precatorius (Indian licorice)  
 C/Date: 21-Feb-1992 #sequence\_revision 31-Dec-1993 #text\_change 20-Aug-1999  
 C/Accession: C39761, S14471  
 R/Jensen, G.; Mathiesen, A.; Sundan, A.  
 J. Biol. Chem. 266, 6848-6852, 1991  
 A/Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
 A/Reference number: A39761; PMID:9120123; PMID:2016300  
 A/Accession: C39761  
 A/Residues: 1-251 <NA>  
 R/Jensen, G.; Mathiesen, A.; Sundan, A.  
 submitted to the EMBL data library, October 1990  
 A/Description: Direct molecular cloning of two distinct abrin A-chains.  
 A/Reference number: S14471  
 A/Accession: S14471  
 A/Molecule type: DNA  
 A/Residues: N, 1-251 <EV2>  
 A/Accession: EMBL:234893; NID:G16088; PIRN:CAA3654.1; PID:G16089  
 C/Comments: This protein belongs to type I ribosomal-inactivating protein  
 C/Keywords: duplication; glycosidase; hydrolase; lectin; toxin  
 F:1-251/Product: abrin (clone 7.2) chain A #status predicted <CH>  
 F:7-246/Dominant: rRNA N-glycosidase homology <RNS>  
 F:74, 113, 195, 196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F:164, 167/Active site: Glu, Arg #status predicted

Query Match  
 Best Local Similarity 16.9%; Score 443; DB 2; Length 251;  
 Matches 106; Conservative 34; Mismatches 97; Indels 6; Gaps 5;

OY 9 THQTKKX 68  
 DB 9 TEGATSGVY 66  
 OY 63 AIDVYKXVY 127

DB 67 GIVYTNKXVY 124  
 OY 128 DQFPGXKX 187  
 DB 125 EQLSGLQNTLALSLASGASDEKARLIVLQMSKXSVYVYVYVYVYVYVYVYVYVY 184  
 OY 188 FLEQYVLELTSNGQSTQYQSHSTQVFNKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 246  
 DB 185 FQDPRKSLKX 244  
 OY 247 FVC 249  
 DB 245 FVC 247

## RESULT 13

OY 275 CSASPTVTRIVGRKXKXVDVDDPHDQIQIIMPESKNDPVOQMTIKEDYTRRSNQC 334  
 DB 4 GMPSEIVIVGNGACVDVADGRFHNGALQIMPCKSNIDNQLMTLEKQNTIRSNKC 63  
 N/Contains: rRNA N-glycosidase (IBC 3.2.2.22)  
 C/Species: Trichosanthes kirilowii var. japonica  
 C/Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 23-May-1997  
 C/Accession: J05032  
 R/Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.  
 J. Biol. Pharm. Bull. 19, 1485-1489, 1996  
 A/Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and  
 A/Reference number: J05032; PMID:9108848; PMID:8951169  
 A/Accession: J05032  
 A/Status: Preliminary  
 A/Residues: 1-247 <NA>  
 A/Residues: 1-247 <CH>  
 C/Comments: This protein belongs to type I ribosomal-inactivating proteins which catalyze  
 C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
 F:4-243/Dominant: rRNA N-glycosidase homology <RNS>

Query Match  
 Best Local Similarity 35.4%; Pred. No. 1, 5a-21;  
 Matches 85; Conservative 46; Mismatches 95; Indels 14; Gaps 9;

OY 11 TGEYFRITLADYVY 72  
 DB 10 TSSGVY 66  
 OY 73 TNYVY 130  
 DB 67 TNYVY 125  
 OY 133 PLGKX 190  
 DB 136 FQDPRKSLKX 244  
 OY 191 DXTVLELTSNGQSTQYQSHSTQVFNKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 246  
 DB 192 DXTVLELTSNGQSTQYQSHSTQVFNKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 244  
 OY 193 STATLSNWSALSKQIQIASTNQCPEYVY 241

## RESULT 14

OY 275 CSASPTVTRIVGRKXKXVDVDDPHDQIQIIMPESKNDPVOQMTIKEDYTRRSNQC 334  
 DB 4 GMPSEIVIVGNGACVDVADGRFHNGALQIMPCKSNIDNQLMTLEKQNTIRSNKC 63  
 N/Contains: rRNA N-glycosidase (IBC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian  
 N/Alternative names: alpha-TCs; type I ribosome-inactivating protein  
 C/Species: Trichosanthes kirilowii (Mongolian snake-poult)  
 C/Date: 30-Sep-1988 #sequence\_revision 26-Jan-1996 #text\_change 23-May-2001  
 C/Accession: J05056; A36274; G10993; A36273; J05003  
 R/Gshaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, M.K.K.; Ng, T.B.; Yeung, H.W.  
 Gene 97, 267-272, 1991  
 A/Title: Cloning of trichosanthin cDNA and its expression in *Escherichia coli*.  
 A/Reference number: J05056; PMID:1915367; PMID:1992921  
 A/Accession: J05056  
 A/Residues: 1-247 <NA>  
 A/Residues: 1-247 <CH>  
 C/Comments: This protein belongs to type I ribosomal-inactivating proteins which catalyze  
 C/Keywords: duplication; glycosidase; hydrolase; lectin; toxin  
 F:1-247/Product: alpha-trichosanthin (clone 1.1) chain A #status predicted <CH>  
 F:1-247/Dominant: rRNA N-glycosidase homology <RNS>  
 F:1-247/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F:1-247/Active site: Glu, Arg #status predicted

Query Match  
 Best Local Similarity 35.4%; Pred. No. 1, 5a-21;  
 Matches 85; Conservative 46; Mismatches 95; Indels 14; Gaps 9;

C:Comment: This protein has strong agglutinating activity and weak cytotoxicity compared  
 C:Superfamily: ricin; rRNA N-glycosidase homology  
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
 F/1-24/Domain: signal sequence #status predicted <S10>  
 F/25-250/Product: agglutinin chain A #status predicted <ACH>  
 F/251-283/Domain: rRNA N-glycosidase homology <RNG>  
 F/283-283/Domain: agglutinin chain B #status experimental <ECH>  
 F/283-283/Domain: agglutinin chain B #status predicted  
 F/319-361,362-402,403-453,454-483,484-509/Region: 10 residue repeats  
 F/319-361,362-402,403-453,454-483,484-509/Region: 10 residue repeats  
 F/319-361,362-402,403-453,454-483,484-509/Region: 10 residue repeats  
 F/104,147,231,232/Binding site: substrate (Gyr, Tyr, Glu, Asn) #status predicted  
 F/200,203/Active site: Glu, Arg #status predicted  
 F/282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted  
 F/324,337,348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted  
 F/397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F/536,557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 41.3%; Score 1101; DB 1; Length 564;  
 Best Local Similarity 45.1%; Pred. No. 9,26-99;  
 Matches 242; Conservative 81; Mismatches 193; Indels 20; Gaps 11;

9 THQTCKEYREFTLLADYSSGS-FSNEPLT-RGRTIPVSDARPVLYELNQXDS 66  
 37 TADATVSTYNEIAYVSHLTGADVHEHLPVLSNWLPTIS-QRIIVLSNHELSV 94  
 67 TAAIDVTNXYVAYOGDQSYFLR-DAPRGAH-TLFTPTDSSSLPFGSYXDLERY 123  
 95 TLADVTNAYVCCRGASNAFFPHDQDEALITHEFL-DVONSEFFAFGANDELQCL 153  
 124 AGRDQPIGLIXOLISYVAL--EKPQSTXQASLILILQMSAARFPILMKRXQ 180  
 154 GGLNSELSTGPLEDAISLTYITSTGCTGFLASSRVCILQMSAARFPILMKRXQ 213  
 181 XINSGSEPLDXYMLELTSNGQCTVQHS-DGVNPPKRLAIXGNFVTLNXYVIA 240  
 214 RIRYRRSAPDSVITLMSVGLSTALQSNQARHSPICLRNMSKFNVTYSLIP 273  
 241 SLALMFVCGEPSSDVRWPIVRYPLAD--DYTSASBPYRYKXGXKVVVDD 297  
 274 IIALWYRACAPPESSQ---FSILREVYRPNADV-CMDEPIYRIYVSGNGLCVVIGE 328  
 298 DPHDNQOIQMPSKSNPNQMLTIRKDXTRISNSGCLTGYGYVYMIPTDNTAVRE 357  
 329 EFDGNPIQDMCKSNTPMOMLTKRCKSTIRSKGCLTISKSPPQVIVYNSSTAVG 388  
 358 AIIQWIKNGTIIIPRSNLVLAASSGKGTITVQTLDTLGGCLMGNTPRPSVITYG 417  
 389 ATRWQIDNRITINPRSGVLAATGNSGKLTITQNNIVANSGMLPTNNQPTVITIG 448  
 418 FRDLQSNKSGVWVETCKSSQXNXXMALYQDGSIRPKNOQCLTARGDSVATVNTY 477  
 449 LVKWCLOANSKGVMLKDCITSKAKQ-QMALYADSGIRPKQNRNCLTTPAKIKGTIVIL 507  
 478 GCSXXSXKXQWVFTKEXAILLAKXXXXXVQAQNPFLKRIIIPATGKPNQMLTPV 533  
 508 SCGPASSGQWVFTNDGTTILNLTGVLVGRSDSLQIIVHFRHNNLQIMLYA 563

RESULT 10  
 562627  
 Agglutinin I precursor - European elder  
 C:Species: Sambucus nigra [European elder]  
 C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Aug-1999  
 F/Accession: S62627; S62619  
 F/Accession: S62627; S62619  
 F/Accession: S62627; S62619  
 A:Title: The Nucleic Acid Sequence of the B-Chain of Ricin Isolated from  
 A:Reference number: S62619; PMID:9603226; PMID:9603131  
 A:Accession: S62627  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-570 <VNW>  
 A:Cross-references: EMBL:U021122; NID:G114772; PID:MAC49158.1; PID:G114773  
 A:Accession: S62619

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 28-39,309-319 <VA2>  
 C:Superfamily: ricin; rRNA N-glycosidase homology  
 F/37-283/Domain: rRNA N-glycosidase homology <RNG>

Query Match 32.4%; Score 851; DB 2; Length 570;  
 Best Local Similarity 38.4%; Pred. No. 1,9e-74;  
 Matches 209; Conservative 79; Mismatches 220; Indels 36; Gaps 17;

8 YHQTCKEYREFTLLADYSSGS-FSNEPLT-RGRTIPVSDARPVLYELNQXDS 65  
 37 YHFLNDYRPTLALQKXVILNHTPDLVLPES-QVSNRFLVPLVPLNSGDT 95  
 66 XTAAIDVTNXYVAYOGDQSYFLR-DAPRGAH-TLFTPTDSSSLPFGSYXDLERY 125  
 96 VTAAIDVTNXYVAYOGDQSYFLR-DAPRGAH-TLFTPTDSSSLPFGSYXDLERY 153  
 126 H-RDQIPGLIXOLISYVALR--PQSTXQASLILILQMSAARFPILMKRXQ 181  
 154 FERYTIPGPKSDQSLSLRTYTLTRDQVPLAGLVVQVMSAARFPILMKRXQ 213  
 214 FDSSEFTDLMLAKENMSKSHSLQVQDQGFAGVGLQDRNMSLEVTNRLES 273  
 239 IASLAIMFVCGEPSSD--DVRWPIVRYPLAD--DYTSASBPYRYKXGXKVVVDD 297  
 274 LVYIAVLVYGCARVTSSTYNNALIDQ--IIMFVRRGGEVEXVSVYETRRISGMD 330  
 290 XNVGVADDPHDNQOIQMPSKSNPNQMLTIRKDXTRISNSGCLTGYGYVYMIPTD 349  
 331 LCVGVYGHYIDNPVQLRP--CGNENQMLTFRDGTIRWGLCL--TASGSAWY 383  
 350 DCTNARENITQWIKNGTIIIPRSNLVLAASSGKGTITVQTLDTLGGCLMGNTPR 409  
 384 DCTNARENITQWIKNGTIIIPRSNLVLAASSGKGTITVQTLDTLGGCLMGNTPR 442  
 410 PEVITYGRLQENSGXS--VWETCKSSQXNXXMALYQDGSIRPKNOQCLTARGD 467  
 443 PLVFTVYGVKQCLRENGENFVLEDVYLRVQ--EMALYDGTIRVNSRSLCVSND 501  
 468 DSVGVYINYSKCSXXKXQWVFTKEXAILLAKXXXXXVQAQNPFLKRIIIPATGKPN 527  
 502 HEPDGLIYILKCR-QSNGRWVFTNGTISNPALMLMDVAGVSLKRIIIPATGKPN 560  
 528 QWET 531  
 561 QWET 564

RESULT 11  
 506330  
 Ricin B - castor bean (fragment)  
 N:Content: Chain B: rRNA N-glycosidase (EC 3.2.2.22) (chain A)  
 C:Species: Ricinus communis (castor bean)  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 20-Aug-1999  
 F/Accession: S06330; S06329  
 F/Accession: S06330; S06329  
 F/Accession: S06330; S06329  
 A:Title: Characterization of a cDNA encoding ricin B, a hybrid ricin-Ricinus communis  
 A:Reference number: S06330  
 A:Accession: S06330  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-263 <LAD>  
 A:Cross-references: EMBL:M17631; NID:G169714; PID:AAA63506.1; PID:G169715  
 A:Accession: S06330  
 A:Status: preliminary  
 A:Molecule type: protein









A:Molecule type: protein  
A:Residues: 1-265 <80>  
C:Superfamily: ricin/ RNA N-glycosidase homology  
C:Keywords: glycoprotein  
P:61,96,136/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 48.7%; Score 1279.5; DB 2; Length 265;  
Best Local Similarity 92.0%; Pred. No. 1,5e-116;  
Matches 243; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

OY 271 DDTCSASEPTVRIWKGXGVYRDDPDNDGNOIAMPSSKNDPNOIATIKEDTIS 330  
DB 1 DDTCSASEPTVRIWKGXGVYRDDPDNDGNOIAMPSSKNDPNOIATIKEDTIS 60

OY 331 NGSCLTATYGTAGYVWFIDCNARVREKATITWIKNGTIPRSMIVLAASSGKFTLT 390  
DB 61 NGSCLTATYGTAGYVWFIDCNARVREKATITWIKNGTIPRSMIVLAASSGKFTLT 120

OY 391 VQIDITLGGMAGNDTAPREVTIYGRDLCEBSNKGWVETCKSSQXQXWALYGD 450  
DB 121 VQIDITLGGMAGNDTAPREVTIYGRDLCEBSNKGWVETCKSSQXQXWALYGD 180

OY 451 GSIRPKNDQCLTKEPDSTYTNVSGSXKXGPMFTNKAIAKXXHXDPA 510  
DB 181 GSIRPKNDQCLTKEPDSTYTNVSGSXKXGPMFTNKAIAKXXHXDPA 240

OY 511 NPKLRITIIIPATGKPKQMW-LPV 533  
DB 241 NPKLRITIIIPATGKPKQMW-LPV 264

RESULT 3  
R:CDSD  
ricin D precursor - castor bean  
N:Contains: RNA N-glycosidase (EC 3.2.2.22)  
C:Species: Ricinus communis (castor bean)  
C>Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #ext change 16-Jul-1999  
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903  
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.  
Nucleic Acids Res. 13: 8019-8033, 1985  
A>Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.  
A:Reference number: A24041; MUID:86067214; PMID:2999712  
A:Accession: A24041  
A:Molecule type: RNA  
A:Residues: 1-576 <RNA>  
R:Rice, J.; Robert, E.; Halling, K.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.  
Plant Mol. Biol. 18: 515-525, 1992  
A:Cross-references: GB:X03179; NID:g21082; PIRN:CAA26939.1; PID:g21083  
A>Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene  
A:Reference number: S20513; MUID:92163016; PMID:1371405  
A:Accession: S20513  
A:Molecule type: DNA  
A:Residues: 1-576 <RNA>  
R:Rice, J.; Robert, E.; Halling, K.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.  
Eur. J. Biochem. 148: 265-270, 1985  
A>Title: Nucleotide sequence of cloned cDNA coding for preprovidin.  
A:Reference number: A24614; MUID:85179479; PMID:3838723  
A:Accession: A24614  
A:Molecule type: mRNA  
A:Residues: 12-75, 'D', '77-550', 'R', '552-576' <LMA>  
R:Koshitake, S.; Funatsu, G.; Funatsu, M.  
Nucleic Acids Res. 22: 4286-4294, 1978  
A>Title: Isolation and characterization of cDNA sequences of peptic peptides, and the complete sequence of the ch  
A:Accession: A03372  
A:Molecule type: protein  
A:Residues: 36-97, 'Q', '99-109', 'S', '111-269', 'D', '272-283', 'V', '285-288', '290-302' <YOS>  
A>Note: this paper cites the others in the series providing experimental details for the  
R:Ataki, T.; Funatsu, G.  
FEBS Lett. 191, 121-124, 1985  
A>Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A:Reference number: A24010  
A:Accession: A24010  
A:Molecule type: protein  
A:Residues: 315-383, 'P', '386-576' <AA>  
R:Funatsu, G.; Kimura, M.; Funatsu, M.  
Agric. Biol. Chem. 43, 2221-2224, 1979  
A>Title: Primary structure of Ala chain of ricin D.  
A:Reference number: A03374  
A:Accession: A03374  
A:Molecule type: protein  
A:Residues: 36-97, 'Q', '99-109', 'S', '111-269', 'D', '272-283', 'V', '285-288', '290-302' <YOS>  
A>Note: this paper, one of a series, summarizes the experimental details for the deter  
R:Ready, M.P.; Kim, Y.; Robertus, J.D.  
Protein 10, 270-278, 1991  
A>Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism  
A:Reference number: A48237; MUID:91352004; PMID:1881883  
A:Accession: A48237  
A:Content: annotation, active site  
R:Nutbier, E.; Robertus, J.D.  
Protein 10, 260-269, 1991  
A>Title: Structure of ricin B-chain at 2.5 angstrom resolution.  
A:Reference number: A48238; MUID:91352005; PMID:1881882  
A:Accession: A48238  
A:Content: annotation, X-ray crystallography, 2.5 angstroms  
R:Nutbier, E.; Robertus, J.D.  
Protein 10, 251-259, 1991  
A>Title: Structure of ricin A-chain at 2.5 angstroms.  
A:Reference number: A48239; MUID:91352004; PMID:1881881  
A:Accession: A48239  
A:Content: annotation, X-ray crystallography, 2.5 angstroms  
C:Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which  
nec the cell of the A chain, B chains are also responsible for cell agglutination (leoc  
C:Comment: This protein is cytotoxic and very poisonous to animals.  
C:Superfamily: ricin/ RNA N-glycosidase homology  
C:Species: Ricinus communis (castor bean)  
C>Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #ext change 16-Jul-1999  
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903  
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.  
Nucleic Acids Res. 13: 8019-8033, 1985  
A>Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.  
A:Reference number: A24041; MUID:86067214; PMID:2999712  
A:Accession: A24041  
A:Molecule type: RNA  
A:Residues: 1-576 <RNA>  
R:Rice, J.; Robert, E.; Halling, K.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.  
Plant Mol. Biol. 18: 515-525, 1992  
A:Cross-references: GB:X03179; NID:g21082; PIRN:CAA26939.1; PID:g21083  
A>Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene  
A:Reference number: S20513; MUID:92163016; PMID:1371405  
A:Accession: S20513  
A:Molecule type: DNA  
A:Residues: 1-576 <RNA>  
R:Rice, J.; Robert, E.; Halling, K.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.  
Eur. J. Biochem. 148: 265-270, 1985  
A>Title: Nucleotide sequence of cloned cDNA coding for preprovidin.  
A:Reference number: A24614; MUID:85179479; PMID:3838723  
A:Accession: A24614  
A:Molecule type: mRNA  
A:Residues: 12-75, 'D', '77-550', 'R', '552-576' <LMA>  
R:Koshitake, S.; Funatsu, G.; Funatsu, M.  
Nucleic Acids Res. 22: 4286-4294, 1978  
A>Title: Isolation and characterization of cDNA sequences of peptic peptides, and the complete sequence of the ch  
A:Accession: A03372  
A:Molecule type: protein  
A:Residues: 36-97, 'Q', '99-109', 'S', '111-269', 'D', '272-283', 'V', '285-288', '290-302' <YOS>  
A>Note: this paper cites the others in the series providing experimental details for the  
R:Ataki, T.; Funatsu, G.  
FEBS Lett. 191, 121-124, 1985  
A>Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

Query Match 46.8%; Score 1229.5; DB 1; Length 576;  
Best Local Similarity 49.2%; Pred. No. 3e-111;  
Matches 264; Conservative 76; Mismatches 176; Indels 21; Gaps 12;

OY 9 TROTQKXFFRTILRDVYSSG-FSENRPL-RGSTIPVSDAGFVLYETNQGXSK 66  
DB 48 TKGAVOSTTFRIRAKRRLTCDVHEHETLVNPKVCLTN--QRTVLVSGHAEALSV 105

OY 67 TAAIDTNNYVYVYQNGOQYR-DAPNGE--THTGTTRPSGSEPYGXHXYR 123  
DB 106 TAAIDTNNYVYVYVYQNGOQYR-DAPNGE--THTGTTRPSGSEPYGXHXYR 164

OY 124 AGH-EDQIFLGLKQILQGVLA--KPPGSTRKQAFIILQVIGSEARFNIMEXR 179  
DB 165 AGH-EDQIFLGLKQILQGVLA--KPPGSTRKQAFIILQVIGSEARFNIMEXR 224

OY 225 TIRNMGARADPSVTLNMRSLNLSALVYVSGTDLPLTARFICQVIGSEARFNIMEXR 224  
DB 225 TIRNMGARADPSVTLNMRSLNLSALVYVSGTDLPLTARFICQVIGSEARFNIMEXR 284

OY 240 ASIALNMFYCGARPSGVRYVPLTIPVD--DYTCASAPFVYVIGKXGYD 286  
DB 240 ASIALNMFYCGARPSGVRYVPLTIPVD--DYTCASAPFVYVIGKXGYD 339

OY 297 DDFHQQGQIAMPSSKNDPNOIATIKEDTISNSCLATYGTAGYVWFIDCNARV 356  
DB 297 DDFHQQGQIAMPSSKNDPNOIATIKEDTISNSCLATYGTAGYVWFIDCNARV 356

Thu Dec 11 16:09:57 2003

us-09-601-667c-40.rpt

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 / Search time 16.5989 seconds  
(without alignments)  
3093.817 Million cell updates/sec

Title: US-09-601-667c-40

Reflect score: 2626

Sequence: 1 TERLRRTHTQTGKEXFRF.....RRILLYPATGKPNQWMLPYX 534

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1290	49.1	264	2 PD0019	mistletoe lectin I
2	1279.5	48.7	265	2 JN0090	lectin-I B chain -
3	1229.5	46.8	576	1 RLCSB	ricin D precursor
4	1190	45.3	528	1 TZLSA	abrin-A precursor
5	1165	44.4	254	2 PD0018	mistletoe lectin I
6	1165	44.3	254	2 PD0022	abrin-C precursor
7	1139	43.3	328	2 S12434	abrin-b precursor
8	1112.5	42.4	570	1 RLCSB	abrin-b precursor
9	1101	41.9	564	1 RLCSB	agglutinin precursor
10	851	32.4	570	2 S06227	agglutinin I precursor
11	822	31.3	263	2 S06230	agglutinin I precursor
12	443	16.9	251	2 C39761	abrin (clone 7.2)
13	302	11.5	247	2 JC5032	karasurin-B - Tric
14	301	11.5	247	2 RL277	karasurin-B - Tric
15	300	11.4	247	2 JN0093	karasurin - Mongol
16	300	11.4	245	2 JC5066	karasurin C - Tric
17	289.5	11.0	245	2 UC4840	RNA N-glycosidase
18	289.5	10.9	245	2 S25560	RNA N-glycosidase
19	280.2	10.7	386	2 UC4335	RNA N-glycosidase
20	273.2	10.4	386	2 UC4335	RNA N-glycosidase
21	254	9.7	278	2 S23612	beta-lactin - smoo
22	253.5	9.7	278	2 RL0P03	RNA N-glycosidase
23	244.5	9.3	277	2 S22494	RNA N-glycosidase
24	239.5	9.1	250	2 JN0108	lactin-B - smoo
25	233.5	8.9	278	2 A39817	RNA N-glycosidase
26	191.5	7.3	261	2 JEO401	activator protein
27	189	7.2	313	2 S17757	RNA N-glycosidase
28	184	6.9	294	2 S28421	RNA N-glycosidase
29	172.5	6.8	106	2 B39761	abrin (clone 3.7)

30	168	6.4	253	2 S28539	RNA N-glycosidase
31	166	6.3	253	2 S28542	RNA N-glycosidase
32	162	6.2	253	2 S29931	RNA N-glycosidase
33	162	6.2	253	2 S05205	RNA N-glycosidase
34	159	6.1	253	2 S28541	RNA N-glycosidase
35	157	6.0	232	1 RL0H02	RNA N-glycosidase
36	150	5.7	272	2 UC4811	beta-lactin - beet
37	141	5.4	272	2 A58923	RNA N-glycosidase
38	139.1	5.3	310	2 S45232	ribosome-inactivat
39	131	5.0	259	2 S17232	RNA N-glycosidase
40	125.5	4.8	377	2 UC7516	RNA N-glycosidase
41	125.5	4.8	377	2 UC7516	RNA N-glycosidase
42	123.5	4.7	289	2 T12573	RNA N-glycosidase
43	120	4.6	281	2 B38664	30K ribosome inact
44	118.5	4.5	477	1 JS0589	endo-l,4-beta-ryla
45	115.5	4.4	383	2 T34603	xylosylase A - strep

ALIGNMENTS

RESULT 1  
PD0019  
mistletoe lectin I B chain - Viscum album (fragment)  
C/Species: Viscum album  
C/Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #ext\_change 07-May-1999  
C/Accession: PD0019  
R/Eschschol, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelker, W.  
Biochem. Biophys. Res. Commun. 247, 367-372, 1998  
A/Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum al  
A/Reference number: PD0018; PMID:98308123; PMID:9642113  
A/Accession: PD0019  
A/Species: Viscum album  
A/Residue: 1-264, protein  
A/Residue: 1-264, protein  
C/Superfamily: Ricin, RNA N-glycosidase homology  
Query Match 49.1%, Score 1290, DB 2, Length 264,  
Best Local Similarity 92.4%, Pred. No. 1, 4e-117,  
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 271 DDVTCASPTVAIVGKXGVYDRODDPHDGNQIQIMPSEKNNDDPQWMTIRKQXTRR 330  
DB 1 DDVTCASPTVAIVGKXGVYDRODDPHDGNQIQIMPSEKNNDDPQWMTIRKQXTRR 60  
QY 331 NQSCITVTGQVAGVYVIGECNTVVEATINQWKNGTINFSNLTVAASGIGKTTTL 390  
DB 61 NQSCITVTGQVAGVYVIGECNTVVEATINQWKNGTINFSNLTVAASGIGKTTTL 120  
QY 391 VQVLDVTCGQVAGVYVIGECNTVVEATINQWKNGTINFSNLTVAASGIGKTTTL 450  
DB 121 VQVLDVTCGQVAGVYVIGECNTVVEATINQWKNGTINFSNLTVAASGIGKTTTL 180  
QY 451 GSIRPQNDQCLTGRDVSIVTINVSQSKXXQKQWFTNEXALINLKXXXXVAVQA 510  
DB 181 GSIRPQNDQCLTGRDVSIVTINVSQSKXXQKQWFTNEXALINLKXXXXVAVQA 240  
QY 511 NPKRILLYPATGKPNQWMLPYX 533  
DB 241 NPKRILLYPATGKPNQWMLPYX 263  
RESULT 2  
JN0090  
lectin-I B chain - European mistletoe  
N/Alternate names: ML-I  
C/Species: Viscum album (European mistletoe)  
C/Date: 18-Jun-1998 #sequence\_revision 10-Jul-1998 #ext\_change 19-May-2000  
A/Accession: JN0090  
A/Species: H. Stoeva, S.; Voelker, W.  
Biochem. Biophys. Res. Commun. 246, 566-601, 1998  
A/Title: Complete amino acid sequence of the B chain of mistletoe lectin I.  
A/Reference number: JN0090; PMID:98289575; PMID:9610256  
A/Accession: JN0090

LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-338-793D-61

Query Match  
Best Local Similarity 30.5%; Score 396; DB 2; Length 267;  
Best Local Similarity 40.2%; Pred. No. 1.9e-33;  
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

9 THQTGDEYFPTLLRDVSSGS-FSNEIFPL-RGSIPTVSDAORFVIVELINOGDSI 66  
13 TGAIVQSYTFIRAVGRGLTGADVREHPIVLRVGLPIN-QRIVELSNHAEISV 70

67 TAAIDVTAIVYVQAGDSYFLR-DAPRGAE--THLFTGTRDSSSLPFGSYTDLERY 123  
71 TLALDVTAIVYVQAGDSYFLR-DAPRGAE--THLFTGTRDSSSLPFGSYTDLERY 129

124 AGH-RDQIPGIEQLQSVSAIY--FGSTRQASSTILITOMISPAAPFPIIMRYR 179  
130 AGH-RNRIELNGFLEALISALYYSVGQQLPLASFTICIMISEAARFQYIBENR 189

180 ODINSSEFLPDWMLETSMQGSYOVCHSTDCVNNPFLAISTGAVTISNYSVI 239  
190 TRIRYRRASAPPSVITLNSWGLSTALQSNQAFASPIQLQRNRSKSVYIVSILI 249

240 ASLAINLFCVGERPSS 255  
250 PITALMYRCAPPPSS 265

DB 250 PITALMYRCAPPPSS 265

RESULT 15  
US-08-839-765-1  
Sequence 1. Application US/08839765  
Patent No. 6146631

GENERAL INFORMATION:  
APPLICANT: Bectel, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studzika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
DORSEY, Andrew, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: Patent in Release #1.0, Version #1.25  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
FIRM: Bectel, Marc D.  
REGISTERED NUMBER: 2,318  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
MOLRECS TYPE: protein  
US-08-839-765-1

Query Match  
Best Local Similarity 30.5%; Score 396; DB 3; Length 267;  
Best Local Similarity 40.2%; Pred. No. 1.9e-33;  
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

9 THQTGDEYFPTLLRDVSSGS-FSNEIFPL-RGSIPTVSDAORFVIVELINOGDSI 66  
13 TGAIVQSYTFIRAVGRGLTGADVREHPIVLRVGLPIN-QRIVELSNHAEISV 70

67 TAAIDVTAIVYVQAGDSYFLR-DAPRGAE--THLFTGTRDSSSLPFGSYTDLERY 123  
71 TLALDVTAIVYVQAGDSYFLR-DAPRGAE--THLFTGTRDSSSLPFGSYTDLERY 129

124 AGH-RDQIPGIEQLQSVSAIY--FGSTRQASSTILITOMISPAAPFPIIMRYR 179  
130 AGH-RNRIELNGFLEALISALYYSVGQQLPLASFTICIMISEAARFQYIBENR 189

180 ODINSSEFLPDWMLETSMQGSYOVCHSTDCVNNPFLAISTGAVTISNYSVI 239  
190 TRIRYRRASAPPSVITLNSWGLSTALQSNQAFASPIQLQRNRSKSVYIVSILI 249

240 ASLAINLFCVGERPSS 255  
250 PITALMYRCAPPPSS 265

DB 250 PITALMYRCAPPPSS 265

Search completed: December 11, 2003, 14:11:37  
Job time: 9.86328 secs

13 TGAATVQSYTNFPAVAGRLTGADVREHIFVLPVRVGLPIN--ORFLVELSNHAEISV 70  
QY 67 TPAIDVTAAVVAQADQSYFLR-DARQAR--THLFTGTDRSSLPFTQSYTDLERY 123  
DB 71 TLADVTAAVVAQADQSYFLR-DARQAR--THLFTGTDRSSLPFTQSYTDLERY 129  
QY 124 RGH-EDQPGICBOLIOSVSAIR--FGSTRQASLILLOMISAPRNPLMNR 179  
DB 130 KQNFEMTELGNGPLEAASLVYVSTGTQPLTASPLICQWISAPARQYIEGMR 189  
QY 180 QDINSGESELPDWMALSTWQSQSTQVSHSTQVNNPFLALSTQNVTLANRSVY 239  
DB 190 TRIVNRSAPDPSVITLNSWGLSTALQESNQASAPFQLORRNGSKFSYVDSILI 249  
QY 240 ASLAIMLVGGERPSS 255  
DB 250 PTLMDVTRKAPRPS 265

## RESULT 13

US-08-646-360-1  
Sequence 1, Application US/08646360  
Patent No. 5837491

GENERAL INFORMATION:  
APPLICANT: Bettec, Marc D.  
INVENTOR: Carroll, Stephen F.  
TITLE OF INVENTION: Immunocytins Compacting Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60641

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: PCT/US94/05348  
PRIOR APPLICATION DATA:  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION DATA:  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/988,430  
PRIOR APPLICATION DATA:  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/901,707  
PRIOR APPLICATION DATA:  
FILING DATE: 04-NOV-1991  
APPLICATION NUMBER: US 07/787,567  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70, P4  
TELEPHONE: 312/777-9155  
TELEFAX: 312/777-9155  
TELEX: 650 388-1248

IMPORTATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-1  
Query Match 30.5%; Score 396; DB 2; Length 267;  
Best Local Similarity 40.2%; Pct. No. 1.9e-35;  
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;  
QY 9 TQRTDDEYFRFTLLADVSSGS-PSNEPLI-RQSTPYSDQRFVLELTVQQDSI 66  
DB 13 TGAATVQSYTNFPAVAGRLTGADVREHIFVLPVRVGLPIN--ORFLVELSNHAEISV 70  
QY 67 TPAIDVTAAVVAQADQSYFLR-DARQAR--THLFTGTDRSSLPFTQSYTDLERY 123  
DB 71 TLADVTAAVVAQADQSYFLR-DARQAR--THLFTGTDRSSLPFTQSYTDLERY 129  
QY 124 RGH-EDQPGICBOLIOSVSAIR--FGSTRQASLILLOMISAPRNPLMNR 179  
DB 130 KQNFEMTELGNGPLEAASLVYVSTGTQPLTASPLICQWISAPARQYIEGMR 189  
QY 180 QDINSGESELPDWMALSTWQSQSTQVSHSTQVNNPFLALSTQNVTLANRSVY 239  
DB 190 TRIVNRSAPDPSVITLNSWGLSTALQESNQASAPFQLORRNGSKFSYVDSILI 249  
QY 240 ASLAIMLVGGERPSS 255  
DB 250 PTLMDVTRKAPRPS 265

## RESULT 14

US-08-338-793D-61  
Sequence 61, Application US/08338793D  
Patent No. 5840521

GENERAL INFORMATION:  
APPLICANT: Bettec, Peter Thomas  
INVENTOR: Barton, Victor  
TITLE OF INVENTION: Immunocytins Compacting Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DAREY CUSHMAN  
ADDRESS: INTELLECTUAL PROPERTY GROUP OF  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C. 20005  
COUNTRY: U.S.A.  
ZIP: 20005-3518

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 1.44 MB storage  
COMPUTER: IBM PC/XT/AT Compatibles  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word or ASCII editors  
CURRENT APPLICATION DATA:  
FILING DATE: 08-NOV-94  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
FILING DATE: 07/842,081  
APPLICATION NUMBER: 9104017.0  
FILING DATE: 26-Feb-91  
APPLICATION NUMBER: 9109188-4  
FILING DATE: 29-APR-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohnle, Paul N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 200-70, P4  
TELEPHONE: 202-661-3000  
TELEFAX: 202-661-3000  
TELEX: 6714627 CUSH

IMPORTATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:

Thu Dec 11 16:09:51 2003

us-09-601-667c-38.ra1

Page 6

US-08-488-113B-1  
Sequence 1, Application US/08488113B  
Patent No. 5,745,610  
GENERAL INFORMATION:  
APPLICANT: Bettef, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
CLASSIFICATION: 530  
FILING DATE: 07-JUN-1995  
PRIORITY DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIORITY DATE: 18-APR-1995  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIORITY DATE: 12-MAY-1993  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIORITY DATE: 09-DEC-1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIORITY DATE: 19-JUN-1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
PRIORITY DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 110220507/200-70-P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-8889  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-1  
Query Match  
Best Local Similarity 40.2%, P-adj. 1.9e-33, Indels 12, Gaps 8,  
Matches 103, Conservative 45, Mismatches 96  
DB 13 TACATVOSYTNFRAVAGRLTGADVREHPLEKRVGLPIN--ORFLVESHAEISLV 70  
QY 9 THQTGDEYFRFTLLRDVYSSGS--FSNEPPL-ROSTIPVSDAORPVLVETNOGOSI 66  
DB 67 TAAIDVNAVYAVQADOSTFLR DAREAR--THLFTGTDRSSSPTGSSYDIERV 123  
QY 71 TLADVTNAIVAGVIRAGNARAFHFDNCEADATLHLEF--DVQKRTYAGAGNDRLDGL 129  
DB 124 AGH-POIRIEHQIOLVSATY--FGSSTRQARSTILICMISAAAPVILAKRY 179  
QY 130 AGNLRNLELNGNGLEBAISLVYTSGTGFLPLANSPTICIMISAAAPVILAKRY 189

QY 180 QDINGSSEFLPDNWKLETSKQGGQGVCHSTGCVENNPRLAISTNIVLSTNYSVY 239  
DB 190 TTRVNRSAADPSVITLNSHSLTALIGSNQARASPTGLARNSGKFSVYVDSILA 249  
QY 240 ASLAIWLPVCGRPSS 285  
DB 250 PIRALVYRCAPPSS 265  
RESULT 12  
US-08-477-484B-1  
Sequence 1, Application US/08477484B  
Patent No. 5,755,639  
GENERAL INFORMATION:  
APPLICANT: Bettef, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
CLASSIFICATION: 530  
FILING DATE: 07-JUN-1995  
PRIORITY DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIORITY DATE: 18-APR-1995  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIORITY DATE: 12-MAY-1993  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIORITY DATE: 09-DEC-1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 04-NOV-1991  
PRIORITY DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 110220507/200-70-P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-8889  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-1  
Query Match  
Best Local Similarity 40.2%, P-adj. 1.9e-33, Indels 12, Gaps 8,  
Matches 103, Conservative 45, Mismatches 96  
QY 9 THQTGDEYFRFTLLRDVYSSGS--FSNEPPL-ROSTIPVSDAORPVLVETNOGOSI 66

Thu Dec 11 16:09:51 2003

us-09-601-667c-38.ra1

Page 5

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US-08-218-303-16
; Sequence 16, Application US/08218303
; Patent No. 5547867
; GENERAL INFORMATION:
; APPLICANT: Kera, Bhupendra V.
; APPLICANT: Hockney, Robert C.
; APPLICANT: Johnson, John E.
; TITLE OF INVENTION: IMMUNOTOXIN PROCESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/218,303
; CLASSIFICATION: 435
; PRIORITY INFORMATION DATA:
; PRIORITY NUMBER: US 07/841,533
; FILING DATE: 26-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerkulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PAK/3893/94908/NAW
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELETYPE: 202-861-3000
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-218-303-16

Query Match 30.5%; Score 396; DB 1; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

QY 9 TQCTGDEYFRFTLLADYSSGS-FSNEPPL-ROSTPVSDQRFLVETLNOQDSI 66
DB 13 TQATVQSYNTPFRAVAGLTTADVREHLPVLPVRVGLPIN--GRFTLVELSHKALSV 70
QY 67 TLAIDTVNAVVAOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSSYTDLERY 123
DB 71 TLAIDTVNAVVAOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSSYTDLERY 129
QY 124 ASH-RQOPLGIBOLIOVSALRY--PGSTRQASILLIOWISEAPRNPLIMNR 179
DB 130 KQNRNIEELGNPLEASLSLVYSTGCTOLPLASFLICOWISEAPRNPLIMNR 189
QY 180 QDINSSESFLPDVWMLSTMSQSQSTOVQASHDGVNPPRLAISTGNFTLSNVSVI 239
DB 190 THINRKSAPDSVITLNSNGSLTALDSNQASAPETQLQRNNSKFSYDVSVILI 249
QY 240 ASLAINLFGCARPPSS 255
DB 250 PTLNLTWRQAPPPSS 265

US-08-425-336-1
; Sequence 1, Application US/08425336
; Patent No. 5621083

US-08-218-303-16
; Sequence 16, Application US/08218303
; Patent No. 5547867
; GENERAL INFORMATION:
; APPLICANT: Kera, Bhupendra V.
; APPLICANT: Hockney, Robert C.
; APPLICANT: Johnson, John E.
; TITLE OF INVENTION: IMMUNOTOXIN PROCESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/218,303
; CLASSIFICATION: 435
; PRIORITY INFORMATION DATA:
; PRIORITY NUMBER: US 07/841,533
; FILING DATE: 26-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerkulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PAK/3893/94908/NAW
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELETYPE: 202-861-3000
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-218-303-16

Query Match 30.5%; Score 396; DB 1; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

QY 9 TQCTGDEYFRFTLLADYSSGS-FSNEPPL-ROSTPVSDQRFLVETLNOQDSI 66
DB 13 TQATVQSYNTPFRAVAGLTTADVREHLPVLPVRVGLPIN--GRFTLVELSHKALSV 70
QY 67 TLAIDTVNAVVAOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSSYTDLERY 123
DB 71 TLAIDTVNAVVAOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSSYTDLERY 129
QY 124 ASH-RQOPLGIBOLIOVSALRY--PGSTRQASILLIOWISEAPRNPLIMNR 179
DB 130 KQNRNIEELGNPLEASLSLVYSTGCTOLPLASFLICOWISEAPRNPLIMNR 189
QY 180 QDINSSESFLPDVWMLSTMSQSQSTOVQASHDGVNPPRLAISTGNFTLSNVSVI 239
DB 190 THINRKSAPDSVITLNSNGSLTALDSNQASAPETQLQRNNSKFSYDVSVILI 249
QY 240 ASLAINLFGCARPPSS 255
DB 250 PTLNLTWRQAPPPSS 265

US-08-425-336-1
; Sequence 1, Application US/08425336
; Patent No. 5621083

US-08-218-303-16
; Sequence 16, Application US/08218303
; Patent No. 5547867
; GENERAL INFORMATION:
; APPLICANT: Kera, Bhupendra V.
; APPLICANT: Hockney, Robert C.
; APPLICANT: Johnson, John E.
; TITLE OF INVENTION: IMMUNOTOXIN PROCESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/218,303
; CLASSIFICATION: 435
; PRIORITY INFORMATION DATA:
; PRIORITY NUMBER: US 07/841,533
; FILING DATE: 26-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerkulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PAK/3893/94908/NAW
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELETYPE: 202-861-3000
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-218-303-16

Query Match 30.5%; Score 396; DB 1; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

QY 9 TQCTGDEYFRFTLLADYSSGS-FSNEPPL-ROSTPVSDQRFLVETLNOQDSI 66
DB 13 TQATVQSYNTPFRAVAGLTTADVREHLPVLPVRVGLPIN--GRFTLVELSHKALSV 70
QY 67 TLAIDTVNAVVAOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSSYTDLERY 123
DB 71 TLAIDTVNAVVAOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSSYTDLERY 129
QY 124 ASH-RQOPLGIBOLIOVSALRY--PGSTRQASILLIOWISEAPRNPLIMNR 179
DB 130 KQNRNIEELGNPLEASLSLVYSTGCTOLPLASFLICOWISEAPRNPLIMNR 189
QY 180 QDINSSESFLPDVWMLSTMSQSQSTOVQASHDGVNPPRLAISTGNFTLSNVSVI 239
DB 190 THINRKSAPDSVITLNSNGSLTALDSNQASAPETQLQRNNSKFSYDVSVILI 249
QY 240 ASLAINLFGCARPPSS 255
DB 250 PTLNLTWRQAPPPSS 265

US-08-425-336-1
; Sequence 1, Application US/08425336
; Patent No. 5621083
```

Thu Dec 11 16:09:51 2003

us-09-601-667c-38.rat

Page 4

APPLICANT: Carroll, Steve F.  
APPLICANT: Lane, Julie A.  
TITLE OF INVENTION: Materials Comprising and Methods of  
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Markell, O'Toole, Gerstein, Murray &  
ADDRESSEE: Markell, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/901,707  
PRIORITY DATA:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 537654and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27129/30910  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-5750  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-901-707-1

Query Match 30.5%; Score 396; DB 1; Length 267;  
Best Local Similarity 40.2%; Pred. No. 1.9e-33;  
Matches 103; Conservative 45; Mismatches 56; Indels 12; Gaps 8;  
QY 9 THQTGDEYFRFTLLADYSSGS-FSNEIFLL-RGSTIPVSDAQRFLVLTNQSDSI 66  
DB 13 TGAIVOSYTNFIRAVGRHLTADVREHPIVLPFRVGLPIN--ORFLVLSHMAISV 70  
QY 67 TAAIDVNAIVYVAVQAGOSYFLR-DAREGAR--THLFTGTDRSSLPFGSYTLERY 123  
DB 71 TLAADVTAIVYVAVQAGOSYFLR-DAREGAR--THLFTGTDRSSLPFGSYTLERY 129  
QY 124 AGH-RDPIGLAIGLQVSAARY--FGSSTAAQASIIILQWISBAARFNIMRYR 179  
DB 130 AGRREHIELGNGPLEBAISALYYSTGCTOLPLAREFTICQWISBAARFNIMRYR 189  
QY 180 QDINSGEFLPDWMLLETSTMGQSTOVQSTGVFNFPRLAISTGNVYTLNRSYI 239  
DB 190 TRIRYRRASAPDSVITLNSMGRSLTAQENQAGAFSPLOLRNGSRFSYDVSIIL 249  
QY 240 ASIAIMLVCGRRPS 255  
DB 250 FTLAMVYRCAPRPS 265

RESULT 8  
US-07-986-430-1  
Sequence 1, Application US/07986430  
Patent No. 5416202  
GENERAL INFORMATION:  
APPLICANT: Bernhard, Susan L.

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Lane, Julie A.  
APPLICANT: Lei, Shau-Ping  
TITLE OF INVENTION: Materials Comprising and Methods of  
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Markell, O'Toole, Gerstein, Murray &  
ADDRESSEE: Markell, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/986,430  
FILING DATE: 19921209  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 537654and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-986-430-1

Query Match 30.5%; Score 396; DB 1; Length 267;  
Best Local Similarity 40.2%; Pred. No. 1.9e-33;  
Matches 103; Conservative 45; Mismatches 56; Indels 12; Gaps 8;  
QY 9 THQTGDEYFRFTLLADYSSGS-FSNEIFLL-RGSTIPVSDAQRFLVLTNQSDSI 66  
DB 13 TGAIVOSYTNFIRAVGRHLTADVREHPIVLPFRVGLPIN--ORFLVLSHMAISV 70  
QY 67 TAAIDVNAIVYVAVQAGOSYFLR-DAREGAR--THLFTGTDRSSLPFGSYTLERY 123  
DB 71 TLAADVTAIVYVAVQAGOSYFLR-DAREGAR--THLFTGTDRSSLPFGSYTLERY 129  
QY 124 AGH-RDPIGLAIGLQVSAARY--FGSSTAAQASIIILQWISBAARFNIMRYR 179  
DB 130 AGRREHIELGNGPLEBAISALYYSTGCTOLPLAREFTICQWISBAARFNIMRYR 189  
QY 180 QDINSGEFLPDWMLLETSTMGQSTOVQSTGVFNFPRLAISTGNVYTLNRSYI 239  
DB 190 TRIRYRRASAPDSVITLNSMGRSLTAQENQAGAFSPLOLRNGSRFSYDVSIIL 249  
QY 240 ASIAIMLVCGRRPS 255  
DB 250 FTLAMVYRCAPRPS 265

RESULT 9



Thu Dec 11 16:09:51 2003

us-09-601-667c-38.ra1

Page 3

US-08-378-761A-71  
Sequence 71, Application US/08378761A  
Patent No. 5635384  
GENERAL INFORMATION:  
INVENTOR: MORGAN, ALICE BE  
APPLICANT: HEY TIMOTHY D  
TITLE OF INVENTION: PEPTIDE-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PEPTIDE-INACTIVATING PROTEINS, INACTIVE  
TITLES OF INVENTION: USING  
CORRESPONDING NUMBERS: 91  
ADDRESSER: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
FILED IN: 1 COPY  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JUN-1995  
PRIORITY CLAIM: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 337-6846  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS  
LENGTH: 350 amino acids.  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
18-08-378-761A-71: protein

[illegible]

RESULT 6  
US-08-485-286-71  
; Sequence 71, Application US/08485286  
; Patent No. 5646026  
; Patent No. 5646026 5646119  
; GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A  
 APPLICANT: RAY, TIMOTHY D  
 INVENTOR: MORAN, ALGER  
 TITLE OF INVENTION: INACTIVATING PROTEIN, INACTIVE  
 TITLE OF INVENTION: PROTEIN FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
 TITLE OF INVENTION: USING  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: ANDREA T. BORUCKI  
 STREET: 9330 ZIONSVILLE ROAD  
 CITY: INDIANAPOLIS  
 STATE: IN  
 COUNTRY: US  
 ZIP: 46268  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,286  
 FILING DATE: 26-JAN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/378761  
 FILING DATE: 26-JAN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BORUCKI, ANDREA T  
 REGISTRATION NUMBER: 33651  
 REFERENCE/DOCKET NUMBER: 38272B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 337-4946  
 INFORMATION: 8317  
 SEQUENCE CHARACTERISTICS: 71:  
 LENGTH: 250 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-485-286-71

Query Match	43.1%;	Score	466.5;	D1;	Length	250;			
Best Local Similarity	45.1%;	Pred. No.	7e-41;						
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Qy	9	THQDGEVPTTLTPYVYSSGSSSTPLGSGTNSDQNPVITNMOCSQIA	68						
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Qy	69	ALDYNNAYVYQAGDQSYFLKDKPRGAEHTLFTGTITDSSSLSEPTQSYTDLKRYGKH-127							
Dh	67	GIDVTNAYVYVYKRGDSIFLNDKAPSSADYLTFTG-DGSHLPYGVYIGLEMAHOSR	124						
Qy	128	DDPIPLGIELQSGSNARVYSGSSRQASRIILLIOMISAAEENPLIMRYQDINSSES	187						
Dh	125	QDPIPLGIELQTHSIFSGSGNDKEKARTIYIILQWAAARFRYSRIRVFSIOTCTA	184						
Qy	188	FLEPMIVLELTSWQSGTGVCHSTGCVFNNPRLIATSTGNFTLLSNWS-	237						
Dh	185	FQPMVNIENLNNL-DNIRGQVSGVQCTFNG-----VILNINNPVYVDSLSH	223						
Qy	238	-VIALSLALFVCC	249						
Dh	234	PYVAVALALFVCC	246						

RESULT 7  
US-07-901-707-1  
Sequence 1, Application US/07901707  
Patent No. 5376546  
GENERAL INFORMATION:  
APPLICANT: Bernhard, Susan L.  
APPLICANT: Better, Marc D.

```
RESULT 2
US-08-776-059-31
/ Sequence 31, Application US/087760598
/ Patent No. 6271368
/ GENERAL INFORMATION:
/ APPLICANT: LENTZEN, Hans
/ APPLICANT: ECK, Jurgen
/ APPLICANT: AXEL, Axel
/ APPLICANT: BAUR, Axel
/ APPLICANT: ZINKE, Holger
/ TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
/ FILE REFERENCE: 674503-2003
/ CURRENT APPLICATION NUMBER: US/08/776, 0598
/ CURRENT FILING DATE: 1999-06-19
/ EARLIER APPLICATION NUMBER: PCT/EP96/02273
/ EARLIER FILING DATE: 1996-06-25
/ EARLIER APPLICATION NUMBER: 95109949.8
/ EARLIER FILING DATE: 1995-06-26
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 31
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Viscum album

US-08-776-059-31
Query Match          90.4%; Score 1174; DB 3; Length 253;
Best Local Similarity 91.7%; Pred. No. 4,76-115;
Matches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 YERIALYVHCTGDEPRFRLILADYVSSGSPSENIPLRGSTIPVSDAQFVLELTVN 60
DB 2 YERIALYVHCTGDEPRFRLILADYVSSGSPSENIPLRGSTIPVSDAQFVLELTVN 61
QY 61 QGQSDITPAIDVNAVVAQADGQSYFLDAPRGAEHLFTGTRRDSGLPTGSYDGL 120
DB 62 QGQSDITPAIDVNAVVAQADGQSYFLDAPRGAEHLFTGTRRDSGLPTGSYDGL 119
QY 121 ERYAGHRDQIPVIGBQILQSVSALRYPGSTPAQASILLIQMISAPARNPILMYR 180
DB 120 ERYAGHRDQIPVIGBQILQSVSALRYPGSTPAQASILLIQMISAPARNPILMYR 179
QY 181 DINGSGEFLPMWMLSTETSWGQSTGVCHSTGCHRNPPRLAISTGNVTLNVSYS 240
DB 180 YINSGASFLPDVWLELSTWQSGSTGVCHSTGCHRNPPRLAISTGNVTLNVSYS 239
QY 241 SLAIVLPGCGRPS 254
DB 240 SLAIVLPGCGRPS 253

RESULT 3
US-08-776-059-39
/ Sequence 39, Application US/087760598
/ Patent No. 6271368
/ GENERAL INFORMATION:
/ APPLICANT: LENTZEN, Hans
/ APPLICANT: ECK, Jurgen
/ APPLICANT: AXEL, Axel
/ APPLICANT: BAUR, Axel
/ APPLICANT: ZINKE, Holger
/ TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
/ FILE REFERENCE: 674503-2003
/ CURRENT APPLICATION NUMBER: US/08/776, 0598
/ CURRENT FILING DATE: 1999-06-19
/ EARLIER APPLICATION NUMBER: PCT/EP96/02273
/ EARLIER FILING DATE: 1996-06-25
/ EARLIER APPLICATION NUMBER: 95109949.8
/ EARLIER FILING DATE: 1995-06-26
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 39
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Viscum album

US-08-776-059-39
Query Match          83.8%; Score 1089; DB 3; Length 235;
Best Local Similarity 92.0%; Pred. No. 3,4e-106;
Matches 218; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 18 FPIITLADYVSSGSPSENIPLRGSTIPVSDAQFVLELTVNQGQSDITPAIDVNAV 77
DB 1 FPIITLADYVSSGSPSENIPLRGSTIPVSDAQFVLELTVNQGQSDITPAIDVNAV 60
QY 78 VAVQADGQSYFLDAPRGAEHLFTGTRRDSGLPTGSYDGLERYAGHRDQIPVIGB 137
DB 61 VAVQADGQSYFLDAPRGAEHLFTGTRRDSGLPTGSYDGLERYAGHRDQIPVIGB 118
QY 138 IQSVSALRYPGSTPAQASILLIQMISAPARNPILMYRQDINGSEFLPMWML 197
DB 119 IQSVSALRYPGSTPAQASILLIQMISAPARNPILMYRQDINGSEFLPMWML 178
QY 198 ETSWQSGSTGVCHSTGCHRNPPRLAISTGNVTLNVSYSVIALVLPVCGRPS 254
DB 179 ETSWQSGSTGVCHSTGCHRNPPRLAISTGNVTLNVSYSVIALVLPVCGRPS 235

RESULT 4
US-09-538-873-3
/ Sequence 3, Application US/09538873
/ Patent No. 6566500
/ GENERAL INFORMATION:
/ APPLICANT: VITETTA, ELLEN S.
/ APPLICANT: GHETTE, VICTOR F.
/ APPLICANT: SHALINSKY, JOAN
/ APPLICANT: BALDWIN, ROXANA G.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
/ FILE REFERENCE: USPD 603
/ CURRENT APPLICATION NUMBER: US/09/538, 873
/ CURRENT FILING DATE: 2000-03-30
/ EARLIER APPLICATION NUMBER: 60/126, 826
/ EARLIER FILING DATE: 1999-03-30
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ TYPE: PRT
/ ORGANISM: Abinus precatorius

US-09-538-873-3
Query Match          36.5%; Score 474; DB 4; Length 251;
Best Local Similarity 43.1%; Pred. No. 1,1e-41;
Matches 109; Conservative 37; Mismatches 81; Indels 26; Gaps 6;

QY 9 THQTCDEYFRPITLADYVSSGSPSENIPLRGSTIPVSDAQFVLELTVNQGQSDIT 68
DB 9 THQTCDEYFRPITLADYVSSGSPSENIPLRGSTIPVSDAQFVLELTVNQGQSDIT 66
QY 69 IDPITNAVVAQADGQSYFLDAPRGAEHLFTGTRRDSGLPTGSYDGLERYAGHR 127
DB 67 IDPITNAVVAQADGQSYFLDAPRGAEHLFTGTRRDSGLPTGSYDGLERYAGHR 124
QY 128 DQIPLDQILQSVSALRYPGSTPAQASILLIQMISAPARNPILMYRQDINGSGS 187
DB 125 DQIPLDQILQSVSALRYPGSTPAQASILLIQMISAPARNPILMYRQDINGSGS 184
QY 188 FLPMWMLSTETSWGQSTGVCHSTGCHRNPPRLAISTGNVTLNVSYS 237
DB 185 FLPMWMLSTETSWGQSTGVCHSTGCHRNPPRLAISTGNVTLNVSYS 234
QY 238 VIALVLPVCGRPS 249
DB 235 VIALVLPVCGRPS 247

RESULT 5
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Thu Dec 11 16:09:51 2003

us-09-601-667c-38.ra1

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 / Search time 8.86328 seconds  
(without alignments)

1222.073 Million cell updates/sec

Title: US-09-601-667C-38

Sequence: 1 YENLKLRYHTQTDYFRFP.....SYLALALKEFYVCGRRSS 256

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: /cgn2\_6/prodata/1/aa/5A.COMB.pep.\*

2: /cgn2\_6/prodata/1/aa/5B.COMB.pep.\*

3: /cgn2\_6/prodata/1/aa/6A.COMB.pep.\*

4: /cgn2\_6/prodata/1/aa/6B.COMB.pep.\*

5: /cgn2\_6/prodata/1/aa/6C.COMB.pep.\*

6: /cgn2\_6/prodata/1/aa/backlist.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1188	91.5	564	3	US-08-776-059-35
2	1174	80.4	253	3	US-08-776-059-31
3	1174	32.8	225	4	US-08-776-059-39
4	474	35.3	250	4	US-08-558-873-3
5	466.5	35.9	250	1	US-08-482-782-71
6	466.5	35.9	250	1	US-08-482-782-71
7	396	30.5	287	1	US-07-901-707-1
8	396	30.5	287	1	US-07-988-430-1
9	396	30.5	287	1	US-08-218-303-16
10	396	30.5	287	1	US-08-425-336-1
11	396	30.5	287	1	US-08-488-1138-1
12	396	30.5	287	1	US-08-477-4848-1
13	396	30.5	287	2	US-08-646-360-1
14	396	30.5	287	3	US-08-932-765-1
15	396	30.5	287	3	US-08-932-765-1
16	396	30.5	287	4	US-08-416-389-1
17	396	30.5	287	4	US-09-818-873-1
18	396	30.5	287	4	US-09-818-873-1
19	396	30.5	287	5	PCT-US92-09487-1
20	396	30.5	288	2	US-08-356-786-8
21	396	30.5	534	2	US-08-356-786-10
22	392.5	30.2	540	1	US-08-378-761A-77
23	392.5	30.2	540	1	US-08-485-286-77
24	392.5	30.2	280	1	US-08-378-761A-27
25	392.5	30.2	280	1	US-08-485-286-27
26	392.5	30.2	280	6	5248606-4
27	392.5	30.2	280	6	5248606-4
28	392.5	30.2	280	6	5248606-4
29	392.5	30.2	280	6	5248606-4
30	392.5	30.2	280	6	5248606-4
31	392.5	30.2	280	6	5248606-4
32	392.5	30.2	280	6	5248606-4
33	392.5	30.2	280	6	5248606-4
34	392.5	30.2	280	6	5248606-4
35	392.5	30.2	280	6	5248606-4
36	392.5	30.2	280	6	5248606-4
37	392.5	30.2	280	6	5248606-4
38	392.5	30.2	280	6	5248606-4
39	392.5	30.2	280	6	5248606-4
40	392.5	30.2	280	6	5248606-4
41	392.5	30.2	280	6	5248606-4
42	392.5	30.2	280	6	5248606-4
43	392.5	30.2	280	6	5248606-4
44	392.5	30.2	280	6	5248606-4
45	392.5	30.2	280	6	5248606-4

#### ALIGNMENTS

28	329	25.3	267	1	US-08-378-761A-74	Sequence 74, Appl
29	329	25.3	267	1	US-08-485-286-74	Sequence 74, Appl
30	327	25.2	247	1	US-08-488-1138-6	Sequence 6, Appl
31	327	25.2	247	1	US-08-477-4848-6	Sequence 6, Appl
32	327	25.2	247	2	US-08-646-360-6	Sequence 6, Appl
33	327	25.2	247	3	US-08-932-765-6	Sequence 6, Appl
34	327	25.2	247	3	US-08-932-765-6	Sequence 6, Appl
35	327	25.2	247	4	US-08-416-389-6	Sequence 6, Appl
36	327	25.2	247	4	US-09-818-873-6	Sequence 6, Appl
37	327	25.2	247	4	US-09-818-873-6	Sequence 6, Appl
38	322	24.8	289	2	US-08-182-327-4	Sequence 4, Appl
39	322	24.8	289	3	US-08-483-502-4	Sequence 4, Appl
40	322	24.8	289	4	US-08-483-502-4	Sequence 4, Appl
41	322	24.8	289	4	US-09-726-651A-4	Sequence 4, Appl
42	314	24.2	263	1	US-07-901-707-4	Sequence 4, Appl
43	314	24.2	263	1	US-07-988-430-4	Sequence 4, Appl
44	314	24.2	263	1	US-08-425-336-4	Sequence 4, Appl
45	314	24.2	263	1	US-08-488-1138-4	Sequence 4, Appl

#### RESULT 1

US-08-776-059-35	Sequence 35, Appl
Patent No. 6271368	Application US/0876059B
GENERAL INFORMATION:	
APPLICANT: LEMZEN, Hans	
APPLICANT: BAK, Axel	
APPLICANT: BAK, Axel	
APPLICANT: BAK, Axel	
TITLE OF INVENTION: RECOMBINANT KISTLETOR LECTIN (RML)	
FILE REFERENCE: 674503-2003	
CURRENT APPLICATION NUMBER: US/08/776, 059B	
EARLIER FILING DATE: 1999-06-19	
EARLIER APPLICATION NUMBER: PCT/EP96/02273	
EARLIER FILING DATE: 1996-06-25	
EARLIER APPLICATION NUMBER: 95109949.8	
EARLIER FILING DATE: 1995-06-26	
NUMBER OF SEQ ID NOS: 56	
SOFTWARE: Patent In Ver. 2.0	
SEQ ID NO: 35	
TYPE: PEP	
ORGANISM: Viscum album	
US-08-776-059-35	

#### Query Match

Best local similarity	31.5%; Score 1188; DB 3; Length 564;
Matches 227; Conservative	5; Mismatches 12; Indels 2; Gaps 1;

Qy	1	YENLKLRYHTQTDYFRFP.....SYLALALKEFYVCGRRSS 256	Sequence 74, Appl
Qy	61	QGGDSITPAIDVTMLVYVAQADGQSFARDAFGHFLVLTOTT-RSLFLPNQSVPL 151	Sequence 151, Appl
Qy	121	ERYAGHDQIPGIEQLQSVSLVYGGSTPAQASILVLIQMSSEALFPIVWYRQ 180	Sequence 180, Appl
Qy	152	ERYAGHDQIPGIEQLQSVSLVYGGSTPAQASILVLIQMSSEALFPIVWYRQ 211	Sequence 211, Appl
Qy	181	DINSGSFLPDWVLELETSKQSTVOVSHDCVNNPFLAISTGPFYLSNVSVA 240	Sequence 240, Appl
Qy	212	YINSGSFLPDWVLELETSKQSTVOVSHDCVNNPFLAISTGPFYLSNVSVA 271	Sequence 271, Appl
Qy	241	SLALKEFYVCGRRSS 256	Sequence 256, Appl
Qy	272	SLALKEFYVCGRRSS 287	Sequence 287, Appl



Thu Dec 11 16:09:52 2003

us-09-601-667c-38.rapb

Page 7

FILING DATE: 23-APR-2002  
CLASSIFICATION: <Unknown>  
PRIORITY NUMBER: 1  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
FILING DATE: 19-JUN-1992  
FILING DATE: 07/901,707  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70, P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 111:  
US-10-127-890-111  
Query Match 22.7%; Score 294.5; DB 12; Length 251;  
Best Local Similarity 34.4%; Pred. No. 7.2e-23;  
Matches 87; Conservative 36; Mismatches 109; Indels 21; Gaps 7;  
QY 8 VTHQGTGDEYFRFTTLADY---VSSGSSNENFLPGSTIPVSDQRFVLEINQGD 64  
DB 5 VSPSTGATYTVVNFLEIRKLEKNSHGIPLKRC--DQPKCFVLAINDMQ 62  
QY 65 SITAIIDVNAVYVYQAGDSYFLDAPRAAEFLFTGTEDSSLPFTGSYTLERYA 124  
DB 63 LAELAIIDVSYVYQVYRNRSYFPDAPRAAYEGFLPKTIKTR--LHFGSYPSLGEK 120  
QY 125 GHRDQPLGIRIOL---IOSVALRYPGSGSTRQAQASILLIOMISGAAR---NPILMR 177  
DB 121 AVEETDDEIEPRTGIGKIDENALINDYKTEFLASLLVYQVSEAAEFTEINQINRN 180  
QY 178 YRQDINSSEFLPDWYLELETSWQOOSTQVQHS--TDGVFNNPFLAISTGNVTLNVR 236  
DB 181 PQGRIR-----PANNITSLNWKGLSFQIRTSQAGNFSBAVELERANKKYYIVAD 234  
QY 237 SYIASLAIIMLYFC 249  
DB 235 QVKEKIALIKFYC 247  
RESULT 15  
US-10-127-890-102  
Sequence 102, Application US/10127890  
Publ. No. 20030906196A1  
GENERAL INFORMATION:  
APPLICANT: Bertier, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois

COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Saccharin Release #1.0, Version #1.25  
CURRENT RELEASE DATE: US/10/127, 890  
FILING DATE: 23-APR-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
FILING DATE: 19-JUN-1992  
FILING DATE: 07/901,707  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70, P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 102:  
US-10-127-890-102  
Query Match 22.4%; Score 290.5; DB 12; Length 251;  
Best Local Similarity 34.0%; Pred. No. 1.9e-22;  
Matches 86; Conservative 37; Mismatches 109; Indels 21; Gaps 7;  
QY 8 VTHQGTGDEYFRFTTLADY---VSSGSSNENFLPGSTIPVSDQRFVLEINQGD 64  
DB 5 VSPSTGATYTVVNFLEIRKLEKNSHGIPLKRC--DQPKCFVLAINDMQ 62  
QY 65 SITAIIDVNAVYVYQAGDSYFLDAPRAAEFLFTGTEDSSLPFTGSYTLERYA 124  
DB 63 LAELAIIDVSYVYQVYRNRSYFPDAPRAAYEGFLPKTIKTR--LHFGSYPSLGEK 120  
QY 125 GHRDQPLGIRIOL---IOSVALRYPGSGSTRQAQASILLIOMISGAAR---NPILMR 177  
DB 121 AVEETDDEIEPRTGIGKIDENALINDYKTEFLASLLVYQVSEAAEFTEINQINRN 180  
QY 178 YRQDINSSEFLPDWYLELETSWQOOSTQVQHS--TDGVFNNPFLAISTGNVTLNVR 236  
DB 181 PQGRIR-----PANNITSLNWKGLSFQIRTSQAGNFSBAVELERANKKYYIVAD 234  
QY 237 SYIASLAIIMLYFC 249  
DB 235 QVKEKIALIKFYC 247  
Search completed: December 11, 2003, 14:46:51  
Job time : 16.497 secs

Thu Dec 11 16:09:52 2003

us-09-601-667c-38.rapb

TYPE: amino acid  
; MOLECULAR WEIGHT: 11661  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-127-890-4

Query Match 24.2%; Score 314; DB 12; Length 263;  
Best Local Similarity 35.0%; Pred. No. 6,6e-25;  
Matches 85; Conservative 49; Mismatches 89; Indels 20; Gaps 9;

QY 13 TGDERTFTLADYVSSGSSFN--EELFQSTIPVSDAQFVYVLELNGQDSITAA 69  
DB 10 TACTTKEF--EDPRATIPFSAKYDIPILIST--ISDRKFTLDDIISAYATISVA 63  
QY 70 IDPTNAYVAYVAYQAGOSYFLDAPRGATLFTGTDRSSLEPTGSYTDLERYAGH--R 127  
DB 64 IDVTNAYVAYVAYTRDVSYPFESPEPAVNLKQIR--KITLPTGMYENLQF--AAKIR 120  
QY 128 DOIPLGIGISVSAIRYGGSTRAQKSEILILQWISBAKFPILMYRQDINSSES 187  
DB 121 ENIDLGIPALSAITTFYMAQSAFSA--LVLIQTTEAKAFKXIERHVAKV--ATN 176  
QY 188 FLPDWMLELETSGQOSTYV--QASTDYVFNPPFLAISTGVPVLSNVSATIAIM 245  
DB 177 FRENALITSLNQSALSKQIFLAQNGKAFNRPVLDITGGERQVATNDDVYAKNIK 236  
QY 246 LPV 248  
DB 237 LLL 239

RESULT 12  
US-09-792-793A-34  
; Sequence 34, Application US/09792793A  
; Patent No. US20020168370A1  
; GENERAL INFORMATION:  
; INVENTOR: McDaniel, John R.  
; APPLICANT: MCCOIN, John R.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
; FILE REFERENCE: 25020-601D  
; CURRENT APPLICATION NUMBER: US/09/792,793A  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Bryonia dioica  
US-09-792-793A-34

Query Match 23.4%; Score 303.5; DB 10; Length 247;  
Best Local Similarity 33.2%; Pred. No. 7,8e-24;  
Matches 82; Conservative 50; Mismatches 98; Indels 17; Gaps 8;  
QY 7 RVHQQTGDEYFFITLADYVSSGSSFNSEIPLRQSTIPVSDAQFVYVLELNGQDSI 66  
DB 5 RLSGATF--TSYGVFIRNREALPYERKYNIPIILSS--ISGERTYLLHNLVYADETI 60  
QY 67 TLAIDVNAVAYVAYQAGOSYFLDAPRGATLFTGTDRSSLEPTGSYTDLERYAGH 126  
DB 61 SVADVNTVYIMGLDGVSYFPBASATEAKAFVDMKAKKVTLPYSGYERELQTAACK 120  
QY 127 --DQIPLGIGISVSAIRYGGSTRAQKSEILILQWISBAKFPILMYRQDINS- 184  
DB 121 IRENIPGLPALDSAITTLVYTAASA--LVLIQSTASAKYKFT---EQQIKR 174  
QY 185 -GSEFLPDWMLELETSGQOSTYV--HSTDYVFNPPFLAISTGVPVLSN--VRSVI 239  
DB 175 VKRTPLSLATISLNNMSLSKQIQIASINNGQFESVVLIDNNQNVSLTNASRYVT 234  
QY 240 ASLAIWL 246  
DB 237 LLL 239

DB 235 SWIALML 241  
RESULT 13  
US-10-375-209A-34  
; Sequence 34, Application US/10375209A  
; Publication No. US20030215423A1  
; GENERAL INFORMATION:  
; INVENTOR: McDaniel, John R.  
; APPLICANT: MCCOIN, John R.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
; FILE REFERENCE: 25020-601S  
; CURRENT APPLICATION NUMBER: US/10/375,209A  
; CURRENT FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Bryonia dioica  
US-10-375-209A-34

Query Match 23.4%; Score 303.5; DB 12; Length 247;  
Best Local Similarity 33.2%; Pred. No. 7,8e-24;  
Matches 82; Conservative 50; Mismatches 98; Indels 17; Gaps 8;

QY 7 RVHQQTGDEYFFITLADYVSSGSSFNSEIPLRQSTIPVSDAQFVYVLELNGQDSI 66  
DB 5 RLSGATF--TSYGVFIRNREALPYERKYNIPIILSS--ISGERTYLLHNLVYADETI 60  
QY 67 TLAIDVNAVAYVAYQAGOSYFLDAPRGATLFTGTDRSSLEPTGSYTDLERYAGH 126  
DB 61 SVADVNTVYIMGLDGVSYFPBASATEAKAFVDMKAKKVTLPYSGYERELQTAACK 120  
QY 127 -DQIPLGIGISVSAIRYGGSTRAQKSEILILQWISBAKFPILMYRQDINS- 184  
DB 121 IRENIPGLPALDSAITTLVYTAASA--LVLIQSTASAKYKFT---EQQIKR 174  
QY 185 -GSEFLPDWMLELETSGQOSTYV--HSTDYVFNPPFLAISTGVPVLSN--VRSVI 239  
DB 175 VKRTPLSLATISLNNMSLSKQIQIASINNGQFESVVLIDNNQNVSLTNASRYVT 234  
QY 240 ASLAIWL 246  
DB 235 SWIALML 241

RESULT 14  
US-10-127-890-111  
; Sequence 111, Application US/10127890  
; Publication No. US2003016616A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; INVENTOR: Carroll, Stephen F.  
; TITLE OF INVENTION: proleins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: McAdams, Heid & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; COMPUTER readable form:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/127,890

Thu Dec 11 16:09:52 2003

us-09-601-667c-38.rapb

Page 5

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: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 6:
:
US-10-127-890-6

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Query Match	25.2%;	Score 327;	DB 12;	Length 247;
Best Local Similarity	36.0%;	Pred. No. 2.5e-26;		
Matches 87; Conservative	52;	Mismatches 85;	Indels 18;	Gaps 10;

QY 13 TGDYERFRTILRDYVSSGFSNEIPLLRQSTIPVSDAQRFLVELLNQGDSTIAIDY 72  
 Db 10 TSSSYGVFISNLKALPNERKLYDIPLR-SSLEGS-QRYALIHILNRYADETISVAIDY 66

Qy 73 TAAVVAAYGAGDGSYYLRDA-PRGAETHLFTGTTRDSRLPFGSYTDLEIRYAGH-RDOI 130  
||:::||| ||| : ::||| : |::| : |::|  
Db 67 TTVYLINGCRACDTSTFFENEASATAPAKYFKQAMR-KTTLPGSGNVERLQPNAGITRENI 125

DY 131 PLGIEOLIGVSALRYPGSTRAQARSLILIMISEARPNILMYRRODINS--GESEF 168  
| | : : : : | : : : : | : :  
Db 126 PLGLPALDSITTFEYNANNSAABA--LMVLTOSTSEAPVEI-----FOOTGVNUNWME 170

[illegible]

200 ML 246  
245 ML 246  
244 ML 246  
243 ML 246  
242 ML 246  
241 ML 246  
240 ML 246  
239 ML 246

DB	240	LT	241
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US-10-280-679B-4  
Sequence 4, Application US/10280679B  
Publication No. US20030150019A1  
GENERAL INFORMATION.

APPLICANT: Large Scale Biology Corporation  
TITLE OF INVENTION: Monoparticle RNA Virus Transformation Vectors  
FILE REFERENCE: LSBC-0109-US03

: CURRENT APPLICATION NUMBER: US/10/280,679E  
 :  
 : CURRENT FILING DATE: 2000-10-24  
 :  
 : PRIOR APPLICATION NUMBER: 09/557,941  
 :  
 : PRIOR FILING DATE: 2000-04-24

; PRIOR APPLICATION NUMBER: 08/484,341  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIOR APPLICATION NUMBER: 07/923,692  
 ; PRIOR FILING DATE: 1993-07-31

/ PRIORITY NUMBER: 07/600,244  
 / PRIORITY DATE: 1992-07-31  
 / PRIORITY NUMBER: 07/600,244  
 / PRIORITY DATE: 1990-10-22  
 / PRIORITY NUMBER: 07/641,617

PRIOR FILING DATE: 1991-01-16  
 PRIOR APPLICATION NUMBER: 07/737,899  
 PRIOR FILING DATE: 1991-07-26  
 PRIOR APPLICATION NUMBER: 07/739,143

; PRIOR FILING DATE: 1991-08-01  
 ; PRIOR APPLICATION NUMBER: 07/310,881  
 ; PRIOR FILING DATE: 1989-02-17  
 ; PRIOR APPLICATION NUMBER: 07/460,744

PRIOR FILING DATE: 1988-02-26  
PRIOR APPLICATION NUMBER: 07/160,771  
PRIOR FILING DATE: 1988-02-26

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

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; LENGTH: 289
; TYPE: PRT
; ORGANISM: Chinese cucumber protein alpha-trichosanthin
; SS-10-280-679B-4

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Query Match	24.8%	Score 322;	DB 12;	Length 289;
Best Local Similarity	36.0%	Pred. No. 1.1e-25;		
March 02 08:00				

QY 13 TGEYFFPITLDRDYSSGGSFNEIPLLRSTIVSDAQRFLVELTNQGSITAAIDV 72  
 Db 33 TSSSYGFISNLKALPNERKLTYPILLR--SLPGS--QRYALHILTNVADETSVAIDV 89

QY 73 TNAVVAAYAGDGSYFLRDA-PRGEHTLFTGTTRDSRLPFNGSYTDLERVAGH-RDQI 130  
|| :: : ||| | | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :  
Db 90 TNVIIMGVRAGDTSYFENESATBAKAYFKDAMR-KYTLPIYSGNVERILOAAGKIRENI 148

QY 131 PLGIHQIQSVSLARYPGSTRAQRSLILIQMISEARFNPFLMKRYQDINS--GESE 188  
||| : : : : : ||| : :  
Db 149 PLGLPADSAITTLFYNNASASA--LWLIQGSTEARPYKFI---EQQIKRVDKTP 202

[illegible]

QY 245 ML 246  
: |  
263 TT 264

200 JUL 2004

RESULT 11

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US-10-127-390-4
; Sequence 4, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
```

APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunizing Composites of Vaccine Antigens

/ **REVIEW OF ANTIMETABOLITES COMPRISING RIBOSOME-INACTIVATING**  
 / **Proteins**  
 / **NUMBER OF SEQUENCES: 173**  
 / **CORRESPONDENCE ADDRESS:**

ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois

```

1      COUNTRY: USA
2      ZIP: 60661
3      COMPUTER READABLE FORM:
4      MEDICAL TYPE: Clinical Trial

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; medium drive: floppy disk
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/10/127,890
3 FILING DATE: 23-Apr-2002
4 CLASSIFICATION: <Unknown>
5

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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US04/06240

? APPLICATION NUMBER: FC1/US94/05348  
 ? FILING DATE: 12-MAY-1994  
 ? APPLICATION NUMBER: US 08/064,691  
 ? FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, James M

REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
DATE RECEIVED: 8-2-76

TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 4:

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;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 263 amino acids
;

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Thu Dec 11 16:09:52 2003

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Page 4

QY 240 ASLAINLFCGGERSS 255  
DB 285 FILALMYRCAPPPSS 300

RESULT 7

US-09-792-793A-39  
Sequence 39, Application US/09792793A  
Patent No. US20020168370A1  
INVENTOR: COGGINS, John R.  
APPLICANT: COGGINS, John R.  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 247  
ORGANISM: Trichosanthems Kirilowii  
US-09-792-793A-39

QY 240 ASLAINLFCGGERSS 255  
DB 285 FILALMYRCAPPPSS 300

Query Match 25.3%; Score 329; DB 10; Length 247;  
Best Local Similarity 36.4%; Pred. No. 1.5e-26;  
Matches 88; Conservative 52; Mismatches 84; Indels 18; Gaps 10;

QY 13 TDEYRFTTLADYVSSGSPANEFLRPGSTPVSDAPRVLYVELTNGQSDITPAIDV 72  
DB 10 TSSGYVFIISNRKALPNERKLYDIFLR-SLPGS--QRYALHLYNADERTISVADIV 66  
QY 73 TNAVVAQADQSYFLRDA-PRGAEHLFTGTRDSSLPFGSTYDLERYAGH-RDOI 130  
DB 67 TWYIMGRADTSYFENEKATEAKYFKDNR-KYLPYSGNTERLTPAKGKIRENT 125  
QY 131 PEGEOLIOSVALRYGSGSTRQASLILLOMISAPARENTILMYRQDINS--GSEF 188  
DB 126 FLGLPALDSATITLFTYNNASASAA--LWVLIQSTSBARKYFI---EQIGKRVDTKF 179  
QY 189 LPMYVLEFSTNGQSTVOV--HSTQVNNPFLAISTGNFVTLNYSVS--VIASLAI 244  
DB 180 LPSLALISLNSMSALSKQIDASTNGQSPVVLINQONRVITTVADAVYNSINL 239  
QY 245 ML 246  
DB 240 LL 241

RESULT 8

US-10-375-209A-39  
Sequence 39, Application US/10375209A  
Publication No. US20030215421A1  
INVENTOR: MCCOY, John R.  
APPLICANT: MCCOY, John R.  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601E  
CURRENT APPLICATION NUMBER: US/10/375,209A  
CURRENT FILING DATE: 2003-02-24  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 247  
ORGANISM: Trichosanthems Kirilowii  
US-10-375-209A-39

Query Match 25.3%; Score 329; DB 12; Length 247;  
Best Local Similarity 36.4%; Pred. No. 1.5e-26;  
Matches 88; Conservative 52; Mismatches 84; Indels 18; Gaps 10;

QY 13 TDEYRFTTLADYVSSGSPANEFLRPGSTPVSDAPRVLYVELTNGQSDITPAIDV 72  
DB 10 TSSGYVFIISNRKALPNERKLYDIFLR-SLPGS--QRYALHLYNADERTISVADIV 66  
QY 73 TNAVVAQADQSYFLRDA-PRGAEHLFTGTRDSSLPFGSTYDLERYAGH-RDOI 130  
DB 67 TWYIMGRADTSYFENEKATEAKYFKDNR-KYLPYSGNTERLTPAKGKIRENT 125  
QY 131 PEGEOLIOSVALRYGSGSTRQASLILLOMISAPARENTILMYRQDINS--GSEF 188  
DB 126 FLGLPALDSATITLFTYNNASASAA--LWVLIQSTSBARKYFI---EQIGKRVDTKF 179  
QY 189 LPMYVLEFSTNGQSTVOV--HSTQVNNPFLAISTGNFVTLNYSVS--VIASLAI 244  
DB 180 LPSLALISLNSMSALSKQIDASTNGQSPVVLINQONRVITTVADAVYNSINL 239  
QY 245 ML 246  
DB 240 LL 241

RESULT 9  
US-10-127-890-6  
Sequence 6, Application US/10127890  
Publication No. US2003016136A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/0/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: D10K0000>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70,74  
TELEPHONE/DOCKET INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9195  
TELEX: 650128-128  
INFORMATION FOR SEQ ID NOS:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids



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Page 3

Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;  
QY 9 THQGTGDEYFREFITLADYVSSGS-FSNEIPL-RGSTIFVSDAQRFVLELWQODSI 66  
DB 13 TAGATVOSYTNFIRAVGRLTGADVHEHIFPYNVGLPYN--GRFIVELSHMAELSV 70  
QY 67 TAAIDVTNAYVAVQAGDSYFIR-DAPKAAE--THLFTGTDRSSLPFGSTYDLERY 123  
DB 71 TAAIDVTNAYVAVQAGDSYFIR-DAPKAAE--THLFTGTDRSSLPFGSTYDLERY 129  
QY 124 AGH-RDQIPGIGBOLIGVSALRY--FGSTRQARSTILILQWISGARFNPILMYR 179  
DB 130 AGH-RDQIPGIGBOLIGVSALRY--FGSTRQARSTILILQWISGARFNPILMYR 189  
QY 180 QDINSGESFLPDWYMELETSWQGSQVQVHSTGVFNNPRLAISTGNFTLSNRSYI 239  
DB 190 TRLRNRSAPDPVSITLNSWRLSTAIQDSNGAFASPIQLORRNSGFSYVDVSIIL 249  
QY 240 ASIAIMLFYQGRSS 255  
DB 250 PIALMYRCAPPS 265

RESULT 5  
US-10-127-890-1  
Sequence 1, Application US/10127890  
Publication No. US2003016136A1  
GENERAL INFORMATION  
APPLICANT: Shudhika, Gary M.  
INVENTOR: Shudhika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 2002-05-21  
CLASSIFICATION: Unknown  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70-P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/777-9155  
TELEFAX: 312/777-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-127-890-1  
Query Match  
Best Local Similarity 40.2%; Pred. No. 1,35-33;  
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;  
QY 9 THQGTGDEYFREFITLADYVSSGS-FSNEIPL-RGSTIFVSDAQRFVLELWQODSI 66  
DB 13 TAGATVOSYTNFIRAVGRLTGADVHEHIFPYNVGLPYN--GRFIVELSHMAELSV 70  
QY 67 TAAIDVTNAYVAVQAGDSYFIR-DAPKAAE--THLFTGTDRSSLPFGSTYDLERY 123  
DB 71 TAAIDVTNAYVAVQAGDSYFIR-DAPKAAE--THLFTGTDRSSLPFGSTYDLERY 129  
QY 124 AGH-RDQIPGIGBOLIGVSALRY--FGSTRQARSTILILQWISGARFNPILMYR 179  
DB 130 AGH-RDQIPGIGBOLIGVSALRY--FGSTRQARSTILILQWISGARFNPILMYR 189  
QY 180 QDINSGESFLPDWYMELETSWQGSQVQVHSTGVFNNPRLAISTGNFTLSNRSYI 239  
DB 190 TRLRNRSAPDPVSITLNSWRLSTAIQDSNGAFASPIQLORRNSGFSYVDVSIIL 249  
QY 240 ASIAIMLFYQGRSS 255  
DB 250 PIALMYRCAPPS 265

RESULT 6  
US-10-083-336A-1  
Sequence 1, Application US/10083336A  
Publication No. US2003018165A1  
GENERAL INFORMATION  
APPLICANT: Shudhika, Gary M.  
INVENTOR: Shudhika, Gary M.  
TITLE OF INVENTION: Ribonuclease and Methods of Making and Using Thereof  
FILE REFERENCE: P6745200 (RIID 01-58)  
CURRENT APPLICATION NUMBER: US/10/083,336A  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO: 576  
TYPE: PPT  
ORGANISM: Ricinus communis  
US-10-083-336A-1  
Query Match  
Best Local Similarity 30.5%; Score 396; DB 12; Length 576;  
Best Local Similarity 40.2%; Pred. No. 4,15-33;  
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;  
QY 9 THQGTGDEYFREFITLADYVSSGS-FSNEIPL-RGSTIFVSDAQRFVLELWQODSI 66  
DB 13 TAGATVOSYTNFIRAVGRLTGADVHEHIFPYNVGLPYN--GRFIVELSHMAELSV 105  
QY 67 TAAIDVTNAYVAVQAGDSYFIR-DAPKAAE--THLFTGTDRSSLPFGSTYDLERY 123  
DB 106 TAAIDVTNAYVAVQAGDSYFIR-DAPKAAE--THLFTGTDRSSLPFGSTYDLERY 164  
QY 124 AGH-RDQIPGIGBOLIGVSALRY--FGSTRQARSTILILQWISGARFNPILMYR 179  
DB 165 AGH-RDQIPGIGBOLIGVSALRY--FGSTRQARSTILILQWISGARFNPILMYR 224  
QY 180 QDINSGESFLPDWYMELETSWQGSQVQVHSTGVFNNPRLAISTGNFTLSNRSYI 239  
DB 225 TRLRNRSAPDPVSITLNSWRLSTAIQDSNGAFASPIQLORRNSGFSYVDVSIIL 264

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us-09-601-667c-38.rapb

QY 121 ERVAGHRDIPGIGLIGSVALRPGSTRQAQNSILLIOMISAPRNPILMRQ 180  
DB 119 ERVAGHRDIPGIGLIGSVALRPGSTRQAQNSILLIOMISAPRNPILMRQ 178  
QY 181 DINSSEFLPDYVWMELETSWGQOSTVOHSTDVGNPNPFLAISTGNPVLTSVSVIA 240  
DB 179 YINSGASFLPDYVWMELETSWGQOSTVOHSTDVGNPNPFLAISTGNPVLTSVSVIA 238  
QY 241 SLAIMFLVCGERS 254  
DB 239 SLAIMFLVCGERS 252

RESULT 2  
US-09-347-064-2  
Sequence 2: Application US/09347064A  
Patent No. US20020045208A1

GENERAL INFORMATION:  
APPLICANT: Beck, Jürgen  
APPLICANT: Schmidt, Arno  
APPLICANT: Zinke, Holger  
TITLE OF INVENTION: Recombinant Fusion Proteins Based on  
TITLE OF INVENTION: Ribosome-inactivating Proteins of the mistletoe viscum  
FILE REFERENCE: 09282-5  
CURRENT APPLICATION NUMBER: US/09/347,064A  
EARLIER FILING DATE: 1999-07-02  
EARLIER APPLICATION NUMBER: PCT/EP98/00009  
EARLIER FILING DATE: 1998-01-02  
EARLIER APPLICATION NUMBER: EP 97 10 0012.0  
EARLIER FILING DATE: 1997-01-02  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
SEQ ID NO 2  
TYPE: PRT  
ORGANISM: Viscum album  
US-09-347-064-2

Query Match 90.1%; Score 1170; DB 9; Length 252;  
Best Local Similarity 91.7%; Pred. No. 8, 8e-116;  
Matches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

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QY 61 OGQSTTAIDVTNAYVVAOAGQSYFLRDAFGAETHLFTGTRDS:LPFGSYTDL 120  
DB 62 OGQSTTAIDVTNAYVVAOAGQSYFLRDAFGAETHLFTGTRDS:LPFGSYTDL 119  
QY 121 ERVAGHRDIPGIGLIGSVALRPGSTRQAQNSILLIOMISAPRNPILMRQ 180  
DB 120 ERVAGHRDIPGIGLIGSVALRPGSTRQAQNSILLIOMISAPRNPILMRQ 179  
QY 181 DINSSEFLPDYVWMELETSWGQOSTVOHSTDVGNPNPFLAISTGNPVLTSVSVIA 240  
DB 180 YINSGASFLPDYVWMELETSWGQOSTVOHSTDVGNPNPFLAISTGNPVLTSVSVIA 239  
QY 241 SLAIMFLVCGERS 253  
DB 240 SLAIMFLVCGERS 252

RESULT 3  
US-10-282-935-3  
Sequence 3: Application US/10282935  
Patent No. US20030143193A1  
GENERAL INFORMATION:  
APPLICANT: VITETTA, ELLEN S.  
APPLICANT: GHETIE, VICTOR F.  
APPLICANT: SMALSHAW, JOAN  
APPLICANT: BALUNA, ROXANA G.

QY 9 THOTGDEFRFILLRDYVSSGSSTVEPIILROSTTVKSDAQRFTVRLN 60  
DB 9 THOTGDEFRFILLRDYVSSGSSTVEPIILROSTTVKSDAQRFTVRLN 61  
QY 69 AIDVTNAYVVAOAGQSYFLRDAFGAETHLFTGTRDS:LPFGSYTDLERYAGH-R 127  
DB 67 GIDVTNAYVVAOAGQSYFLRDAFGAETHLFTGTRDS:LPFGSYTDLERYAGH-R 124  
QY 128 DQIPGIGLIGSVALRPGSTRQAQNSILLIOMISAPRNPILMRQ 180  
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DB 186 FQDDYVWMELETSWGQOSTVOHSTDVGNPNPFLAISTGNPVLTSVSVIA 234  
QY 238 -VIAIAIMFLVC 249  
DB 235 PIVAVIALMFLVC 247

US-10-282-935-3  
Sequence 3: Application US/10282935  
Patent No. US20030143193A1

GENERAL INFORMATION:  
APPLICANT: VITETTA, ELLEN S.  
APPLICANT: GHETIE, VICTOR F.  
APPLICANT: SMALSHAW, JOAN  
APPLICANT: BALUNA, ROXANA G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
TITLE OF INVENTION: PROTEINACIOUS COMPOUNDS  
FILE REFERENCE: US/10/282,935  
CURRENT APPLICATION NUMBER: US/10/282,935  
EARLIER FILING DATE: 2002-10-29  
EARLIER APPLICATION NUMBER: 09/538,873  
EARLIER FILING DATE: 2000-03-30  
EARLIER APPLICATION NUMBER: 60/126,826  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
SEQ ID NO 2  
TYPE: PRT  
ORGANISM: Abirus precatorius  
US-10-282-935-3

Query Match 36.5%; Score 474; DB 12; Length 251;  
Best Local Similarity 49.1%; Pred. No. 6, 6e-42;  
Matches 109; Conservative 37; Mismatches 81; Indels 26; Gaps 6;  
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DB 9 THOTGDEFRFILLRDYVSSGSSTVEPIILROSTTVKSDAQRFTVRLN 61  
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QY 128 DQIPGIGLIGSVALRPGSTRQAQNSILLIOMISAPRNPILMRQ 180  
DB 125 DQIPGIGLIGSVALRPGSTRQAQNSILLIOMISAPRNPILMRQ 184  
QY 188 FLDDYVWMELETSWGQOSTVOHSTDVGNPNPFLAISTGNPVLTSVSVIA 240  
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QY 238 -VIAIAIMFLVC 249  
DB 235 PIVAVIALMFLVC 247

RESULT 4  
US-10-282-935-1  
Sequence 1: Application US/10282935  
Patent No. US20030143193A1  
GENERAL INFORMATION:  
APPLICANT: VITETTA, ELLEN S.  
APPLICANT: GHETIE, VICTOR F.  
APPLICANT: SMALSHAW, JOAN  
APPLICANT: BALUNA, ROXANA G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
TITLE OF INVENTION: PROTEINACIOUS COMPOUNDS  
FILE REFERENCE: US/10/282,935  
CURRENT APPLICATION NUMBER: US/10/282,935  
EARLIER FILING DATE: 2002-10-29  
EARLIER APPLICATION NUMBER: 09/538,873  
EARLIER FILING DATE: 2000-03-30  
EARLIER APPLICATION NUMBER: 60/126,826  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
SEQ ID NO 2  
TYPE: PRT  
ORGANISM: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-282-935-1

Query Match 30.5%; Score 396; DB 12; Length 267;  
Best Local Similarity 40.2%; Pred. No. 1, 3e-33;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 ; Search time 16.4973 Seconds  
(without alignments)

2886.029 Million cell updates/sec

Title: US-09-601-667C-38

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Sequence: 1 YERIALRVHTQGTGDRFRP.....SVTASIALMFCGERSSS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	1174	90.4	252	9	US-09-347-064-8	Sequence 8, Appl1
2	1170	90.1	252	9	US-09-347-064-2	Sequence 2, Appl1
3	174	90.1	251	12	US-10-127-890-3	Sequence 3, Appl1
4	336	36.5	251	12	US-10-127-890-1	Sequence 1, Appl1
5	336	30.5	257	12	US-10-127-890-1	Sequence 1, Appl1
6	336	30.5	257	12	US-10-127-890-1	Sequence 1, Appl1
7	339	25.3	247	10	US-09-792-793A-39	Sequence 39, Appl1
8	339	25.3	247	12	US-10-375-209A-39	Sequence 39, Appl1
9	327	25.2	247	12	US-10-127-890-6	Sequence 6, Appl1
10	322	24.8	289	12	US-10-280-679B-4	Sequence 4, Appl1
11	314	24.2	263	12	US-10-127-890-4	Sequence 4, Appl1
12	303.5	23.4	247	12	US-09-792-793A-34	Sequence 34, Appl1
13	303.5	23.4	247	12	US-10-375-209A-34	Sequence 34, Appl1
14	303.5	23.4	247	12	US-10-127-890-111	Sequence 111, Appl1
15	290.5	22.4	251	12	US-10-127-890-102	Sequence 102, Appl1

16	286	22.0	263	12	US-10-127-890-7	Sequence 7, Appl1
17	285.5	22.0	251	12	US-10-127-890-101	Sequence 101, Appl1
18	285.5	22.0	251	12	US-10-127-890-110	Sequence 110, Appl1
19	284.5	21.9	251	12	US-10-127-890-99	Sequence 99, Appl1
20	282.5	21.7	251	12	US-10-127-890-100	Sequence 100, Appl1
21	282.5	21.7	251	12	US-10-127-890-105	Sequence 105, Appl1
22	282.5	21.7	251	12	US-10-127-890-106	Sequence 106, Appl1
23	282.5	21.7	198	12	US-10-083-336A-3	Sequence 3, Appl1
24	282	21.7	198	12	US-10-083-336A-7	Sequence 7, Appl1
25	282	21.7	199	12	US-10-083-336A-5	Sequence 5, Appl1
26	282	21.7	200	12	US-10-083-336A-10	Sequence 10, Appl1
27	281.5	21.7	251	12	US-09-765-527-247	Sequence 247, Appl1
28	281.5	21.7	251	12	US-10-127-890-2	Sequence 2, Appl1
29	281.5	21.7	251	12	US-10-127-890-103	Sequence 103, Appl1
30	281.5	21.7	251	12	US-10-127-890-108	Sequence 108, Appl1
31	281.5	21.7	251	12	US-10-127-890-109	Sequence 109, Appl1
32	281.5	21.7	251	12	US-10-074-586-11	Sequence 11, Appl1
33	281.5	21.7	251	12	US-10-074-586-11	Sequence 11, Appl1
34	280.5	21.6	251	12	US-10-127-890-108	Sequence 108, Appl1
35	278.5	21.4	251	12	US-10-127-890-107	Sequence 107, Appl1
36	278.5	21.4	251	12	US-09-765-527-259	Sequence 259, Appl1
37	278.5	21.4	309	9	US-09-765-527-253	Sequence 253, Appl1
38	278.5	21.4	312	9	US-09-765-527-251	Sequence 251, Appl1
39	268.5	20.7	185	12	US-10-083-336A-9	Sequence 9, Appl1
40	260	20.0	188	12	US-10-083-336A-8	Sequence 8, Appl1
41	260	20.0	188	12	US-10-083-336A-6	Sequence 6, Appl1
42	260	20.0	189	12	US-10-083-336A-6	Sequence 6, Appl1
43	247.5	19.1	190	12	US-10-083-336A-11	Sequence 11, Appl1
44	247.5	19.1	250	12	US-09-792-793A-36	Sequence 36, Appl1
45	247.5	19.1	250	12	US-10-127-890-8	Sequence 8, Appl1

#### ALIGNMENTS

RESULT 1

US-09-347-064-8

Sequence 8, Application US/09347064A

Patent No. US20020045208A1

GENERAL INFORMATION:

APPLICANT: SCH. DUREN

INVENTOR: SCH. DUREN

APPLICANT: ZINKE, Holger

TITLE OF INVENTION: Recombinant Fusion Proteins Based on

TITLE OF INVENTION: Ribosome Inactivating Proteins of the mistletoe Visum

FILE REFERENCE: 09282-5

CURRENT FILING DATE: US/09/347, 064A

EARLIER FILING DATE: 1999-07-02

EARLIER FILING DATE: 1998-01-02

EARLIER APPLICATION NUMBER: PCT/EP98/00009

EARLIER APPLICATION NUMBER: EP 97 10 0012.0

NUMBER OF CLAIMS: 1

INVENTOR: DUREN, Holger

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 252

TYPE: PRT

ORIGIN: Viscum album

US-09-347-064-8

Query Match 90.4%; Score 1174; DB 9; Length 252;

Best Local Similarity 91.7%; Pctd. No. 3,36-116;

Natches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

1 YERIALRVHTQGTGDRFRP.....SVTASIALMFCGERSSS 256

1 YERIALRVHTQGTGDRFRP.....SVTASIALMFCGERSSS 256

61 QGQDSIALIVNNAVVAQADQSYFRLDPKGAETHFTGTRRNSLFPFGSYTDL 120

61 QGQDSIALIVNNAVVAQADQSYFRLDPKGAETHFTGTRRNSLFPFGSYTDL 120

Thu Dec 11 16:09:51 2003

us-09-601-667c-38.rag

Page 10

FT /label= Asp, Glu  
FT Misc-difference 141  
FT /label= Ser, Thr  
FT Misc-difference 145  
FT /label= Phe, Tyr  
FT Misc-difference 152  
FT /label= Thr, Ala  
FT Misc-difference 157  
FT /label= Ala, Tyr  
FT Misc-difference 160  
FT /label= Tyr, Asp  
FT Misc-difference 185  
FT /label= Ala, Glu  
FT Misc-difference 191  
FT /label= Val, Met  
FT Misc-difference 219  
FT /label= Ile, Phe  
FT Misc-difference 224  
FT /label= Pro, Ser  
FT Misc-difference 225  
FT /label= Pro, Thr  
FT Misc-difference 232  
FT /label= Thr, Ser  
FT Misc-difference 236  
FT /label= Asp, Ser  
XX DE19804210-AL.  
XX 12-AUG-1999.  
XX 03-FEB-1998; 98DE-1004210.  
XX 03-FEB-1998; 98DE-1004210.  
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
XX Morris P, Siefert T, Voelter W, Welbers P;  
XX WPI, 1999-44535/38.  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX Claim 41; Page 39; 78pp; German.  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumor and immunostimulatory activity. The A-chain (MAA)  
XX of the mistletoe lectin binds to, and inhibits, the 28S subunit of  
XX ribosomes. The invention provides a method for preparing the A-chain of  
XX lymphokine-producing macrophages, so stimulate immunity (I) and its  
XX fragments are used to treat uncontrolled cell growth (particularly  
XX cancers) and if they lack cytotoxicity, to increase the strength of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a consensus sequence of the mistletoe lectin A chain (MAA)  
XX described in the invention.  
SQ Sequence 255 Aa;  
Query Match 90.2%; Score 1171.5; DB 20; Length 255;  
Best Local Similarity 91.8%; Pred. No. 1.5e-113;  
Matches 235; Conservative 0; Mismatches 20; Indels 1; Gaps 1;  
Qy 1 YERLRNTHQTTGSEFFFTLLADRYSSGSRNEPIFAGCTTPVSDAGRPVWATN 60  
Db 1 YERLRNTHQTTGSEFFFTLLADRYSSGSRNEPIFAGCTTPVSDAGRPVWATN 60  
Qy 61 QGDSITVAIDVTNAYVAVYAGDSYFLDAPGAEFTLPTGTRRSSLPFGSYTDL 120  
Db 61 QGDSITVAIDVTNAYVAVYAGDSYFLDAPGAEFTLPTGTRRSSLPFGSYTDL 120  
Qy 61 QGDSITVAIDVTNAYVAVYAGDSYFLDAPGAEFTLPTGTRRSSLPFGSYTDL 119  
Db 61 QGDSITVAIDVTNAYVAVYAGDSYFLDAPGAEFTLPTGTRRSSLPFGSYTDL 119

Qy 121 ERYAGHRDQIPIGIEQLIOSVSLNRYGSTRQAQASILLIOMISSARFNPILWRYRQ 180  
Db 120 ERYAGHRDQIPIGIXQLIOSVSLNRYGSTRQAQASILLIOMISSARFNPILWRYRQ 179  
Qy 181 DINGSESEFLDMMWLELTENKQSTGVGHSTDCVFNPPRLAISTNPTLISNVSYIA 240  
Db 180 XINSKXSLDMMWLELTENKQSTGVGHSTDCVFNPPRLAISTNPTLISNVSYIA 239  
Qy 241 SLATMLPVGGERPSSS 256  
Db 240 SLATMLPVGGERPSSS 255

Search completed: December 11, 2003, 14:07:47  
Job time : 26.2959 secs

XX Mistletoe lectin A chain MIA consensus protein sequence 2.  
 XX  
 KM Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KM ribosome; 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KM cancer; cytotoxicity; antigen; isoform.  
 XX  
 OS viscum album.  
 XX  
 FH Key Location/Qualifiers  
 FH Misc-difference 15  
 FT Misc-difference 63 /label= Asp, Glu  
 FT Misc-difference 66 /label= Gly, Gln  
 FT Misc-difference 75 /label= Ile, Val  
 FT Misc-difference 107 /label= Leu, Ala  
 FT Misc-difference 113 /label= Asp, Arg, none  
 FT Misc-difference 117 /label= Asn, Thr  
 FT Misc-difference 120 /label= Pro, Thr  
 FT Misc-difference 141 /label= Ser, Thr  
 FT Misc-difference 145 /label= Phe, Tyr  
 FT Misc-difference 152 /label= Thr, Ala  
 FT Misc-difference 177 /label= Ala, Tyr  
 FT Misc-difference 180 /label= Tyr, Asp  
 FT Misc-difference 185 /label= Ala, Glu  
 FT Misc-difference 191 /label= Val, Met  
 FT Misc-difference 219 /label= Ile, Phe  
 FT Misc-difference 224 /label= Phe, Ser  
 FT Misc-difference 225 /label= Pro, Thr  
 FT Misc-difference 232 /label= Thr, Ser  
 FT Misc-difference 236 /label= Asp, Ser  
 FT  
 XX DE19804210-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX (BIOS-) BIOSYN ARANWITTEL GMBH.  
 XX  
 XX Morris P, Stiefel T, Voelker W, Walters P.  
 XX WPI, 1999-44535/38.  
 XX  
 XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX Claim 5; Page 30; 78pp; German.  
 XX  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)

CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC recombinant chains in many different isoforms  
 CC and on a large scale at any time of year. Anticancer products are  
 CC free from toxins present in natural mistletoe extracts.  
 CC represents a consensus sequence of the mistletoe lectin A chain (MIA)  
 CC described in the invention.  
 XX  
 XX Sequence 255 AA;  
 XX  
 XX Query Match 90.24; Score 1171.5; DB 20; Length 255;  
 XX Best Local Similarity 91.84; Pred. No. 1.5e-113;  
 XX Matches 235; Conservative 0; Mismatches 20; Indels 1; Gaps 1;  
 XX  
 XX 1 YERLRAPYHQTGDEYFETILRDYVSSGFSNTEFLRQSTIVSDAQRVYVLTN 60  
 XX 1 YERLRAPYHQTGDEYFETILRDYVSSGFSNTEFLRQSTIVSDAQRVYVLTN 60  
 XX 61 QGQDSITADIDVNAVYVAYQKQDQYFLDAPRQETLFTGTDRSSIPPTGSYTDL 120  
 XX 61 QGQDSITADIDVNAVYVAYQKQDQYFLDAPRQETLFTGTDRSSIPPTGSYTDL 120  
 XX 61 QGQDSITADIDVNAVYVAYQKQDQYFLDAPRQETLFTGTDRSSIPPTGSYTDL 119  
 XX 121 ERVAGRDQIPIGIEOLISVALRPGGSTRQARSLILHOMISEAARPNILMYRQ 180  
 XX 120 ERVAGRDQIPIGIEOLISVALRPGGSTRQARSLILHOMISEAARPNILMYRQ 179  
 XX 181 DINGGSETPPMYMLFETSMGQSTQVORHSDQVFNPRALSTGFTLSNRYVLA 240  
 XX 180 XINGGSETPPMYMLFETSMGQSTQVORHSDQVFNPRALSTGFTLSNRYVLA 239  
 XX  
 XX 241 SLAHMFCVCEPSSS 256  
 XX 240 SLAHMFCVCEPSSS 255  
 XX  
 XX RESULT 15  
 XX X123977 standard; protein; 255 AA.  
 XX ID X123977  
 XX AC X123977  
 XX XX X123977  
 XX DE 18-OCT-1999 (first entry)  
 XX  
 XX Mistletoe lectin A chain MIA consensus protein sequence 3.  
 XX  
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KM ribosome; 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KM cancer; cytotoxicity; antigen; isoform.  
 XX  
 OS viscum album.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FH Misc-difference 15 /label= Asp, Glu  
 FT Misc-difference 63 /label= Gly, Gln  
 FT Misc-difference 66 /label= Ile, Val  
 FT Misc-difference 75 /label= Leu, Ala  
 FT Misc-difference 107 /label= Asp, none  
 FT Misc-difference 113 /label= Asn, Thr  
 FT Misc-difference 117 /label= Pro, Thr  
 FT Misc-difference 141 /label= Ser, Thr  
 FT Misc-difference 145 /label= Phe, Tyr  
 FT Misc-difference 152 /label= Thr, Ala  
 FT Misc-difference 177 /label= Ala, Tyr  
 FT Misc-difference 180 /label= Tyr, Asp  
 FT Misc-difference 185 /label= Ala, Glu  
 FT Misc-difference 191 /label= Val, Met  
 FT Misc-difference 219 /label= Ile, Phe  
 FT Misc-difference 224 /label= Phe, Ser  
 FT Misc-difference 225 /label= Pro, Thr  
 FT Misc-difference 232 /label= Thr, Ser  
 FT Misc-difference 236 /label= Asp, Ser  
 FT  
 XX DE19804210-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX (BIOS-) BIOSYN ARANWITTEL GMBH.  
 XX  
 XX Morris P, Stiefel T, Voelker W, Walters P.  
 XX WPI, 1999-44535/38.  
 XX  
 XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX Claim 5; Page 30; 78pp; German.  
 XX  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)

Db 2 YERILAVYHTQGTGERFPIITLADYVSSGSFSENFILROSTIPVSDAQFVLELTN 61  
 QY 61 QGQDSITPAIDVTNAVVAVYAGADSYFLADAPGAEHLPTGTTRDRSSLPFTGSYTDL 120  
 Db 62 QGQDSITPAIDVTNLVVAVYAGADSYFLADAPGAEHLPTGTTRDRSSLPFTGSYTDL 119  
 QY 121 ERYAGHRDQIPGIGIOLQSVSALRYPGQSTRAQAKSILLIOMISKAAPFPIIMRQ 180  
 Db 120 ERYAGHRDQIPGIGIDLIQSVTLRPGQSTRTQARSILLIOMISKAAPFPIIMRQ 179  
 QY 181 DINSGESLPDMYMLERSTMGQSTQVQHSIDGVNRPFLAISTGNPFTLSMNSVIA 240  
 Db 180 YINSASLPDPYMLERSTMGQSTQVQHSIDGVNRPFLAISTGNPFTLSMNSVIA 239  
 QY 241 SLAINLFCGGERPS 254  
 Db 240 SLAINLFCGGERPS 253

## RESULT 13

AAV25971 standard; protein; 255 AA.

AAV25971;

18-OCT-1999 (first entry)

Mistletoe lectin A chain MIA consensus protein sequence 1.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

Ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;

Lymphokine-producing macrophage; uncontrolled cell growth; treatment;

cancer; cytotoxicity; antigen; isoform.

viscum album.

Key

Location/Qualifiers

Misc-difference 15 /label= Asp, Glu

Misc-difference 63 /label= Gly, Glu

Misc-difference 66 /label= Ile, Val

Misc-difference 75 /label= Leu, Ala

Misc-difference 107 /label= Asp, Arg or none

Misc-difference 113 /label= Asp, Thr

Misc-difference 117 /label= Asn, Thr

Misc-difference 134 /label= Pro, Glu

Misc-difference 141 /label= Asp, Thr

Misc-difference 145 /label= Ser, Thr

Misc-difference 152 /label= Phe, Tyr

Misc-difference 177 /label= Thr, Ala

Misc-difference 180 /label= Ala, Tyr

Misc-difference 185 /label= Tyr, Asp

Misc-difference 191 /label= Ala, Glu

Misc-difference 219 /label= Val, Met

Misc-difference 223 /label= Ile, Phe

Misc-difference 225 /label= Pro, Ser

FT Misc-difference 232 /label= Thr, Ser  
 FT Misc-difference 236 /label= Asp, Ser  
 XX DE19804210-A1.  
 PN 12-AUG-1999.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX (Bios-) BIOCYN AFZNEIMTTTEL CMH.  
 PA Morris P, Stiefel T, Voelter W, Welters P.  
 PI WPI; 1999-44535/38.  
 DR Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX Chain 2; Page 27; 78pp; German.

This invention describes a novel mistletoe lectin (1) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (1) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancer) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered method of production of  
 CC (immune-activated) and its individual chains in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC fire from toxins present in natural mistletoe extracts. This sequence  
 CC represents a consensus sequence of the mistletoe lectin A chain (MIA)  
 CC described in the invention.

Sequence 255 AA;

Query Match 90.2%; Score 1171.5; DB 20; Length 255;

Best Local Similarity 91.8%; First Match 128-113; Gaps 1;

Matches 235; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 1 YERILAVYHTQGTGERFPIITLADYVSSGSFSENFILROSTIPVSDAQFVLELTN 60  
 Db 1 YERILAVYHTQGTGERFPIITLADYVSSGSFSENFILROSTIPVSDAQFVLELTN 60  
 QY 61 QGQDSITPAIDVTNAVVAVYAGADSYFLADAPGAEHLPTGTTRDRSSLPFTGSYTDL 120  
 Db 61 QGQDSITPAIDVTNLVVAVYAGADSYFLADAPGAEHLPTGTTRDRSSLPFTGSYTDL 119  
 QY 121 ERYAGHRDQIPGIGIOLQSVSALRYPGQSTRAQAKSILLIOMISKAAPFPIIMRQ 180  
 Db 120 ERYAGHRDQIPGIGIDLIQSVTLRPGQSTRTQARSILLIOMISKAAPFPIIMRQ 179  
 QY 181 DINSGESLPDMYMLERSTMGQSTQVQHSIDGVNRPFLAISTGNPFTLSMNSVIA 240  
 Db 180 YINSASLPDPYMLERSTMGQSTQVQHSIDGVNRPFLAISTGNPFTLSMNSVIA 239  
 QY 241 SLAINLFCGGERPS 256  
 Db 240 SLAINLFCGGERPS 255

## RESULT 14

AAV25974 standard; protein; 255 AA.

AAV25974;

18-OCT-1999 (first entry)

QY 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPLAKOSTIPVSDAKRFVVELTN 60  
 DB 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPLAKOSTIPVSDAKRFVVELTN 60  
 QY 61 QGQDSITPAIDVTNAYVAYQADQSYFLDAPRAKATHTFTTTRDSSLPFGSYTDL 120  
 DB 61 QGQDSITPAIDVTNAYVAYQADQSYFLDAPRAKATHTFTTTRDSSLPFGSYTDL 118  
 QY 121 ERYAGHRDQIPLGIEQLQSVNLRYPGSGSTRQAQASILLIQMISEARFNPILMRQ 180  
 DB 119 ERYAGHRDQIPLGIDQLQSVNLRYPGSGSTRQAQASILLIQMISEARFNPILMRQ 178  
 QY 181 DINGSESTPEMVMLELTSWGQOSTOVQSHTDGVNNEPFLAISTGNFVLISVRSVTA 240  
 DB 179 YINSGASTPEMVMLELTSWGQOSTOVQSHTDGVNNEPFLAISTGNFVLISVRSVTA 238  
 QY 241 SLAIMEFVCGERS 254  
 DB 239 SLAIMEFVCGERS 252

## RESULT 11

AA10022 standard; Protein: 253 AA.

AA10022;

18-DEC-1997 (first entry)

Prepro mistletoe lectin A chain.

Mistletoe lectin; cytotoxic; A chain; B chain; dimer.

Viscum album.

EP751221-A1.

02-JAN-1997.

26-JUN-1995; 9SEP-0109949.

26-JUN-1995; 9SEP-0109949.

(MADU) MADANUS KOELEN AG.

Baur A, Eck J, Lentzen H, Zinke H;

WPI; 1997-054678/06.

N-PSDB; AAT70474.

Nucleic acid encoding pre-pro form of mistletoe lectin - for therapeutic or diagnostic use

Claim 12; Fig 4A; 30pp; German.

Mistletoe lectin is a cytotoxic agent that has been used for tumour therapy. It can be used in immunotoxic and medicaments. Nucleic acid fragments can be used in diagnostic methods. Mistletoe lectin (AAT70473) comprises an A chain (AAT70474) and a B chain (AAT70475).

Sequence 253 AA;

Query Match 90.4%; Score 1174; DB 18; Length 253;

Best Local Similarity 91.7%; Pred. No. 8 1e-114;

Matches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPLAKOSTIPVSDAKRFVVELTN 60  
 DB 2 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPLAKOSTIPVSDAKRFVVELTN 61  
 QY 61 QGQDSITPAIDVTNAYVAYQADQSYFLDAPRAKATHTFTTTRDSSLPFGSYTDL 120  
 DB 62 QGQDSITPAIDVTNAYVAYQADQSYFLDAPRAKATHTFTTTRDSSLPFGSYTDL 119

QY 121 ERYAGHRDQIPLGIEQLQSVNLRYPGSGSTRQAQASILLIQMISEARFNPILMRQ 180  
 DB 120 ERYAGHRDQIPLGIDQLQSVNLRYPGSGSTRQAQASILLIQMISEARFNPILMRQ 179  
 QY 181 DINGSESTPEMVMLELTSWGQOSTOVQSHTDGVNNEPFLAISTGNFVLISVRSVTA 240  
 DB 180 YINSGASTPEMVMLELTSWGQOSTOVQSHTDGVNNEPFLAISTGNFVLISVRSVTA 239  
 QY 241 SLAIMEFVCGERS 254  
 DB 240 SLAIMEFVCGERS 253

## RESULT 12

AA190125 standard; Protein: 253 AA.

AA190125;

20-MAR-2003 (updated)

30-APR-1999 (first entry)

Mistletoe ML A-chain protein.

ML; mistletoe lectin; MUA; A-chain; transgenic plant; glycosylation; dimer; immunotoxin; large-scale production; diagnosis; therapeutic;

cancer.

Viscum album.

EP884388-A1.

16-DEC-1998.

26-JUN-1995; 9SEP-0105660.

26-JUN-1995; 9SEP-0109949.

26-JUN-1995; 9SEP-0105660.

(MADU) MADANUS KOELEN AG.

Baur A, Eck J, Lentzen H, Zinke H;

WPI; 1999-026582/03.

N-PSDB; AAT74180.

New transgenic plant expressing mistletoe lectin - useful for producing recombinant lectin in e.g. cancer diagnosis and therapy

Disclosure; Fig 4a; 30pp; German.

This invention describes a novel transgenic plant transformed with a vector capable of encoding a mistletoe (Viscum album) lectin. The plant also describes a polypeptide produced by the plant which is the polypeptide that occurs in Viscum album or the polypeptide is a fusion protein, a mistletoe lectin polypeptide dimer and an immunotoxin comprising the polypeptide or the polypeptide dimer. The plants are used for large-scale production of mistletoe lectin for diagnostic or therapeutic purposes (e.g. in cancer therapy). This sequence represents the mistletoe lectin A-chain which is contained in expression vector pTMAA.

(Updated on 20-MAR-2003 to correct PF field.)

Sequence 253 AA;

Query Match 90.4%; Score 1174; DB 20; Length 253;

Best Local Similarity 91.7%; Pred. No. 8 1e-114;

Matches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPLAKOSTIPVSDAKRFVVELTN 60

ID	AAV25392 standard; Protein; 532 AA.
AC	AAV25392;
NC	
CC	
PP	18-OCT-1999 (first entry)
DE	Mistletoe lectin I (variant) protein fragment.
XX	
KM	Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
KW	ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KV	lymphokine-producing macrophages; uncontrolled cell growth; treatment;
KX	cancer; cytotoxicity; antigen; isoform; lectin I.
XX	
OS	Viscum album.
XX	
PN	DR19604210-A1.
XX	
DD	12-AUG-1999.
XX	
PF	03-FEB-1998; 98DE.1004210.
XX	
PR	03-FEB-1998; 98DE.1004210.
XX	
PA	(EIO8-) BIODIV ARDENNIMTEL GMBH.
XX	
PI	Morris P, Stiefel T, Voelter W, Weilers P,
XX	
DR	WFI; 1999-445335/78.
XX	
DR	W-PSDB; A0259106.
PT	Preparation of mistletoe lectins in heterologous systems,
PT	particularly for use as anticancer agents and immunostimulants
XX	
PS	Disclosure; Fig 4B; 78pp; German.
XX	
CC	This invention describes a novel mistletoe lectin (I) and its fragments
CC	which have antitumor and immunostimulatory activity. The A-chain (HA)
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC	ribosomes. Non-cytotoxic forms of (I) stimulate immunity (I) and its
CC	lymphokine-producing macrophages stimulate immunity (I) and its
CC	carcinomas are used to treat uncontrolled cell growth (particularly
CC	cancers) and if they lack cytotoxicity, to increase the strength of the
CC	immune response, particularly to a co-administered antigen
CC	(tumour-associated, bacterial or viral). The method allows production of
CC	mistletoe lectin, and its individual chains, in many different isoforms
CC	and on a large scale, at any time of the year. Recombinant products are
CC	free from toxins present in natural mistletoe extracts. This sequence
CC	represents a fragment of a mistletoe lectin I protein variant.
XX	
XX	Sequence 532 AA;
XX	
QY	Query Match 91.1%; Score 1184; DB 20; Length 532;
QY	Best Local Similarity 92.2%; Pred. No. 2.2e-114;
QY	Matches 226; Conservative 6; Mismatches 12; Indels 2; Gaps 1.
QY	
QY	1 YERLARATVQTQGEYFEFFITLLRDVYSSGSFSNEMILPQSTTPVSDAKPSFLVLYTN 60
DB	1 YERLARATVQTQGEYFEFFITLLRDVYSSGSFSNEMILPQSTTPVSDAKPSFLVLYTN 60
QY	61 QGQSDITADITVATVAVYQADQSGYFLDPAFCATFLCTGTTRDSRLDFPGSYDL 120
DB	61 QGQSDITADITVATVAVYQADQSGYFLDPAFCATFLCTGTTRDSRLDFPGSYDL 118
QY	121 ERYVAGRCRQPLGFIQGLQGSALRYPGSTPAQASRIILIIQMSSEAFKFLIKRRQ 180
DB	119 ERYVAGRCRQPLGFIQGLQGSALRYPGSTPAQASRIILIIQMSSEAFKFLIKRRQ 178
QY	181 DINGSEFLDEPMNMLELQSGQSGQSTVOQASTDGVFNNEPFLAISTGNPYLLSNVSVYA 240
DB	179 YINGSGASFLPDVPMLELETSSMOQSTVOQASTDGVFNNEFLALPQSGPVLLINVDVYA 238
QY	241 SLATNLFPGGRSSS 256

D6		239 SLAINLFCVCGPERSS 254
		RESULT 10
AAW64661		AAM64661 standard; Protein; 252 AA.
XX		PAM64661;
XX		23-OCT-1998 (first entry)
DE		Mistletoe rMLA variant protein.
XX		Lectin A-chain; mistletoe; rMLA; fusion protein; effector; cytotoxic;
KM		intracellular; processing module; protease recognition; targeting module;
KW		immunisation; allergy; disorder; cell proliferation; activation;
XK		autoimmune disease; treatment; tumour; clinic; translocation; ss.
XX		Viscum album.
PH	Key	Location/Qualifiers
FT	Protein	1..252
PT		/note="partial"
PR	MOJ829350-A2.	
PN	09-JUL-1998.	
PD	02-JAN-1998;	98NO-BE00009.
PP	02-JAN-1997;	97EP-0100012.
PA	(BRAI-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.	
PI	Bock J., Schmidt A., Zinke H;	
DR	WPI; 1998-388122/33.	
N-PEDS:	AAVS1343.	
XX		Nucleic acid encoding fusion protein containing mistletoe lectin A
PT		chain - useful for treatment of proliferative and autoimmune
PS		diseases, allergies and tumours
XX		Disclosure; Fig 11a'; 115pp; German.
XX		This sequence encodes a variant mistletoe lectin A-chain. rMLA. This
CC		sequence can be used in combination with the extracellular domain of a fusion protein which
CC		comprises a fusion protein module that is cytotoxic intracellularly, a
CC		targeting module covalently bonded to the effector module and
CC		containing a protease recognition sequence, and a targeting module
CC		covalently bonded to the processing module, able to bind specifically to
CC		the surface of a cell so as to mediate internalisation of the fusion
CC		protein. Such a fusion protein can be used for treating disorders
CC		involving proliferation and/or elevated activation of cells, especially
CC		autoimmune disease, allergy and tumours. The proteins can be injected
CC		e.g. by injection topically or especially by i.v. infusion at a dose of
CC		at 1 ng to 500 mu g/kg/day, or for example at 1 mg to 500 ng/ml.
CC		Fusion proteins can developable prevents extracellular dissociation, and
CC		calca. monoclonal antibody activity in a wide range of target
CC		than those based on ricin and do have the associated problems of
CC		non-specific toxicity. The protein may be expressed in a non-glycosylated
CC		form that does not bind to sugar receptors in the liver, and which has a
CC		long half-life in the blood. Where the mistletoe lectin B-chain is used,
CC		it actively assists in translocation of the M <sub>H</sub> A-chain from the
CC		endoplasmic reticulum to the cytoplasm.
SQ	Sequence	252 AA;
XX		
Query Match	90.4%;	Score 1174; DS 19; Length 252;
Best local similarity	91.7%;	Pred. No. 8..1e-114;
Matches 233; Conservative	7;	Indels 2; Gaps 1



KM	dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
KX	cancer.
KX	
KX	Viscum album.
PN	Bp864388-A1.
PD	16-DEC-1998.
PP	26-JUN-1995; 98EP-0105660.
XX	26-JUN-1995; 95EP-0109949.
XX	26-JUN-1995; 98EP-0105660.
XX	(MADU ) MADDAUS KOEHL AG.
PI	Baur A., Eck U., Lentzen H., Zinke H,
DR	WPI: 1999-026582/03.
N-	PSDB; AA74182.
PT	New transgenic plant expressing mistletoe lectin - useful for
PT	producing recombinant lectin in e.g. cancer diagnosis and therapy
CC	Claim 1a: Fig 4c; 30pp; German.
CC	This invention describes a novel transgenic plant transformed with a
CC	vector capable of encoding a mistletoe ( <i>Viscum album</i> ) lectin
CC	proprotein or a biologically active fragment. The specification
CC	also describes a polypeptide produced by a plant where the polypeptide
CC	exhibits at least one enzymatic modification other than the glycosylation
CC	that occurs in <i>Viscum album</i> or the polypeptide is a fusion protein, a
CC	mistletoe lectin polypeptide dimer and an immunotoxin comprising the
CC	polypeptide or the polypeptide dimer. The plants are used for large-scale
CC	production of mistletoe lectin for diagnostic or therapeutic purposes
CC	used in the method of the invention. The sequence represents the mistletoe lectin
CC	(updated on 20-MAR-2003 to correct PF field.)
XX	
XX	Sequence 564 AA:
QY	
Query Match	91.5%; Score 1188; DB 20; Length 564;
Best Local Similarity	92.6%; Pred. No. 9.3e-115;
Matches 237; Conservative	5; Mismatches 12; Indels 2; Gaps 1
Dy	1 YERLANTVHQTGDETRFRFTLLADIVSSGSFSENEPLRSTPEVSADKGVVELTN 60
Dy	34 YERLANTVHQTGDETRFRFTLLADIVSSGSFSENEPLRSTPEVSADKGVVELTN 93
OY	61 OGQDSIPALADVTVAAVVAVOADOSVFELDAPGAETHLPGTTPRRSLPFGSYTL 120
Dy	94 OGQDSIPALADVTVAAVVAVOADOSVFELDAPGAETHLPGT--RSLEPFMSYEDL 151
OY	121 ERYAHRKDQPIGLIEQLIQSVSALKVRQGSTTAQASTILLIOMISRAEPFLIRVQ 180
Dy	152 ERYAHRKDQPIGLIEQLIQSVSALKVRQGSTTAQASTILLIOMISRAEPFLIRVQ 211
OY	181 ENKSRHFAPDMWTMLSTLSMGOGSTGYHSIDCVNRPFLATSTGNPTLTSGVSYIA 240
Dy	212 VINSAGAFPLDPVWVLLETSMWGOSTGYHSIDCVNRPFLATSTGNPTLTINVEDVIA 271
OY	241 SLAIATLVCGSPFPSS 256
Dy	272 SLAIATLVCGSPFPSS 287
RESULT 8	
ID	AAZ5979 standard; Protein; 531 AA.
AC	AAZ5979;
XX	
XX	18-OCT-1999 (first entry)

D	DE	Mistletoe lectin I protein fragment.
XX	MM	Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
XX	KW	lysozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX	KM	lysozyme-producing macrophage; uncontrolled cell growth; treatment;
XX	OS	cancer; cytotoxicity; antigen; isoform; lectin I.
XX	XX	Viscum album.
FN	PX	DE13604210-A1.
FD	PD	12-AUG-1999.
XX	PX	03-FEB-1998; 98DE-1004210.
XX	PX	03-FEB-1998; 98DB-1004210.
XX	PX	(EPOS-) EPOSIN AKENEMITTEL GMBH.
PI	P1	Morris P, Stiefel T, Voelter W, Walters P,
DR	DR	WPI; 1999-44535/38.
DR	NR	N-PSDB; AA209103.
PT	P1	Preparation of mistletoe lectins in heterologous systems,
XX	XX	particularly for use as anticancer agents and immunostimulants
XX	XX	Claim 7; Fig 1B; 78pp; German.
CC	CC	This invention describes a novel mistletoe lectin (I) and its fragments
CC	CC	which have antitumor and immunostimulatory activity. The A-chain (MHA)
CC	CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC	CC	ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC	CC	lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC	CC	fragments are used to treat uncontrolled cell growth (particularly of the
CC	CC	sarcomas) and if they lack cytotoxicity, to increase the strength of the
CC	CC	immune system by stimulating bacterial or viral infection and production of
CC	CC	tumor-associated bacterial or viral antigens. The method allows production of
CC	CC	mistletoe lectin, and its individual chains, in many different isoforms
CC	CC	and on a large scale, at any time of the year. Recombinant products are
CC	CC	free from toxins present in natural mistletoe extracts. This sequence
CC	CC	represents a mistletoe lectin I protein fragment.
SQ	SQ	Sequence 531 AA;
Query Match		91.1%; Score 1184; DB 20; Length 531;
Blast Similarity		92.2%; Free NO. 2,26-113; Indels 2; Gaps 1
Matches 236;		Conservative 6; Mismatches 12;
D	OY	1 YEHLRLVHQCTGDEYRRLLTLDVSSGSFSENFPLRGSTPSPAGRPVLVELTN 60
D	OY	1 YEHRLVHQCTGGEYRRILLDVSSGSFSENFELRGSTPSPAGRPVLVELTN 60
D	OY	61 QGGDSITPAIDVTNAVVAAYAGDGYFLRAAPGRKETHLFTGTTRDRSSLPEFGSYTDL 120
D	Db	61 QGGDSITPAIDVTNAVVAAYAGDGYFLRAAPGRKETHLFTGTTRDRSSLPEFGSYTDL 118
OY	CY	ERRAHNRDDIPGIGDLQSVAARPGSGSRROAASITLIOMTSFAARRNPILWRFRQ 180
D	Db	119 ERAGHDHPDGIGDLQSVAARPGSGSRRTQAISITLIQMISFAARRNPILWRARQ 178
OY	OY	181 DINSSESFPEDMWMLSTSMQSGSTVOGHSTDGVNPNPRLLATGTGNFVLTLSNVSVYA 240
Db	OY	179 YINGSASFEPDYVMLEMTSMQSGSTVOGHSDVDVNNPRLALPPGNFVLTIVADVIA 238
OY	OY	241 SLAINLVCGGRSSS 256
Db	OY	239 SLAINLVCGGRSSS 254



XX 03-FEB-1998; 98DB-1004210.  
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 XX MPI; 1999-445335/38.  
 XX N-PSDB; AA209104.  
 XX  
 XX Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX  
 XX Disclosure; Fig 2b, 78pp; German.  
 XX  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumor and immunostimulatory activity. The 286 subunit of  
 XX of the mistletoe lectin binds to, and inactivates, the 286 subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX of a large scale, at any time of the year. Recombinant products are  
 XX free from toxins present in natural mistletoe extracts. This sequence  
 XX represents a fragment of the mistletoe lectin A1 protein.

SO Sequence 254 AA;  
 Query Match 92.7%; Score 1204; DB 20; Length 254;  
 Best Local Similarity 93.0%; Pred. No. 6.1e-117;  
 Matches 238; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 1 YERLRKRYHQTDEYFRPFTLLADVYSSGSFSENEIPILRGSTIPVSDAQRFVLELTN 60  
 DB 1 YERLRKRYHQTDEYFRPFTLLADVYSSGSFSENEIPILRGSTIPVSDAQRFVLELTN 60  
 QY 61 QGDSITRAIDVTNAVVAAGQGSYFLRDPAGAEHLFTGTRDRSPLPFVGSYDL 120  
 DB 61 QGDSITRAIDVTNAVVAAGQGSYFLRDPAGAEHLFTGTRDRSPLPFVGSYDL 120  
 QY 61 QGDSITRAIDVTNAVVAAGQGSYFLRDPAGAEHLFTGTRDRSPLPFVGSYDL 118  
 DB 61 QGDSITRAIDVTNAVVAAGQGSYFLRDPAGAEHLFTGTRDRSPLPFVGSYDL 118  
 QY 121 ERYAGHRDQIPGLIGIOLIOSVSAIRYGGSTRAQASLILILOMISEAARFPIIMRYQ 180  
 DB 121 ERYAGHRDQIPGLIGIOLIOSVSAIRYGGSTRAQASLILILOMISEAARFPIIMRYQ 180  
 QY 119 ERYAGHRDQIPGLIGIOLIOSVSAIRYGGSTRAQASLILILOMISEAARFPIIMRYQ 178  
 DB 119 ERYAGHRDQIPGLIGIOLIOSVSAIRYGGSTRAQASLILILOMISEAARFPIIMRYQ 178  
 QY 181 DINGSEFLPDYMLLETSMGQSTVOYHSTQVYNNPFLAISTNPFVLTSMVASYA 240  
 DB 181 DINGSEFLPDYMLLETSMGQSTVOYHSTQVYNNPFLAISTNPFVLTSMVASYA 240  
 QY 179 YNSGASFLPDYMLLETSMGQSTVOYHSTQVYNNPFLAISTNPFVLTSMVASYA 238  
 DB 179 YNSGASFLPDYMLLETSMGQSTVOYHSTQVYNNPFLAISTNPFVLTSMVASYA 238  
 QY 241 SLATMLFVCGRRPSSS 256  
 DB 241 SLATMLFVCGRRPSSS 254  
 DB 239 SLATMLFVCGRRPSSS 254

RESULT 4  
 AA25983  
 ID AA25983 standard; Protein; 254 AA.  
 XX AA25983;  
 XX  
 XX 18-OCT-1999 (first entry)  
 XX  
 XX Mistletoe lectin A1 (variant) protein fragment.  
 XX  
 XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;  
 XX ribosome 286 subunit; non-cytotoxic; T-cell activation; immune response;  
 XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
 XX cancer; cytotoxicity; antigen; isoform; lectin A1.  
 XX  
 XX Viscum album.

PN DE19804210-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 03-FEB-1998; 98DB-1004210.  
 XX  
 XX 03-FEB-1998; 98DB-1004210.  
 XX  
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 XX MPI; 1999-445335/38.  
 XX N-PSDB; AA209107.  
 XX  
 XX Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX  
 XX Disclosure; Fig 5b; 78pp; German.  
 XX  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumor and immunostimulatory activity. The A-chain (MIA)  
 XX of the mistletoe lectin binds to, and inactivates, the 286 subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX of a large scale, at any time of the year. Recombinant products are  
 XX free from toxins present in natural mistletoe extracts. This sequence  
 XX represents a fragment of a mistletoe lectin A1 protein variant.

SO Sequence 254 AA;  
 Query Match 92.7%; Score 1204; DB 20; Length 254;  
 Best Local Similarity 93.0%; Pred. No. 6.1e-117;  
 Matches 238; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 1 YERLRKRYHQTDEYFRPFTLLADVYSSGSFSENEIPILRGSTIPVSDAQRFVLELTN 60  
 DB 1 YERLRKRYHQTDEYFRPFTLLADVYSSGSFSENEIPILRGSTIPVSDAQRFVLELTN 60  
 QY 61 QGDSITRAIDVTNAVVAAGQGSYFLRDPAGAEHLFTGTRDRSPLPFVGSYDL 120  
 DB 61 QGDSITRAIDVTNAVVAAGQGSYFLRDPAGAEHLFTGTRDRSPLPFVGSYDL 120  
 QY 61 QGDSITRAIDVTNAVVAAGQGSYFLRDPAGAEHLFTGTRDRSPLPFVGSYDL 118  
 DB 61 QGDSITRAIDVTNAVVAAGQGSYFLRDPAGAEHLFTGTRDRSPLPFVGSYDL 118  
 QY 121 ERYAGHRDQIPGLIGIOLIOSVSAIRYGGSTRAQASLILILOMISEAARFPIIMRYQ 180  
 DB 121 ERYAGHRDQIPGLIGIOLIOSVSAIRYGGSTRAQASLILILOMISEAARFPIIMRYQ 180  
 QY 119 ERYAGHRDQIPGLIGIOLIOSVSAIRYGGSTRAQASLILILOMISEAARFPIIMRYQ 178  
 DB 119 ERYAGHRDQIPGLIGIOLIOSVSAIRYGGSTRAQASLILILOMISEAARFPIIMRYQ 178  
 QY 181 DINGSEFLPDYMLLETSMGQSTVOYHSTQVYNNPFLAISTNPFVLTSMVASYA 240  
 DB 181 DINGSEFLPDYMLLETSMGQSTVOYHSTQVYNNPFLAISTNPFVLTSMVASYA 240  
 QY 179 YNSGASFLPDYMLLETSMGQSTVOYHSTQVYNNPFLAISTNPFVLTSMVASYA 238  
 DB 179 YNSGASFLPDYMLLETSMGQSTVOYHSTQVYNNPFLAISTNPFVLTSMVASYA 238  
 QY 241 SLATMLFVCGRRPSSS 256  
 DB 241 SLATMLFVCGRRPSSS 254  
 DB 239 SLATMLFVCGRRPSSS 254

RESULT 5  
 AB79450  
 ID AB79450 standard; Protein; 551 AA.  
 XX AB79450;  
 XX  
 XX 08-JUL-2002 (first entry)  
 XX  
 XX Galactose-recognising mistletoe lectin.  
 XX  
 XX Mistletoe; galactose-recognising mistletoe lectin; MIII.





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us-09-601-667c-38.rsp

QY	9	THQTDGDEYFEFTLLADYVSSGSPNEPILRO-STIPVSDAORFVVELNQGDS-I	66
DB	40	TKRATYTSYQFIELBAQLASGEFHGIDPVRREHSTVP--DSKRFIVELSNWADSV	97
QY	67	TAIDVTNAYVVAQAGDOSYELR-DAPGAEHTLFTGTEDRSSLPFTGSYTDLEKYAG	125
DB	98	TLAVDTNAYVVAFTGOSOFLEEDNDPALENLAPDT--KRYTFPSGSYTDLEGVAG	155
QY	126	HRDQPIGIEQLIOSVSNLRTG-GSTRQARSIIILQWISBAAPNFIEMARODIN	183
DB	156	ERREHILGMDPLENKLISNLSNNOGRLARSLIVLQWYHAYRFRFEYKRGIS	215
QY	184	SGESFLPDMNLELETSNQQOSTQVGHSTD-GVNNPFLAISTGNVYLSNYS-VIAS	241
DB	216	RAWFFRDPBMLSTENNGALSNAVOGNGGVPSSEVELNSISNRPVYVGSVDVIGS	275
QY	242	LATMLFVC--GESPSS	255
DB	276	LATMLFICRSTDRASS	291

Search completed: December 11, 2003, 14:01:05  
JOB time : 20.732 secs







QY 9 TQCTGDEYFFETTLADYVSSGSPNEPLRSGTTPVSDAQRFVTLVETLNOGQDSITA 68  
DB 9 TQCTGDEYFFETTLADYVSSGSPNEPLRSGTTPVSDAQRFVTLVETLNOGQDSITA 68  
QY 69 AIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 127  
DB 69 AIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 127  
QY 67 GIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 124  
DB 67 GIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 124  
QY 128 DOIPLGIEQLQSVLALRYPGSTPAQASILLIOMISBAAPNPLIMRYODINSSES 187  
DB 128 DOIPLGIEQLQSVLALRYPGSTPAQASILLIOMISBAAPNPLIMRYODINSSES 187  
QY 125 QOILPLGLOALTHGISFFRSGNDMEKARTLIVILQWVAALAFRISNRVYSIQOTA 184  
DB 125 QOILPLGLOALTHGISFFRSGNDMEKARTLIVILQWVAALAFRISNRVYSIQOTA 184  
QY 186 FLPDMVYMLBETNSWQOSTVQVHSTDGVFNNPRLAISTGNFTVLSNVS----- 237  
DB 186 FLPDMVYMLBETNSWQOSTVQVHSTDGVFNNPRLAISTGNFTVLSNVS----- 237  
QY 238 -VIASLAIMLFCV 249  
DB 238 -VIASLAIMLFCV 249  
QY 235 PTVAVALMLFCV 247  
DB 235 PTVAVALMLFCV 247

## RESULT 9

Q96237 PRELIMINARY; PRT; 251 AA.  
ID Q96237  
AC Q96237 (TREMELREL. 02, Created)  
DT 01-FEB-1997 (TREMELREL. 02, Last sequence update)  
DE 01-OCT-2002 (TREMELREL. 22, Last annotation update)  
PC PDBAAC-1:EI64A/R167 protein (EC 3.2.2.22) (RNA N-glycosidase)  
DE (Fragment)  
OS Abrus precatorius (Indian licorice) (Crab's eye).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
OX NCBI\_TaxID:3816;  
RN 11  
RS SEQUENCE FROM N.A.  
RC TISSUE=Seed.  
RX MEDLINE=94139756; PubMed=8307038;  
RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;  
RT "Cloning and expression of three abrin A-chains and their mutants  
derived by site-specific mutagenesis in Escherichia coli.",  
RL Eur. J. Biochem. 219:83-87(1994).  
CC -1- CATALYTIC ACTIVITY: ENDOPHYLLOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR HSRP; P11140; IABR.  
DR PIRAT; P00157; R1P.  
DR PIRAT; P00157; R1P.  
DR PRINTS; PR00396; SHIGARICIN.  
KW Hydrolase; Toxin.  
FT NON TER 1  
FT NON TER 251  
SQ SEQUENCE 251 AA; 28055 MW; 6F6475C9DEAFB79 CRC64;

Query Match 36.4%; Score 473; DB 10; Length 251;  
Best Local Similarity 43.1%; Pred. No. 4,2e-37;  
Matches 109; Conservative 37; Mismatches 81; Indels 26; Gaps 6;

QY 9 TQCTGDEYFFETTLADYVSSGSPNEPLRSGTTPVSDAQRFVTLVETLNOGQDSITA 68  
DB 9 TQCTGDEYFFETTLADYVSSGSPNEPLRSGTTPVSDAQRFVTLVETLNOGQDSITA 68  
QY 69 AIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 127  
DB 69 AIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 127  
QY 67 GIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 124  
DB 67 GIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 124  
QY 128 DOIPLGIEQLQSVLALRYPGSTPAQASILLIOMISBAAPNPLIMRYODINSSES 187  
DB 128 DOIPLGIEQLQSVLALRYPGSTPAQASILLIOMISBAAPNPLIMRYODINSSES 187  
QY 125 QOILPLGLOALTHGISFFRSGNDMEKARTLIVILQWVAALAFRISNRVYSIQOTA 184  
DB 125 QOILPLGLOALTHGISFFRSGNDMEKARTLIVILQWVAALAFRISNRVYSIQOTA 184  
QY 186 FLPDMVYMLBETNSWQOSTVQVHSTDGVFNNPRLAISTGNFTVLSNVS----- 237  
DB 186 FLPDMVYMLBETNSWQOSTVQVHSTDGVFNNPRLAISTGNFTVLSNVS----- 237

DB 186 FLPDMVYMLBETNSWQOSTVQVHSTDGVFNNPRLAISTGNFTVLSNVS----- 234  
QY 238 -VIASLAIMLFCV 249  
DB 238 -VIASLAIMLFCV 249  
QY 235 PTVAVALMLFCV 247  
DB 235 PTVAVALMLFCV 247

## RESULT 10

Q96235 PRELIMINARY; PRT; 251 AA.  
ID Q96235  
AC Q96235;  
DT 01-FEB-1997 (TREMELREL. 02, Created)  
DE 01-OCT-2002 (TREMELREL. 22, Last annotation update)  
PC PDBAAC-1:EI64A/R167 (EC 3.2.2.22) (RNA N-glycosidase)  
DE (Fragment)  
OS Abrus precatorius (Indian licorice) (Crab's eye).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
OX NCBI\_TaxID:3816;  
RN 11  
RS SEQUENCE FROM N.A.  
RC TISSUE=Seed.  
RX MEDLINE=94139756; PubMed=8307038;  
RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;  
RT "Cloning and expression of three abrin A-chains and their mutants  
derived by site-specific mutagenesis in Escherichia coli.",  
RL Eur. J. Biochem. 219:83-87(1994).  
CC -1- CATALYTIC ACTIVITY: ENDOPHYLLOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR HSRP; P11140; IABR.  
DR PIRAT; P00157; R1P.  
DR PIRAT; P00157; R1P.  
DR PRINTS; PR00396; SHIGARICIN.  
KW Hydrolase; Toxin.  
FT NON TER 1  
FT NON TER 251  
SQ SEQUENCE 251 AA; 27997 MW; 3B60351839AEFBE78 CRC64;

Query Match 36.0%; Score 467; DB 10; Length 251;  
Best Local Similarity 42.7%; Pred. No. 1,6e-36;  
Matches 108; Conservative 37; Mismatches 82; Indels 26; Gaps 6;

QY 9 TQCTGDEYFFETTLADYVSSGSPNEPLRSGTTPVSDAQRFVTLVETLNOGQDSITA 68  
DB 9 TQCTGDEYFFETTLADYVSSGSPNEPLRSGTTPVSDAQRFVTLVETLNOGQDSITA 68  
QY 69 AIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 127  
DB 69 AIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 127  
QY 67 GIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 124  
DB 67 GIDVTNAYVVAQAGOSYFLNDAPRGAKTHLFTGTRDSSLPFGSYTDLERYAGH-R 124  
QY 128 DOIPLGIEQLQSVLALRYPGSTPAQASILLIOMISBAAPNPLIMRYODINSSES 187  
DB 128 DOIPLGIEQLQSVLALRYPGSTPAQASILLIOMISBAAPNPLIMRYODINSSES 187  
QY 125 QOILPLGLOALTHGISFFRSGNDMEKARTLIVILQWVAALAFRISNRVYSIQOTA 184  
DB 125 QOILPLGLOALTHGISFFRSGNDMEKARTLIVILQWVAALAFRISNRVYSIQOTA 184  
QY 186 FLPDMVYMLBETNSWQOSTVQVHSTDGVFNNPRLAISTGNFTVLSNVS----- 237  
DB 186 FLPDMVYMLBETNSWQOSTVQVHSTDGVFNNPRLAISTGNFTVLSNVS----- 237  
QY 238 -VIASLAIMLFCV 249  
DB 238 -VIASLAIMLFCV 249  
QY 235 PTVAVALMLFCV 247  
DB 235 PTVAVALMLFCV 247

## RESULT 11

Q98760 PRELIMINARY; PRT; 255 AA.  
ID Q98760  
AC Q98760;  
DT 01-NOV-1998 (TREMELREL. 08, Created)

RA Do M.-S., Song S.K.;  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL, AF508916; AAM46934.1; -.  
 DR InterPro; IPR001574; RIF.  
 DR Pfam; PF00161; RIF\_1.  
 DR PRINTS; PR00275; SHIGARICIN.  
 DR KX Glycosidase; Toxin.  
 KY Hydrolase; Toxin.  
 FT NON TER 251  
 FT 251  
 SQ SEQUENCE 251 AA; 28090 MW; A1177489012B989 CRC64;  
 Query Match 79.1%; Score 1027; DB 10; Length 251;  
 Best Local Similarity 84.1%; Pred. No. 2,7e-90;  
 Matches 212; Conservative 9; Mismatches 25; Indels 6; Gaps 3;  
 DB 1 YERLNLNTHQTDGTYRFTLLADVVSSGSPSENEIFLRQSTTPVSDAQPVLVELTN 60  
 QY 1 YERLNLNTHQTDGTYRFTLLADVVSSGSPSENEIFLRQSTTPVSDAQPVLVELTN 60  
 DB 1 YERLNLNTHQTDGTYRFTLLADVVSSGSPSENEIFLRQSTTPVSDAQPVLVELTN 59  
 QY 61 C---GGDSITAIIDVTAAVYVAGQSGSYFLADPQATGTHFTGTGDDSSLPRTGTY 117  
 DB 60 QLAKWDSITAIIDVTNLVYVAYVAGQSGYFLADPQATGTHFTGTG--SSLPRTGTY 117  
 QY 118 TDLERYAGRDQIFLGIEQLGVSAALRPGSGSTRQARSTILLQMSLAAAPNELMR 177  
 DB 118 ADLERYAGRDQIFLGIEQLGVSAALRPGSGSTRQARSTILLQMSLAAAPNELMR 177  
 QY 178 YRODNGSGSELPDWTMLLEPISNGQSGTQVGHSTGTFNNPRLAISTGNFVLSNRS 237  
 DB 178 ARQYINSGVSLPDVTMLLSHNSMQQSGTQVGHSTGTFNNPRLAISTGNFVLSNRS 237  
 QY 238 VTSALATMLPVC 249  
 DB 238 VTSALATMLPVC 249  
 QY 238 VTSALATMLPVC 249  
 DB 238 VTSALATMLPVC 249  
 RESULT 7  
 Q38761 PRELIMINARY; PRT; 252 AA.  
 AC Q38761; Q96234;  
 DT 01-NOV-1996 (TREMBLrel. 02, Created)  
 DT 01-NOV-1996 (TREMBLrel. 02, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Ricin A-chain type 73 (EC 3.2.2.22) (RNA N-glycosidase)  
 GN RIP.  
 OS Abrus precatorius (Indian licorice) (Crab's eye).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosoid I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
 CX NCBI\_TaxID:3816;  
 RX NCBI\_TaxID:3816;  
 RN SEQUENCE FROM N.A.  
 RA TissueSeed;  
 RC TissueSeed;  
 RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE OF 2-252 FROM N.A.  
 RC TissueSeed;  
 RX MEDLINE-94139756; PubMed-8107038;  
 RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;  
 RT Cloning and expression of three abrin A-chains and their mutants  
 RT derived by site-specific mutagenesis in Escherichia coli.";  
 RX J Biol Chem. 211:83-87(1996)HYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL, X54873; CA43855.1; -.  
 DR EMBL, X76720; CA45138.1; -.  
 DR HSSP; P11140; IABR.

DR InterPro; IPR001574; RIF.  
 DR Pfam; PF00161; RIF\_1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PR00275; SHIGARICIN. 1.  
 KW Glycosidase; Hydrolase; Toxin.  
 FT NON TER 252  
 FT 252  
 SQ SEQUENCE 252 AA; 28229 MW; 167B894E134EC65 CRC64;  
 Query Match 37.0%; Score 450; DB 10; Length 252;  
 Best Local Similarity 33.5%; Pred. No. 9e-30;  
 Matches 110; Conservative 37; Mismatches 80; Indels 26; Gaps 6;  
 DB 9 THQTGDIYRFTLLADVVSSGSPSENEIFLRQSTTPVSDAQPVLVELTNQGGDSTTA 68  
 QY 9 THQTGDIYRFTLLADVVSSGSPSENEIFLRQSTTPVSDAQPVLVELTNQGGDSTTA 68  
 DB 10 TQATGSGYQFTEALREELRGDLIHDPVLPDPTLTQERNRYITVELSNEDTSIEV 67  
 QY 69 AIDVTAAVYVAGQSGSYFLADPQATGTHFTGTGDDSSLPRTGTY 127  
 DB 68 GIDVTAAVYVAGQSGSYFLADPQATGTHFTGTGDDSSLPRTGTY 125  
 QY 128 DQIFLGIEQLGVSAALRPGSGSTRQARSTILLQMSLAAAPNELMRQDINSQS 187  
 DB 126 QQLIDQLTHGIFRSGDNDKAKILVILQVADPKRRYLSMKRYVSLQGVH 185  
 QY 188 FLDPWTMLLEPISNGQSGTQVGHSTGTFNNPRLAISTGNFVLSNRS 237  
 DB 186 FQPDAAITSLNNMNDNSGVSQDTFPCV-----VLTININHPVYVDSLSH 235  
 QY 238 -VTSALATMLPVC 249  
 DB 236 FTVAVIALMLPVC 248  
 RESULT 8  
 Q96236 PRELIMINARY; PRT; 251 AA.  
 AC Q96236;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Abrin A chain (EC 3.2.2.22) (B164a) (RNA N-glycosidase)  
 GN (Fragment).  
 GN PCDNA6-1-5164A.  
 OS Abrus precatorius (Indian licorice) (Crab's eye).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosoid I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
 CX NCBI\_TaxID:3816;  
 RX NCBI\_TaxID:3816;  
 RN SEQUENCE FROM N.A.  
 RA TissueSeed;  
 RC TissueSeed;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE OF 2-251 FROM N.A.  
 RC TissueSeed;  
 RX MEDLINE-94139756; PubMed-8107038;  
 RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;  
 RT Cloning and expression of three abrin A-chains and their mutants  
 RT derived by site-specific mutagenesis in Escherichia coli.";  
 RX J Biol Chem. 211:83-87(1996)HYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL, X76721; CA45139.1; -.  
 DR HSSP; P11140; IABR.  
 DR InterPro; IPR001574; RIF.  
 DR Pfam; PF00161; RIF\_1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 KW Hydrolase; Toxin.  
 FT NON TER 251  
 FT 251  
 SQ SEQUENCE 251 AA; 28040 MW; D57CB192E0EC69 CRC64;  
 Query Match 36.5%; Score 474; DB 10; Length 251;  
 Best Local Similarity 43.1%; Pred. No. 3.4e-37;  
 Matches 109; Conservative 37; Mismatches 81; Indels 26; Gaps 6;

DE Lectin chain A isoform 1 (EC 3.2.2.22) (tRNA N-glycosidase)  
 DE (Fragment).  
 DE Viscum album subsp. coloratum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Santalales; Viscaceae; Viscum.  
 OC NCBI\_TaxID=159976;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21566752; PubMed=11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RA Mol. Cells 12:215-220(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOPOLYMERIZATION OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; AF508914; AA046932.1; -  
 DR InterPro; IP001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR Hydrolase; Toxin.  
 FM NON TER  
 FT NON TER  
 SQ SEQUENCE 254 AA; 28446 MW; 6DB5C318FAFE90 CRC64;

Query Match 87.9%; Score 1142; DB 10; Length 254;  
 Best Local Similarity 89.5%; Pred. No. 2.5e-101;  
 Matches 229; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 1 YERLRARVHTQGTGDEYFFETLLRDVYSGSPSENEIPILKQSTIPVSDAQFVLELTN 60  
 DB 1 YERLRARVHTQGTGDEYFFETLLRDVYSGSPSENEIPILKQSTIPVSDAQFVLELTN 60  
 QY 61 GGGSTTAIDVTNAYVAVAGDQSYFLRPAKAEHTLFTGTTDRSSLPPTGSYTDL 120  
 DB 61 GGGSTTAIDVTNAYVAVAGDQSYFLRPAKAEHTLFTGTTDRSSLPPTGSYTDL 118  
 QY 121 ERYAGRRDQIPLGIGELIOVSALRFPQSGTRARQSSILLIOMISBARPNFLIMARYO 180  
 DB 119 ERYAGRRDQIPLGIGELIOVSALRFPQSGTRARQSSILLIOMISBARPNFLIMARYO 178  
 QY 181 DINGSGSLPDMTMELETSWQSQSTOVQHSITDGVFNNPRLAISTGNFTLSNRSVYA 240  
 DB 179 YISGSGSLPDMTMELETSWQSQSTOVQHSITDGVFNNPRLAISTGNFTLSNRSVYA 238  
 QY 241 SLATMLFVCERRSSS 256  
 DB 239 SLATMLFVCERRSSS 254

RESULT 5  
 QBLK05  
 ID QBLK05 PRELIMINARY; PRT; 249 AA.  
 AC QBLK05; T-REMBLrel. 22. Created)  
 DT 01-OCT-2002 (T-REMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (T-REMBLrel. 22, Last annotation update)  
 DE Lectin chain A isoform 2 (EC 3.2.2.22) (tRNA N-glycosidase)  
 DE (Fragment).  
 OS Viscum album subsp. coloratum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Santalales; Viscaceae; Viscum.  
 OC NCBI\_TaxID=159976;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,

RX MEDLINE=21566752; PubMed=11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RA Mol. Cells 12:215-220(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOPOLYMERIZATION OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; AF508915; AA046933.1; -  
 DR InterPro; IP001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR Hydrolase; Toxin.  
 FM NON TER  
 FT NON TER  
 SQ SEQUENCE 249 AA; 27821 MW; 3C5870F8338D85 CRC64;

Query Match 84.0%; Score 1091; DB 10; Length 249;  
 Best Local Similarity 86.7%; Pred. No. 1.9e-96;  
 Matches 216; Conservative 15; Mismatches 16; Indels 2; Gaps 1;

QY 1 YERLRARVHTQGTGDEYFFETLLRDVYSGSPSENEIPILKQSTIPVSDAQFVLELTN 60  
 DB 1 YERLRARVHTQGTGDEYFFETLLRDVYSGSPSENEIPILKQSTIPVSDAQFVLELTN 60  
 QY 61 GGGSTTAIDVTNAYVAVAGDQSYFLRPAKAEHTLFTGTTDRSSLPPTGSYTDL 120  
 DB 61 GGGSTTAIDVTNAYVAVAGDQSYFLRPAKAEHTLFTGTTDRSSLPPTGSYTDL 118  
 QY 121 ERYAGRRDQIPLGIGELIOVSALRFPQSGTRARQSSILLIOMISBARPNFLIMARYO 180  
 DB 119 ERYAGRRDQIPLGIGELIOVSALRFPQSGTRARQSSILLIOMISBARPNFLIMARYO 178  
 QY 181 DINGSGSLPDMTMELETSWQSQSTOVQHSITDGVFNNPRLAISTGNFTLSNRSVYA 240  
 DB 179 YISGSGSLPDMTMELETSWQSQSTOVQHSITDGVFNNPRLAISTGNFTLSNRSVYA 238  
 QY 241 SLATMLFVCE 249  
 DB 239 SLATMLFVCE 247

RESULT 6  
 QBLK04  
 ID QBLK04 PRELIMINARY; PRT; 251 AA.  
 AC QBLK04; T-REMBLrel. 22. Created)  
 DT 01-OCT-2002 (T-REMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (T-REMBLrel. 22, Last annotation update)  
 DE Lectin chain A isoform 3 (EC 3.2.2.22) (tRNA N-glycosidase)  
 DE (Fragment).  
 OS Viscum album subsp. coloratum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Santalales; Viscaceae; Viscum.  
 OC NCBI\_TaxID=159976;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21566752; PubMed=11710524;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RA Mol. Cells 12:215-220(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,



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us-09-601-667c-38.rpt

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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18, Search time 19.7321 seconds

3347.915 Million cell updates/sec

Title: US-09-601-667C-38

Perfect score: 1299

Sequence: 1 YERLNAVHTQTDYFRF.....SVIASIAMFVCGSPSS 256

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting First 45 summaries

Database: 1: SP archaea:\*

2: SP bacteria:\*

3: SP fungi:\*

4: SP human:\*

5: SP invertebrate:\*

6: SP mammal:\*

7: SP muc:\*

8: SP organelle:\*

9: SP plant:\*

10: SP protist:\*

11: SP rodent:\*

12: SP virus:\*

13: SP vertebrate:\*

14: SP unclassified:\*

15: SP viroin:\*

16: SP bacteriopl:\*

17: SP archaeosp:\*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1186	91.1	249	Q08XK7	Q08XK7 viscum albu
2	1186	89.8	249	Q08XK8	Q08XK8 viscum albu
3	1166	89.8	249	Q08XK9	Q08XK9 viscum albu
4	1142	87.9	249	Q08XK5	Q08XK5 viscum albu
5	1091	84.0	249	Q08XK6	Q08XK6 viscum albu
6	1027	79.1	251	Q08XK4	Q08XK4 viscum albu
7	480	37.0	252	Q08XK1	Q08XK1 viscum albu
8	474	36.5	251	Q08XK3	Q08XK3 viscum albu
9	473	36.4	251	Q08XK2	Q08XK2 viscum albu
10	467	36.0	251	Q08XK7	Q08XK7 viscum albu
11	462	35.6	251	Q08XK8	Q08XK8 viscum albu
12	459	34.9	251	Q08XK9	Q08XK9 viscum albu
13	450.5	34.7	549	Q08XK2	Q08XK2 viscum albu
14	449.5	34.6	581	Q08XK5	Q08XK5 viscum albu
15	448	34.5	528	Q06076	Q06076 abrus prec

17	401	30.9	570	10	Q41358	Q41358 sambucus ni
18	393	30.3	541	10	Q41174	Q41174 ricinus com
19	392	30.2	570	10	Q22415	Q22415 sambucus ni
20	390	30.0	547	10	Q06659	Q06659 abrus prec
21	387.5	29.8	564	10	Q06659	Q06659 abrus prec
22	386	29.7	592	10	Q06659	Q06659 abrus prec
23	384.5	29.6	555	10	Q06659	Q06659 abrus prec
24	384	29.6	573	10	Q06659	Q06659 abrus prec
25	384	29.6	573	10	Q06659	Q06659 abrus prec
26	384	29.6	573	10	Q06659	Q06659 abrus prec
27	384	29.6	573	10	Q06659	Q06659 abrus prec
28	384	29.6	573	10	Q06659	Q06659 abrus prec
29	384	29.6	573	10	Q06659	Q06659 abrus prec
30	384	29.6	573	10	Q06659	Q06659 abrus prec
31	384	29.6	573	10	Q06659	Q06659 abrus prec
32	384	29.6	573	10	Q06659	Q06659 abrus prec
33	384	29.6	573	10	Q06659	Q06659 abrus prec
34	384	29.6	573	10	Q06659	Q06659 abrus prec
35	384	29.6	573	10	Q06659	Q06659 abrus prec
36	384	29.6	573	10	Q06659	Q06659 abrus prec
37	384	29.6	573	10	Q06659	Q06659 abrus prec
38	384	29.6	573	10	Q06659	Q06659 abrus prec
39	384	29.6	573	10	Q06659	Q06659 abrus prec
40	384	29.6	573	10	Q06659	Q06659 abrus prec
41	384	29.6	573	10	Q06659	Q06659 abrus prec
42	384	29.6	573	10	Q06659	Q06659 abrus prec
43	384	29.6	573	10	Q06659	Q06659 abrus prec
44	384	29.6	573	10	Q06659	Q06659 abrus prec
45	384	29.6	573	10	Q06659	Q06659 abrus prec

ALIGNMENTS

RESULT 1

ID Q08XK7

AC Q08XK7

DT 01-JUN-2002 (TrEMBL)

DT 01-JUN-2002 (TrEMBL)

DT 01-JUN-2002 (TrEMBL)

DT 01-JUN-2002 (TrEMBL)

DT 01-JUN-2002 (TrEMBL)

DT 01-JUN-2002 (TrEMBL)

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DT 01-JUN-2002 (TrEMBL)

DT 01-JUN-2002 (TrEMBL)

DT 01-JUN-2002 (TrEMBL)

RL Structure 2:7-16 (1994).  
 RN 153  
 RN X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).  
 RX MEDLINE=94192822; PubMed=8143659;  
 RA Husain J., Tickle I.J., Wood S.P.;  
 RT "Crystal structure of momordin, a type I ribosome inactivating  
 RT protein from the seeds of Momordica charantia.";  
 RL FEBS Lett. 342:154-158 (1994).  
 RN [6]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RA Husain J., Tickle I.J., Wood S.P., Wang Y.;  
 RA Huang Q., Lin S., Tang Y., Jin S.;  
 RT "Studies on crystal structures active-centre geometry and  
 RT dephasing mechanism of two ribosome-inactivating proteins.";  
 RL Biochem. J. 309:285-298 (1995).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC  
 CC EMBL; X57682; CAA04069.1; -  
 DR PIR; S14273; RLP034.  
 DR PDB; 1A8H; 22-JUN-94.  
 DR PDB; 1A8J; 22-JUN-94.  
 DR PDB; 1A8C; 22-JUN-94.  
 DR PDB; 1A8M; 31-MAY-94.  
 DR PDB; 1A8G; 07-FEB-95.  
 DR PDB; 1A8H; 07-FEB-95.  
 DR PDB; 1A8I; 07-FEB-95.  
 DR PDB; 1A8Q; 21-NOV-01.  
 DR GlycoStatedB; E16094; -  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00101; RIP.  
 DR SMART; SM00106; RIP.  
 DR PROSITE; PS00275; SHIGA\_SICIN\_1.  
 KW plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;  
 KW Glycoprotein; 3D-structure.  
 FT SIGNAL 1 23  
 FT CHAIN 24 269  
 FT PROPEP 270 286  
 FT ACT SITE 183 183  
 FT CARBOHYD 250 250  
 FT STRAND 25 28  
 FT HELIX 34 47  
 FT STRAND 50 54  
 FT TURN 55 56  
 FT STRAND 57 60  
 FT HELIX 66 69  
 FT STRAND 70 76  
 FT TURN 76 79  
 FT STRAND 82 88  
 FT TURN 88 93  
 FT STRAND 93 99  
 FT TURN 100 101  
 FT STRAND 102 105  
 FT HELIX 109 114  
 FT TURN 115 117  
 FT STRAND 120 121  
 FT STRAND 124 127  
 FT STRAND 134 135  
 FT HELIX 141 144  
 FT STRAND 150 150  
 FT HELIX 152 162  
 FT TURN 163 163  
 FT TURN 163 163

RIBOSOME-INACTIVATING PROTEIN MOMORDIN I.  
 MISSING IN MATURE PROTEIN.  
 N-LINKED (GLCNAC...)  
 /FTID=CAR\_000082.

FT HELIX 167 186  
 FT STRAND 187 189  
 FT HELIX 188 195  
 FT TURN 196 197  
 FT STRAND 202 202  
 FT HELIX 206 225  
 FT TURN 226 230  
 FT STRAND 231 238  
 FT TURN 240 241  
 FT STRAND 246 250  
 FT STRAND 250 258  
 FT HELIX 254 258  
 FT TURN 259 259  
 FT STRAND 260 260  
 FT STRAND 263 263  
 FT HELIX 266 268  
 SQ SEQUENCE 286 AA; 31532 MW; E18013ABEC316CF CRC64;  
 Query Match 22.1%; Score 286.5; DB 1; Length 286;  
 Best Local Similarity 32.3%; 44; From 198-193; Indels 33; Gaps 9;  
 Matches 85; Conservative 44; Identical 33; Gaps 9;  
 14 GDEYR-----PILLRDUVSSGSFSENEIPILPOSTIPVSDAQRVYLVELTNOG 62  
 23 GDVSRFLSGADPRYKGFIDKLNMLPFREKVMIFLLPS--VSGAQRVILMLHFNVD 79  
 63 QDSITPAIDVTNAVYVQAGDSYFLRD-APRGATRLFTGTRDSSLPPTGSYDLS 121  
 80 GKTIIVADVNTVINGTADITTSIFENRPAELASQVFRDNR-KITLPSNTERLQ 138  
 122 RYAGE-EDQIPICQEQLOSALVPGSRPAQASITLITOMSSAARPIILWR-- 177  
 139 IAKGPKREKIFIGPRLDSALITLH-YDSIAAGALVLIQTAAARAFVIEQIOE 196  
 178 --YQDINSSESEFLPPMVMLELETSWCOQSTQV--HSDGVNPPRLATSTGNVPLS 233  
 197 RAYREYV-----PSLATISLENSWGLSKXIOQLAQQNGIFRPIPLVLDNKNVQIT 249  
 234 NVESVYSLAIKLFV 248  
 250 NVTSKAVTSNIQILL 264

Search completed: December 11, 2003, 14:09:08  
 Job time : 5.48263 secs

FT CONFLICT 152 152 A -> S (IN REF. 2).  
 FT CONFLICT 174 174 C -> S (IN REF. 2).  
 FT CONFLICT 245 245 N -> H (IN REF. 2).  
 SQ SEQUENCE 294 AA; 32234 MW; DA4F8YCE3290994 CRC64;

Query Match  
 Best Local Similarity 33.6%; Pred. No. 1,6e-15;  
 Matches 81; Conservative 45; Mismatches 100; Indels 15; Gaps 7;

13 TGPYRPTTLRDPYSSGSFNEIPLRKSTIPVSDQSPFVLVELTNGQSDITLADY 72  
 29 TKKYSSEFTLRDLALPTQGVCGIPLPST--AGSGQWFFPFLTNDETVAVNV 85  
 73 TNAVVAQMDQSYFLNDA-FRGAETLFTGTTRDSLSLPTGSYTLDERVAG-GRDQIP 131  
 86 TNAVIVAPADVSYFEDTPBAKILFAGKIVK--LVYSANIDLOSVAQKORWIE 143  
 132 LQTEOLQSVSLARPQGSTRAQASILLIQLMISAPENPILMKRYKODINGSSELPD 191  
 144 LQIPALSAIINWY--YDQSTKALVYVACCTAKAKKXKILBOVSLSIS--NFTN 199  
 192 MWLELETSWQSGSTQVQ--HSTQGVNPNPRLAISTGNFTLNVNS--VIRSLATL 246  
 200 QAVISLNNWGLSKQIQIANKTGQFNPVELYVDPGTRRESVNTSAGVAKNIKLL 259

DB 247 F 247  
 QY 260 Y 260

RESULT 14  
 RIPI\_CUOPI STANDARD; PRT; 286 AA.  
 AC Q9FRX4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)  
 DE EC 3.2.2.22  
 OS Cucumis flacres.  
 CC Cucurbitales; Cucurbitaceae; Cucumiss.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eucosids I; Cucurbitales; Cucurbitaceae; Cucumiss.  
 CX NCBI\_Taxid=331071;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamada T., Ohts. S.T., Osaka T.;  
 RA "Cloning and analysis of a cDNA coding a putative ribosome-  
 RA inactivating protein from Cucumis flacres.";  
 RA Plant Biotechnol. 17:337-340(2000).  
 RL -1- CATALYTIC ACTIVITY: Endoglycosylase of the N-glycosidic bond at one  
 RL -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL: AB045560; BAB1677.1; -  
 DR HSSP: P16094; IARC.  
 DR InterPro: IPR001574; RIF.  
 DR Pfam: PF00336; SIBDALIGN.  
 DR PROSITE: PS000275; SHOG\_RICH1.  
 DR Pfam: P16094; IARC.  
 DR Toxic: signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 23 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.

FT ACT SITE 185 185 BY SIMILARITY.  
 FT CARBOHYD 103 103 N-LINKED (GLUCAC... ) (POTENTIAL).  
 FT CARBOHYD 110 110 N-LINKED (GLUCAC... ) (POTENTIAL).  
 FT CARBOHYD 252 252 N-LINKED (GLUCAC... ) (POTENTIAL).  
 SQ SEQUENCE 286 AA; 31771 MW; 4EPD96B604D41 CRC64;

Query Match  
 Best Local Similarity 22.4%; Score 290.5; DB 1; Length 286;  
 Matches 79; Conservative 49; Mismatches 94; Indels 15; Gaps 8;

17 YRFTTLRDPYSSGSFNEIPLRKSTIPVSDQSPFVLVELTNGQSDITLADY 76  
 40 YRFTTLRDPYSSGSFNEIPLRKSTIPVSDQSPFVLVELTNGQSDITLADY 76  
 77 VNAVQMDQSYFLNDA-FRGAETLFTGTTRDSLSLPTGSYTLDERVAG-GRDQIP 134  
 97 TNAVIVAPADVSYFEDTPBAKILFAGKIVK--LVYSANIDLOSVAQKORWIE 143  
 132 LQTEOLQSVSLARPQGSTRAQASILLIQLMISAPENPILMKRYKODINGSSELPD 191  
 144 LQIPALSAIINWY--YDQSTKALVYVACCTAKAKKXKILBOVSLSIS--NFTN 199  
 192 MWLELETSWQSGSTQVQ--HSTQGVNPNPRLAISTGNFTLNVNS--VIRSLATL 246  
 200 QAVISLNNWGLSKQIQIANKTGQFNPVELYVDPGTRRESVNTSAGVAKNIKLL 259

DB 247 F 247  
 QY 260 Y 260

RESULT 15  
 RIPI\_CUOPI STANDARD; PRT; 286 AA.  
 AC P16094; P24697;  
 DT 01-MAR-1990 (Rel. 14, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ribosome-inactivating protein precursor (rRNA N-glycosidase)  
 DE EC 3.2.2.22 (Alpha-momocharitin) (Alpha-IMC).  
 OS Momordica charantia (Bitter melon) (Balsam pear).  
 CC Cucurbitales; Cucurbitaceae; Cucurbitaceae; Cucumiss.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC Cucurbitales; Cucurbitaceae; Cucurbitaceae; Cucumiss.  
 CX NCBI\_Taxid=3673;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-91159486; PubMed=200104;  
 RA Ho W.K.K., Liu S.C., Shaw P.C., Young W.W., Ng T.B., Chan W.Y.;  
 RA "Cloning of the cDNA of alpha-momocharitin: a ribosome inactivating  
 RA protein.";  
 RA Biochem. Biophys. Acta 1088:311-314(1991).  
 RL -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
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 CC EMBL: AB045560; BAB1677.1; -  
 DR HSSP: P16094; IARC.  
 DR InterPro: IPR001574; RIF.  
 DR Pfam: PF00336; SIBDALIGN.  
 DR PROSITE: PS000275; SHOG\_RICH1.  
 DR Pfam: P16094; IARC.  
 DR Toxic: signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 23 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.

KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;  
3D-structure; Multigene family; Glycoprotein; signal.  
FT SIGNAL 1 23  
FT CHAIN 24 270  
FT PROPER 271 290  
FT ACT\_SITE 212 212  
FT ACT\_SITE 212 212  
FT CARBOHYD 256 256  
FT MITRAGEN 212 212  
FT CONFLICT 61 65  
FT STRAND 25 28  
FT TURN 30 31  
FT HELIX 34 46  
FT TURN 47 47  
FT STRAND 50 54  
FT TURN 55 56  
FT STRAND 57 60  
FT HELIX 62 69  
FT STRAND 72 78  
FT TURN 82 88  
FT TURN 89 92  
FT STRAND 93 99  
FT TURN 100 101  
FT STRAND 102 105  
FT HELIX 109 114  
FT TURN 115 117  
FT TURN 120 121  
FT STRAND 124 127  
FT HELIX 134 141  
FT STRAND 142 147  
FT HELIX 147 150  
FT STRAND 152 163  
FT TURN 164 165  
FT HELIX 167 186  
FT STRAND 187 187  
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FT TURN 226 238  
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FT STRAND 263 263  
FT HELIX 266 266  
SQ SEQUENCE 290 AA; 31798 MW; B966CD9C031A42DB CRC64;  
Query Match 23.4%; Score 303.5; DB 1; Length 290;  
Best Local Similarity 33.2%; Pred No. 5; 7e-20;  
Matches 82; Conservative 50; Mismatches 98; Indels 17; Gaps 8;  
QY 7 RVHQTGDEPPPTITLADYVSSGSENEIPALQSTIPVSDAQPVLVELTQGGDI 66  
DB 28 RLSGATV-TSGVPIKRLKALPYERKYNIPLEKSS--ISGSGRYLILHLYNADETI 83  
QY 67 TAAIDYNAVVAAGDQDQSYFLNDPFGARTHLFTGTGRRSLPFTGSGYTDLERYAGH 126  
DB 84 SAVADYNAVIMSTLADYVSSGSENEIPALQSTIPVSDAQPVLVELTQGGDI 143  
QY 127 -RQDITGLTGLQVSLAPVSGSTPQARSLITLQMLISAPRNILAKRYRQDINS- 184  
DB 144 IRENIPLGLPDLDSATILTYLTYTMSAASN--LIVLQSTKASRYKI---EQIGKR 197  
QY 185 -GSEPLPDMYMLEETSGQSGTQVQ--HSDGVNPNPRLAISTQNYPLAN--VASYI 239  
DB 198 VKTFEPLSLATILENMSALSKQIQTSTNGQSPVPLDNGRVSITNARAVYT 257  
QY 240 ASLAIML 246  
DB 258 SNIALML 264  
PROTEIN 13  
ID RIPL\_TPTAN STANDARD; PRT; 294 AA.  
AC P56656; 09207; 1  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Type I ribosome-inactivating protein trichoangulina precursor (RNA  
N-glycosidase) (EC 3.2.2.22) (RIPI) (trichoangulin).  
OS Trichosanthes angulina (Snake gourd).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core Eudicotyledons;  
OC Cucurbitales; Cucurbitaceae; Trichosanthes.  
OX NCBI\_TaxID:50544;  
RN [1]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.  
RC SPRAIN-CV, Anguina; TISSUE=Seed;  
RX MEDLINE=99132006; PubMed=99131318;  
RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,  
Lin J.-Y.;  
RT "Purification, characterization and molecular cloning of trichoangulin,  
a novel type I ribosome-inactivating protein from the seeds of  
Trichosanthes angulina.";  
RU J. Biochem. Sci. 338:211-219 (1999).  
RP SEQUENCE OF 20-264.  
RA Chow L.-P., Kano M., Lin J.-Y., Wang S.-H., Ueno Y., Tsugita A.;  
RT "Amino acid sequence of trichoangulina, a ribosomal-inactivating  
protein from Trichosanthes angulina seeds.";  
RL J. Biochem. Sci. 3:178-186 (1996).  
CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN  
CC RIBOSOMES.  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
CC specific adenosine on the 28S ribosome.  
CC -1- TYPE 1 RIP SUBFAMILY.  
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DB EMBL: A053086; A052686.1; -  
DB HSB: P33132; P33132.1; -  
DB PIR: P00161; P00161.1; -  
DR PRINTS: P000396; SHIGARICIN.  
DR PROSITE: P500275; SHIGA\_RICIN; FALSE NEG.  
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;  
FT SIGNAL 1 19  
FT CHAIN 20 264  
FT PROPER 265 294  
FT ACT\_SITE 170 170  
FT CARBOHYD 220 220  
FT CONFLICT 51 51  
FT CONFLICT 65 65  
FT CONFLICT 84 84  
TYPE I RIBOSOME-INACTIVATING PROTEIN  
TRICHOANGULINA.  
BY SIMILARITY.  
N-LINKED (GLCNAC... ) (PROBABILE).  
C -> Y (IN REF. 2).  
W -> R (IN REF. 2).  
N -> D (IN REF. 2).





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FT HELIX 109 114
FT TURN 115 117
FT TURN 117 121
FT STRAND 121 124
FT HELIX 134 141
FT TURN 142 147
FT HELIX 145 147
FT STRAND 150 150
FT HELIX 152 153
FT TURN 154 155
FT TURN 151 151
FT TURN 181 181
FT STRAND 182 186
FT STRAND 187 187
FT HELIX 188 195
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FT STRAND 263 263
FT TURN 266 269
SQ SEQUENCE 289 AA; 31676 MW; 5CE09B63075B89 CRC64;

Query Match 25.3%; Score 329; DB 1; Length 289;
Best local similarity 36.4%; Pred. No. 2, 9e-22;
Matches 89; Conservative 52; Mismatches 84; Indels 18; Gaps 10;

QY 13 TGDFFRFTLLRDYVSGSFNSNEPLLRQSTIPVSDAQFVVLVLTNQGDSITPAIDV 72
DB 33 TSSYGVFISNLRALPNERLVDIPILR-SLTPGS--QVYLHLINVADETSIADIV 89
QY 73 TNAVVAVQAGOSYFLADA-PRGAETHLFTGTDRRESLPTSGYTDLEEVAGH-RDQI 130
DB 90 TNAVYVAGDGTSTYFENBATEKAYVFDGAR-KVLPFGSNERLQIAAGKIRBN 148
QY 131 PLAGIQLQSVALKRPGSGTRAPQASILLIILQMSKAAKPNILKRWKQINS--GESP 188
DB 149 PLALPDLDSAITLTFYNNANSASLR--LWVLQSTSEAAKRF---EQDIKRVKDT 202
QY 189 LPMVMELETSWQOOSTVOV--HSTQGVNPPRLAISTGNVTLNVSRS--VIASIAL 244
DB 203 LPSALISLNSNSGALSRLQIQLASTNNGOFSEFVLINAGNORVITINVDAGVYSIAL 262
QY 245 ML 246
DB 263 LL 264

RESULT 10
RIP2 MOWBA ID R1P2 MOWBA STANDARD; PRT; 289 AA.
AC P23335;
DT 01-MAR-1992 (Rel. 21; Created)
DT 15-DEC-1998 (Rel. 37; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Ribosome-inactivating protein karasurin precursor (rRNA
DB N-glycosidase) (EC 3.2.2.22).
OS Trichosanthes kirticowli (Mongolian snake-sourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Equisetopsida; Equisetales; Equisetaceae; Equisetum;
OC Equisetum; Equisetum; Equisetum; Equisetum; Equisetum;
OC NCBI_TaxId=3677;

SEQUENCE FROM N.A.
RIP2 MOWBA ID R1P2 MOWBA STANDARD; PRT; 286 AA.
AC P23335;
MEDLINE=97356562; PubMed=9212398;

```



RL Plant Mol. Biol. 22:1181-1186(1993).  
CC -1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN  
CC PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN  
CC SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN  
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATING PROTEIN  
CC SUBUNIT. B1 KENOVIRUS-INDUCED INACTIVATION OF 32S OF 28 S RNA. THE  
CC B1 KENOVIRUS-INDUCED INACTIVATION OF 32S OF 28 S RNA. THE  
CC BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES  
CC ENDOTOXICITY.  
CC -1- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.  
CC -----  
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CC -----  
DR EMBL, U41299; AAB39475.1; -  
DR PIR, S37382; S37382.  
DR InterPro; IPR000772; Ricin\_B\_lectin.  
DR Pfam; P000622; Ricin\_B\_lectin.6.  
DR PRINTS; PR00366; SHIGARICIN.  
DR SMART; SM00458; RICIN.2.  
DR PROSITE; PS00275; SHIGA\_RICIN.1.  
DR PROSITE; PS50231; RICIN\_B\_LECTIN.2.  
DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
KM Glycoprotein; Lectin; Signal.  
FT SIGNAL 1 25  
FT CHAIN 26 297 NIGRIN B A CHAIN.  
FT DOMAIN 298 563 NIGRIN B B CHAIN.  
FT DOMAIN 302 421 RICIN B-TYPE LECTIN 1.  
FT REPEAT 324 352 1 ALPHA.  
FT REPEAT 329 397 1-BETA.  
FT REPEAT 400 432 1-GAMMA.  
FT REPEAT 445 482 2-ALPHA.  
FT REPEAT 486 524 2-BETA.  
FT REPEAT 527 554 2-GAMMA.  
FT ACT\_SITES 188 188 BY SIMILARITY.  
FT DISULFID 274 302 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 319 338 BY SIMILARITY.  
FT DISULFID 360 377 BY SIMILARITY.  
FT DISULFID 448 462 BY SIMILARITY.  
FT DISULFID 463 482 BY SIMILARITY.  
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 39 39 K -> V (IN REP. 2).  
SQ SEQUENCE 563 AA; 62300 MW; P250CB2461BF14 CRC64;

Query Match 27.2%; Score 35; DB 1; Length 563;  
Best Local Similarity 37.2%; Posed No. 5; 1e-24;  
Matches 92; Conservative 87; Mismatches 8; Indels 18; Gaps 10;

QY 17 YRFTITLADYSSGS--NEPLLCSTIPVDQRVAVLNGQDSITLADVTNA 75  
DB 43 YDFPLNLEKTVAGGVGVGPIARER--SVQVSRVAVLNVNGVITLADVTNL 101  
QY 76 YVAVYQAGQGYFLDAPRGATVTLFTGTTRSSSLPTQSYTLDSRYAG--HSDQIFLST 134  
DB 102 YVAVFSGRANSTFFKLTREYQNSLNVGL--KQNTLSTFNTDNLNLEKTRRSHSLD 159

QY 135 ROLIGSVALRPGSTPRKQNSLILLOVTESEARNDPILMRRODNGSGSFLPDPM 194  
DB 160 SPLDNLITSL-YHDSV--ARSLVLIQVSEARFRRYEGEVRSLQDQNSFTPMALM 215  
QY 195 LELSTWQOQSTGVGHTGTFVNNPRLAISTGNF---VTLSSRVSV--IASLALMEPV 248  
DB 216 LSNENWNSLSLEIQAGKNV--SPFQVQLNDYDTRFLVDFEELVYCTGAILLFLR 273  
QY 249 GGRPSS 255  
DB 274 GSS-FSN 279  
RESULT B  
RIP2 BRVDI  
ID RIP2 BRVDI STANDARD; PRT; 282 AA.  
AC P98163; Q98800;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein Bryodin II precursor (RNA N-  
glycosidase) (EC 3.2.2.22) (B02).  
OS Bryonia dioica (Red Bryon); Streptophyta; Embryophyta; Tracheophyta;  
OC Eukaryota; Bryonia; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;  
OC Eucosida; Cucurbitales; Cucurbitaceae; Bryonia.  
OX NCBI\_Taxid:3652;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Segall C.B., Gawlak S.L., Margardt H.;  
RT "Bryodin 2, a ribosome-inactivating protein isolated from the plant  
Bryonia dioica.";  
RL Patent number US5597569, 28-JAN-1997.  
RN [2]  
RP SEQUENCE OF 22-42.  
RA MEDLINE-95151812; PubMed-7849072;  
RT Margardt H.;  
RA Segall C.B., Gawlak S.L., Chase D., Wolfe B.A., Mixan B.;  
RT "Characterization of ribosome-inactivating proteins isolated from  
Bryonia dioica and their utility as carcinoma-reactive  
immunokonjugates.";  
RL Bioconj. Chem. 5:423-429(1994).  
CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS  
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC -1- TYPE 1 RIP SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL, I14718; -; NOT\_ANNOTATED\_CDS.  
DR HSSP; P09989; IMB1.  
DR InterPro; IPR001574; RIP.  
DR Pfam; P00151; RIP.1.  
DR PRINTS; PR00366; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN.1.  
DR Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;  
KM Multigene family; Glycoprotein; Signal.  
FT SIGNAL 1 81  
FT CHAIN 1 81 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.  
FT ACT\_SITES 22 282  
FT CARBOHYD 25 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 282 AA; C58BZF6A873769C CRC64;  
SQ SEQUENCE 282 AA; 30754 MW; C58BZF6A873769C CRC64;

Query Match 25.7%; Score 34; DB 1; Length 282;





FT DOMAIN 272 399 RICIN B-TYPE LECTIN 1.  
 FT REPEAT 402 526 RICIN B-TYPE LECTIN 2.  
 FT REPEAT 282 324 1-ALPHA.  
 FT REPEAT 325 365 1-BETA.  
 FT REPEAT 365 400 2-GAMMA.  
 FT REPEAT 400 440 2-DELTA.  
 FT REPEAT 440 482 2-EPSILON.  
 FT REPEAT 482 527 2-GAMMA.  
 FT ACT SITE 163 163 BY SIMILARITY.  
 FT DISTALD 246 268 INTERCHAIN (BY SIMILARITY).  
 FT DISTALD 285 304 BY SIMILARITY.  
 FT DISTALD 328 345 BY SIMILARITY.  
 FT DISTALD 416 429 BY SIMILARITY.  
 FT MOD\_RES 455 472 BY SIMILARITY.  
 FT MOD\_RES 1 1 BY SIMILARITY.  
 FT CARBOHYD 110 110 N-LINKED (GLYCAN. . .) (POTENTIAL).  
 FT CARBOHYD 360 360 N-LINKED (GLYCAN. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLYCAN. . .) (POTENTIAL).  
 FT CONFLICT 282 282 N -> D (IN REF. 2).  
 FT CONFLICT 291 291 D -> N (IN REF. 2).  
 FT CONFLICT 350 351 AR -> PQ (IN REF. 2).  
 FT CONFLICT 378 378 S -> N (IN REF. 2).  
 FT CONFLICT 426 426 L -> M (IN REF. 2).  
 FT CONFLICT 428 428 Y -> D (IN REF. 2).  
 FT CONFLICT 431 431 N -> S (IN REF. 2).  
 FT CONFLICT 431 431 R -> K (IN REF. 2).  
 FT CONFLICT 434 434 N -> S (IN REF. 2).  
 FT CONFLICT 434 434 H -> Q (IN REF. 2).  
 FT CONFLICT 502 502 E -> G (IN REF. 2).  
 FT CONFLICT 509 509 H -> W (IN REF. 2).  
 FT CONFLICT 513 513 H -> T (IN REF. 2).  
 FT CONFLICT 516 516  
 SQ SEQUENCE 527 AA; 5914 MW; 3253AD490CE9494A CRC64;  
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 Best Local Similarity 42.4%; Pred. No. 2.1e-30;  
 Matches 103; Conservative 40; Mismatches 93; Indels 7; Gaps 6;  
 QY 9 THQTGDEYFRITLIDYVSSSSRSNIPILROSTIPVSDAQRVYELTNGQSDITR 68  
 DB 9 TEGATSGYKQFIENLQRI--TGLHGLVLPDPF--TLQERNKIVSLSDSTSLIA 66  
 QY 69 AIDVNAVVAAYQAGDSYFRLDAPRGAETHEFTGTRDRESLPEFTGSYDDEYAGH-R 127  
 DB 67 GIDVSAVVAAYRANSSYFRLDPTPSASRYFLTGT--QQSYLRPGSYIDLERLAQR 124  
 QY 128 DQIPGIBOLIOSVALRYPGSTRPAKRSIILQITSEASAFNFIIMFYKQDINSGES 187  
 DB 125 QQLPDELQRLRAISFLQ--SGDDQELRLLTVIIQWSEASARFISYVAVSIRPNA 183  
 QY 188 FLDPNMLFETSGQSTQVCSHTDGYFNPFRL-AISTGAEVTLNVAISYSLAINT 246  
 DB 184 FQDDAMISLENNONISGQSTQVCSHTDGYFNPFRLNVAISYSLAINT 243  
 QY 247 FVC 249  
 DB 244 FVC 246  
 RESULT 5  
 RCT\_RICCO STANDARD; PRT; 576 AA.  
 AC P02879; P02880; Rel. 01. Created  
 DT 21-JUN-1986 (Rel. 01. Last sequence update)  
 DT 13-AUG-1987 (Rel. 05. Last sequence update)  
 DT 15-SEP-2003 (Rel. 42. Last annotation update)  
 DB Ricin precursor [Contains: Ricin A chain (RNA N-glycosidase)  
 (EC 3.2.2.22); Ricin B chain).  
 DB Ricinus communis (Castor bean).  
 DB Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Eumariophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  
 OX NCBI\_TaxID=3988;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=66067214; PubMed=2999712;  
 RA Halling K.C., Halling A.C., Murray E.B., Ladin B.F., Houston L.L.,  
 RA Weaver R.F.;  
 RT "Genomic cloning and characterization of a ricin gene from Ricinus  
 RT Nucleic Acids Res. 13:8019-8033(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92163016; PubMed=1371405;  
 RA Tregear J.W., Roberts L.M.;  
 RT "The lectin gene family of Ricinus communis: cloning of a functional  
 RT ricin gene and three lectin pseudogenes.";  
 RT Plant Mol. Biol. 18:515-525(1992).  
 RN [3]  
 RP SEQUENCE OF 12-576 FROM N.A.  
 RX MEDLINE=85174479; PubMed=338723;  
 RA Lamb A., Roberts L.M., Lord J.M.;  
 RT "Nucleotide sequence of cloned cDNA coding for preproricin.";  
 RT Eur. J. Biochem. 148:265-270(1985).  
 RN [4]  
 RP SEQUENCE OF 36-302.  
 RA Yoshitake S., Funatsu G., Funatsu M.;  
 RT "Isolation and sequences of peptide peptides, and the complete  
 RT sequence of the chain of ricin D.";  
 RT Agric. Biol. Chem. 42:1267-1274(1978).  
 RN [5]  
 RP SEQUENCE OF 315-576.  
 RA Yoshitake S., Funatsu M.;  
 RT "Primary structure of A1b chain of ricin D.";  
 RT Agric. Biol. Chem. 43:2221-2224(1979).  
 RN [6]  
 RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.  
 RX MEDLINE=90344223; PubMed=168517;  
 RA Kimura Y., Kusuhara H., Tada M., Takagi S., Funatsu G.;  
 RT "Structural analyses of sugar chains from ricin A-chain variant.";  
 RT Agric. Biol. Chem. 54:157-162(1990).  
 RN [7]  
 RP REVIEW  
 RX MEDLINE=21480122; PubMed=11595634;  
 RA "Ricin.";  
 RT Toxicol. 39:1723-1728(2001).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=97165983; PubMed=358397;  
 RA Montefiore W., Villatransa J.E., Montenegro A.F., Ernst S.R., Katzin B.,  
 RA Rutenber E., Xiong N.H., Hamlin R., Robertus J.D.;  
 RT "The three-dimensional structure of ricin at 2.8 A.";  
 RT J. Biol. Chem. 262:5398-5403(1987).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE=91352004; PubMed=1881881;  
 RA Katzin B.J., Collins B.J., Robertus J.D.;  
 RT "Structure of ricin A-chain at 2.5 A.";  
 RT Proteins 10:251-259(1991).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.  
 RX MEDLINE=91352005; PubMed=1881882;  
 RA Rutenber E., Robertus J.D.;  
 RT "Structure of ricin B-chain at 2.5-A resolution.";  
 RT Proteins 10:260-269(1991).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE=95082010; PubMed=7901010;  
 RA Weston S.A., Tucker A.D., Thatcher D.R., Debyehtre D.J.,  
 RA Pauptit R.A.;  
 RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";  
 RT J. Mol. Biol. 244:410-422(1994).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.

CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.  
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.  
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 CC -----  
 CC EMBL: X55667; CAA39202.1; -  
 CC PIR: S16022; S16022.  
 CC HSSP: P1140; 1ABR.  
 CC InterPro: IPR000572; Ricin\_B\_lectin.  
 CC Pfam: PF00652; Ricin\_B\_lectin; 6.  
 CC PRINTS: PR00366; SHIGARICIN.  
 CC SMART: SM00458; RICIN; 2.  
 CC PROSITE: PS00231; RICIN\_B\_LECTIN; 2.  
 CC PROSITE: PS00275; SHIGA\_RICIN; 1.  
 CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 CC Glycoprotein; Lectin; Signal; Pyroglutamate carboxylic acid.  
 CC SIGNAL: 1 34  
 CC CHAIN: 35 285  
 CC PEPTIDE: 286 295  
 CC CHAIN: 296 562  
 CC DOMAIN: 307 424  
 CC REPEAT: 317 321  
 CC REPEAT: 360 400  
 CC REPEAT: 403 435  
 CC REPEAT: 448 483  
 CC REPEAT: 487 526  
 CC REPEAT: 529 562  
 CC ACT\_SITE: 198 198  
 CC DISULFID: 261 303  
 CC DISULFID: 320 339  
 CC DISULFID: 363 380  
 CC DISULFID: 451 464  
 CC DISULFID: 452 464  
 CC MOD\_RES: 35 35  
 CC CARBOHYD: 234 234  
 CC CARBOHYD: 395 395  
 CC CARBOHYD: 435 435  
 CC SEQUENCE: 562 AA; 62817 MW; 1FD0AC7D7BA6278 CEC64;  
 CC  
 CC Query Match 34.5%; Score 448; DB 1; Length 562;  
 CC Best Local Similarity 44.4%; Freq. No. 1.5e-32;  
 CC Matches 108; Conservative 36; Mismatches 93; Indels 6; Gaps 5;  
 CC  
 CC 9 THQTDGDEYRFTLLADVYSSGSSRNEPILRLRGSTIPYDAQRYVLYELVTCQOOSITR 68  
 CC 43 TEATSGSYKQFLEKRLQELTGLAHIVLPDPVTIERRRYIVLHLSRRSRIEV 100  
 CC  
 CC 69 AIDVNNVAVVAVQAGQSYFLPAPAGAEHFLFTGRBRSGLPFGSYVDLERYAGH-R 137  
 CC 101 GIDVNNVAVVAVRAGQSYFLPAPASASTVLFGLT--GRSIRPDSGYDLEKMAHQIR 158  
 CC  
 CC 128 DQPLGRIQLQSVSALRPGSGTRAPGRSILILHQTENAPRPIIMWRQDINSGES 167  
 CC 159 EELSLDQALTRALRIFLKSQSNDEKRLTIVILQGEDEKAKRILSNVGSIRGIR 218  
 CC  
 CC 188 PLPDWYMLEFSGWGSGTQVGSIDVDF--NRPRLAISTANTYTLASVAVSIATLT 246  
 CC 219 FQDPDMVLSLENNMDNLGGVQSGVQDFPNNVLLSIRNPVVVDSLSPTVAVALLML 278  
 CC  
 CC 247 FVC 249

DB 279 FVC 281  
 |||  
 RESULT 4  
 ABRB ABRER STANDARD; PRT; 527 AA.  
 AC 006077; 281374; (Created)  
 DT 15-DEC-1998 (Rel. 37)  
 DT 28-FEB-2003 (Rel. 41) (Last annotation update)  
 DE Ayrin-b precursor (Contains: Ayrin-b A chain (RNA N-glycosidase)  
 DE (RC 3.2.2.22); Ayrin-b B chain).  
 OS Ayrus pectoratus (Indian licorice) (Crab's eye).  
 CC Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eumids I; Fabales; Fabaceae; Papilionoideae; Abrasae; Abrus.  
 CC NCBI\_TaxID:3816;  
 CC [1]  
 RN SEQUENCE FROM N.A. Pubmed:412113;  
 RP MEDLINE:9316798; Jpn J -Y;  
 RX "Primary structure of three distinct isoenzymes determined by cDNA  
 RT sequencing. Conservation and significance".  
 RT J. Mol. Biol. 229:263-267 (1993).  
 RN [2]  
 RP SEQUENCE OF 260-537.  
 RC TISSUE=Seed;  
 RA MEDLINE:93169023; Pubmed:7763422;  
 RA Kimura M., Sumizawa T., Funatsu G.;  
 RT "The complete amino acid sequences of the B-chains of ayrin-a and  
 RT ayrin-b, toxic proteins from the seeds of Abrus precatorius".  
 RL Bioest. Biochemol. Biochem. 57:168-169 (1993)  
 CC -1- SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL  
 CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,334 OF 28 S RNA.  
 CC ABRIN-A IS MORE TOXIC THAN RICIN.  
 CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT  
 CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT  
 CC PRECEDES ENDOCYTOSIS.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.  
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.  
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 CC -----  
 CC EMBL: M9315; AAA3225.1; -  
 CC PIR: S32430; S32430.  
 CC HSSP: P1140; 1ABR.  
 CC InterPro: IPR000572; Ricin\_B\_lectin.  
 CC Pfam: PF00652; Ricin\_B\_lectin; 6.  
 CC PRINTS: PR00366; SHIGARICIN.  
 CC SMART: SM00458; RICIN; 2.  
 CC PROSITE: PS00231; RICIN\_B\_LECTIN; 2.  
 CC PROSITE: PS00275; SHIGA\_RICIN; 1.  
 CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 CC Glycoprotein; Lectin; Signal; Pyroglutamate carboxylic acid.  
 CC CHAIN: 1 250  
 CC PEPTIDE: 251 260  
 CC CHAIN: 261 527  
 CC ABRIN-B B CHAIN.



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FT TURN 10 11
FT HELIX 14 38
FT STRAND 34 32
FT TURN 32 32
FT STRAND 36 38
FT TURN 44 43
FT HELIX 47 49
FT STRAND 51 57
FT STRAND 63 69
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FT TURN 124 126
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FT TURN 346 348
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FT TURN 367 370
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FT STRAND 387 387
FT HELIX 393 395
FT STRAND 399 399
FT STRAND 406 408
FT STRAND 410 411
FT HELIX 413 415
FT STRAND 421 421
FT TURN 422 423

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FT STRAND 424 428
FT TURN 432 433
FT HELIX 435 437
FT STRAND 439 441
FT TURN 443 444
FT STRAND 447 449
FT TURN 451 451
FT STRAND 452 453
FT TURN 464 465
FT STRAND 467 472
FT TURN 474 475
FT HELIX 478 480
FT STRAND 483 484
FT TURN 486 487
FT STRAND 490 492
FT TURN 493 496
FT STRAND 497 501

Query Match 37.0% Score 480, DB 1, Length 528,
Best local similarity 47.9%, 18e-36, 30, indels 26, Gaps 6,
Matches 110, Conservative 37, Mismatches 30, Indels 26, Gaps 6:

Qy 9 TQTTGDEYFPFTILRDYVSSGSFSEIPLRQSTFVSDAQREVLVATLMOQOSITA 68
Db 9 TEGATOSYKQFIETALRRLRGLIHIDIPVLPDPFLQERNRYITVELNSPTESIEV 66

Qy 69 AIDYNAVYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 127
Db 69 AIDYNAVYVAYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 127

Qy 67 GIDVNAVYVAYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 124
Db 67 GIDVNAVYVAYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 124

Qy 128 DQIPFGHDTQSVYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 187
Db 128 DQIPFGHDTQSVYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 187

Qy 125 QDIPFGHDTQSVYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 184
Db 125 QDIPFGHDTQSVYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 184

Qy 188 FLDPVYVAYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 237
Db 188 FLDPVYVAYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 237

Qy 185 FQDPAVYVAYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 247
Db 185 FQDPAVYVAYVAYQGDQSYETLNDAPRGATTHLPFTYTRDSRLPTGQSYTDLERYVGH-R 247

Qy 238 -VIASLALMFVC 249
Db 238 -VIASLALMFVC 249

Qy 235 PTVATLALMFVC 247
Db 235 PTVATLALMFVC 247

RESULT 3
ID ABERC ABERP STANDARD; FRT; 562 AA.
AC P28590;
DT 01-DEC-1992 (Rel. 24, Created)
DE 01-DEC-1992 (Rel. 24, Last sequence update)
DR 28-FEB-2003 (Rel. 41, Last annotation update)
DE ABERC precursor (containing: ABERC-A chain (rRNA N-glycosidase)
OS ABERC precursor (containing: ABERC-A chain (rRNA N-glycosidase)
OS ABERC precursor (containing: ABERC-A chain (rRNA N-glycosidase)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons; Rosidae;
OC Eucosids I; Fabales; Fabaceae; Papilionoideae; Alysae; Abrus.
NCBI_TaxID=3816;
RN [1]_SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RC MEDLINE=9126657; PubMed=2050149;
RA Wood K.A., Lord C.M., Wawrzyniak E.J., Patak M.;
DE "Peptide:in: genomic cloning, characterization and the expression of
the A-chain in Escherichia coli."
FT 1-1000 (1-1000)
CC SUBUNIT: BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RIBOSOMAL
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RIBOSOMAL
B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
BINDING OF ABERC TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
-1- CATALYTIC ACTIVITY: Endoglycosylase of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

```





F:70,158,161/Active site: Tyr, Glu, Arg #status predicted  
F:155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 23.8%; Score 309.5; DB 2; Length 245;  
Best Local Similarity 34.8%; Pred. No. 1.9e-20;  
Matches 84; Conservative 42; Mismatches 100; Indels 15; Gaps 7;

QY 13 TGEYFRITLADYVSSGSSNSAIPILRGSTIFVSDAQFVLVEITNGQDSTTAIDV 72  
DB 10 IKSISSPITQMDALPTGTVYGLIPST---ASGGRFRFNLINVDVTVYV 66  
QY 73 TNAYVVAACAGGQGYFLPDAFGAETHLFTGTBBSGLPTGQYTDLERVAG-HRDLP 131  
DB 67 TNYIVAVRADAVSFEEEDTPAEPKLIFFAGKTVK--LPYSGNYDKLGSTVQKRDWIR 124  
QY 113 LGIEOLIOSVALRYPGSGSTRAQASITLILQIMISEARFNPIIRYRQDINSGESFLPD 191  
DB 125 LGIPALSSAITMNVY--VDYOSTAALIVLIQSTAEKARYKIEQVSHIS--NRYPN 180  
QY 192 MWMLELTSNGQOSTVQ--HSTDGVPNPFRLAISTG--FTLSNVSYSIAALML 246  
DB 181 QAVISLKKWALSKOIQANRKGQCHENPVELYNPDTRFSYIRISAGVKNRIHL 240  
QY 247 F 247  
DB 241 Y 241

Search completed: December 11, 2003, 13:55:47  
Job time : 8.95754 secs

QY TCGRPFITLADIVVSSGSPENELROSTIPVSDQGFVUEVLTQKQSDITALIDIV 72  
Db 10 TSSSGVFSNLRKALPYEKSLYDIPLR-STPLSS-QRYVALIHITVYADETISALIDV 66  
QY TAAYVAYQADSDSYFLADA-PRQGRHFLFTGTSTDRSHPFTSYTLERYVGH-RDOI 130  
Db 67 TNVYVQYADQSTYFPEHESKTEBAKYVFDKAR-KYTLVPYSENKRLQCAQKQTEHVI 125  
QY 73 TAAYVAYQADSDSYFLADA-PRQGRHFLFTGTSTDRSHPFTSYTLERYVGH-RDOI 130  
Db 11 PGCFIQLOISVSLARPGSGTTPAQRSLITLITQMSAPNARVLRIDQNS-GESE 186  
QY 126 PEGMPLDLSITLFLFYANSLKSS-ANVQIQSISBANKTFE----EQIQEKVDYKAI 179  
Db 189 IEDPMVLEFETSGQSGTQVQ-ISTSGYVFNRPFLASLQNFYLTSSVSS-VYSALAI 244  
QY 180 LPSLAIISLSSMSALSQIQIQLASTNNQGFETPVYLLINQORVTTINVDAGVTSIAL 239  
Db 245 ML 246  
Db 240 LL 241

RESULT 13

Karsaurin C - *Trichosanthes kirilowii* var. *japonica*

N>Contactins: Karsaurin A

CSpecies: *Trichosanthes kirilowii* var. *japonica*

CAccession: JCS606

CComment: This protein belongs to type I ribosomal-inactivating proteins which catalyze

CSuperfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

P:24-270/Product: Karsaurin C #status predicted <MC>

P:27-266/Domains: rRNA N-glycosidase homology <MG>

A:Reference number: JC6506; PMID:9715562; PMID:9212998

A:Accession: JCS606

A:Molecule type: DNA

A:Accessions: 1,269,497PZ

R:Kondo, T.; Mizukami, H.; Tanaka, T.; Ogihara, Y.

Biol. Pharm. Bull. 18, 1485-1489, 1996

A:File: Amino acid sequences and ribosome-inactivating activities of Karsaurin-B and Karsaurin-C

A:Reference number: JC6503; PMID:9710848; PMID:8951169

A:Accession: JCS033

A>Status: Preliminary

A:Residues: 272/270/KON

CComment: This protein is a ribosome-inactivating protein and exhibit cytotoxic activity

CSuperfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

P:24-270/Product: Karsaurin C #status predicted <MC>

P:27-266/Domains: rRNA N-glycosidase homology <MG>

Query Match	25.3%;	Score 328;	DB 2;	Length 289;
Best Local Similarity	37.2%;	Pred. No. 5.2e-22;		
Matches 90;	Conservative 48;	Mismatches 86;	Indels 18;	Gaps 10;

QY 13 QDDEFFPFTLLDPIYSSGSEFNEBLDPOSTPIPSDAGFUEVLTUQODSITALITY 72  
Db 33 TSSSYGVFISNLRKALPFEKRYXOPIRDLN-STLSS--QVXALHINADSEIYALV 89  
QY 73 TAAVAYAOAGDSYFLND-PRAGFETHFGTGTDESEIPECTSYTOLEEVAGH-PDO 130  
Db 90 TAAVAYAOAGDSYFNEBASTAEKAYVFXDKR-KYLLPYSGNVERLOAGKIRENI 148  
QY 131 PGIPIOLIOVSALRPGSGTAAQSRSLIIILIOMLSEAPPLRYKRODINS--GSEF 188  
Db 149 PGIPIALDSAITLLPFYANSAAS--LWVIOSTSEKAYFYF---EQOICKVAKAF 202  
QY 189 LPMWMLLETSWQGSOTVO--HSTDGVFNNEFFRLATSGNPFYLSNVR--VIASLAI 244  
Db 203 LSLAIIISLNSMSALSKQICIASTNGQETPYVLLINAMONORVTTWADGVYSNIAL 262  
QY 245 ML 246  
:|

**D8**

263 LL 264

**RESULT 14**

S25560

rRNA N-glycosidase (EC 3.2.2.22) momordin II - balsam apple

CSpecies: Momordica balsamina (balsam apple)

CDate: 25-Feb-1999 #sequence\_revision 03-Aug-1995 #text\_change 20-Aug-1999

AAccession: S25560

FAccession: S25560

FAccVersion: 1.0

FReleaseDate: 1992

FTitle: Momordin II, a ribosome-inactivating protein from Momordica balsamina, is homologous to the rRNA N-glycosylase family.

AReference number: S25560; PMID:9307170; PMID:1408971

AAccession: S25560

AStatus: preliminary

AStature: preliminary

AMolecule type: mRNA

AResidues: 1..286 <ORF>

ACross-references: EMBL:Z12175; NID:g19525; PDB:CAAT6.1; PID:g19525

CSuperfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

CKeywords: Glycosidase; hydrolase

I:27-264/Domain: rRNA N-glycosidase homology <RNG>

Query Match	34.2%	Score 314	DB 2	Length 286
Seac. Local Similarity	35.0%	Pred. No.9.55-21		
Matches	Consecutive	49	Mismatches 89	Indels 20
			Gaps	9
QY	13	TGDEHF <del>FF</del> ITLLRDVYSSGSFEN--EILPLRGSTLPVSDAQFVVLNLTNGQSDSTFA	69	
Db	13	TKATYHFF--EPLFA <del>IT</del> PSUKYDILPLVST--IDSR <del>RI</del> LLDLSVAVETLSA	86	
QY	70	IDVNAVVAVQAQGDOSYFLRDAPFGAETHLFTYTRRSLSLFFGGSYDLERVAGH--R	127	
Db	87	IDVNVVVAARTDVSFFRESPEAKNITLKRTR--KILLYGNGNELO <del>T</del> --AAKIR	143	
QY	128	DOIPLGIELOLSVSLATVQSGSTQASITILLTOMKSEAAEPLIMRYNDIOMSGS	187	
Db	144	ENIDLG <del>IG</del> PLSSATITLLVYNAQSDPSA--LLVITQTZAAAFYIRRVAKVY--AIN	199	
QY	188	FLPDWVMELETNSGQSTQYV--QHSITGVYNNFELATISTGNFVLTNSRVSATIAIM	245	
Db	200	FKNALITIELBWSALSKQIFLAQNGQKPNRVDLIFLTSRGVQVNTDSDVKNKX	259	
QY	246	LEFV 248		
Db	260	LLT 262		

## RESULT 15

C/Species: *Trichosanthes anguina* (snake gourd)  
rRNA: N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd

Cdate: 15-Nov-1995 #sequence, revision 24-Oct-1997 #next\_change 05-Dec-1997  
C:accession J04840, J07071, J076677  
R:Chou, L.P.; Kamo, M.; Ito, T.Y.; Wang, S.H.; Yeno, Y.; Tsugita, A.  
Biomol. Sci. 3, 179-186, 1996  
A:Accession: J04840 #sequence of trichangina, a ribosomal-inactivating protein from  
A:Accession: J07071  
A:Accession: J076677  
A:Molecule type: protein  
A:Residues: 1-133, 'S', 134-245 <CHO>  
A:Experimental source: seed  
A:Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Ta  
R:Chou, L.P.; Kamo, M.; Ito, T.Y.; Yeno, Y.; Tsugita, A.  
Submitted to JPEB, August 1995  
A:Accession: J04840 #sequence of trichangina, a ribosomal-inactivating protein  
A:Reference number: J076677  
A:Accession: J07071  
A:Molecule type: protein  
A:Residues: 1-50, 'V', 52-245 <CHO2>  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed  
A:422/Domain: rRNA N-glycosidase homology <RNS>  
A:51,201/Binding site: carbonyldate (Asn) (covalent) #status experimental









Db 125 EGISLQALFHAISFASGASNDSEKXPTLIVLIOMASENARYETINSRVSIRCTA 184  
OY 188 FLPMYVLELSTSGQSTVOYHSTDCVFRNPFEL-AISTGNFVTLSNVSVASIAIATL 246  
Db 185 FQEPDPAFLSLNNWMDLSRGVGSVQDTFPAVTLTRVNNQPIVDSLTHGSAVALATL 244  
OY 247 FVC 249  
Db 245 FVC 247

## RESULT 4

S32431 abrin-d precursor - Indian licorice (fragment)

N/contains: rRNA N-glycosidase (EC 3.2.2.22)

C/species: Abrus precatorius (Indian licorice)

C/date: 30-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 01-Aug-1997

C/accession: S32431, S34408

R/mod: Biol 229, 263-267 1993

J/mol: Biol 229, 263-267 1993

A/title: Primary structure of three distinct isobabins determined by cDNA sequencing.

A/reference number: S32429; PMID:9132798; PMID:842313

A/accession: S32431

A/molecule type: mRNA

A/residues: 1-528 <HUN>

A/cross-references: GB:M98346

R/hung, C.; Lee, M.; Lee, T.; Lin, J.

submitted to the EMBL Data Library, March 1993

A/reference number: S34408

A/accession: S32431

A/molecule type: mRNA

A/residues: 1-169 'C', 171-320 'U', 322-628 <HD>

A/cross-references: GB:M98346

C/comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating

The A and B chains are linked by a single disulfide bond, which is essential for toxicity

C/superfamily: ricin; rRNA N-glycosidase homology

C/keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F

F/1-251/Product: abrin-d chain A #status predicted <RCH>

F/1-251/Domains: rRNA N-glycosidase homology <RCH>

F/261-328/Product: abrin-d chain B #status predicted <RCH>

F/261-328/Domains: rRNA N-glycosidase homology <RCH>

F/1/Modified site: pyroglutamate (Glu) #status predicted

F/174,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted

F/164,167/Active site: Glu, Arg #status predicted

F/200,253,361,401,402/Binding site: carboxylate (Asp) (covalent) #status predicted

F/247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted

F/288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F/500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 34.5%; Score 448; DB 2; Length 528;  
Best Local Similarity 44.4%; Pred. No. 1.7e-32;

Matches 108; Conservative 36; Mismatches 93; Indels 6; Gaps 5;

OY 9 THCTGDEYRFTLLADYVSSGSPNPLRQSTIPVSDAQSPVAVELYNQGDQSTRA 68

Db 9 TEGATSSQYKQFTEALRQEL-TGGLIHDPVLPDPT-TVEERNRITVELNSRSRSIEV 66

OY 69 AIDVTNAYVAVAYQAGQSYFLDARGLRGLFTGTNRASRLPTQSYTDLERYGH-R 127

Db 67 GIDVTNAYVAVAYQAGQSYFLDARGLRGLFTGTNRASRLPTQSYTDLERYGH-R 124

OY 128 DQIPGIGELQISVARSYFGSTPAQARSILLIOMISEAHPNPLIWRQDINSSES 187

Db 125 EGISLQALFHAISFASGASNDSEKXPTLIVLIOMASENARYETINSRVSIRCTA 184

OY 188 FLPMYVLELSTSGQSTVOYHSTDCVFRNPFEL-AISTGNFVTLSNVSVASIAIATL 246

Db 185 FQEPDPAFLSLNNWMDLSRGVGSVQDTFPAVTLTRVNNQPIVDSLTHGSAVALATL 244

OY 247 FVC 249

Db 245 FVC 247

## RESULT 5

S16022 abrin-c precursor - Indian licorice

N/contains: rRNA N-glycosidase (EC 3.2.2.22)

C/species: Abrus precatorius (Indian licorice)

C/date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999

C/accession: S16022, S16023

R/mod: X-ray, Lord, J.M.; Mawryczak, E.J.; Plazak, M.

Eur. J. Biochem. 199, 723-732, 1991

A/title: Precursor: genomic cloning, characterization and the expression of the A-chain

A/reference number: S16022; PMID:9166957; PMID:2050149

A/accession: S16022

A/status: preliminary

A/molecule type: DNA

A/residues: 1-562 <MOD>

A/cross-references: EMBL:X55667; NID:916084; PIDN:CA92920.1; PID:916085

C/comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating

The A and B chains are linked by a single disulfide bond, which is essential for toxicity

C/keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamate ac

F/41-280/Product: abrin-c chain A #status predicted <RCH>

F/295-562/Product: abrin-c chain B #status predicted <RCH>

F/317-359,360-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats

F/35/Modified site: pyroglutamate carboxylic acid (Glu) (in mature form) #status predicted

F/108,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted

F/199,201/Active site: Glu, Arg #status predicted

F/234,287,335,435,436/Binding site: carboxylate (Asn) (covalent) #status predicted

F/321-343,320-359,363-380,454,464,480-507/Disulfide bonds: #status predicted

F/534,555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F/534,555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 34.5%; Score 448; DB 2; Length 562;  
Best Local Similarity 44.4%; Pred. No. 1.9e-32;

Matches 108; Conservative 36; Mismatches 93; Indels 6; Gaps 5;

OY 9 THCTGDEYRFTLLADYVSSGSPNPLRQSTIPVSDAQSPVAVELYNQGDQSTRA 68

Db 9 TEGATSSQYKQFTEALRQEL-TGGLIHDPVLPDPT-TVEERNRITVELNSRSRSIEV 66

OY 69 AIDVTNAYVAVAYQAGQSYFLDARGLRGLFTGTNRASRLPTQSYTDLERYGH-R 127

Db 67 GIDVTNAYVAVAYQAGQSYFLDARGLRGLFTGTNRASRLPTQSYTDLERYGH-R 124

OY 128 DQIPGIGELQISVARSYFGSTPAQARSILLIOMISEAHPNPLIWRQDINSSES 187

Db 125 EGISLQALFHAISFASGASNDSEKXPTLIVLIOMASENARYETINSRVSIRCTA 184

OY 188 FLPMYVLELSTSGQSTVOYHSTDCVFRNPFEL-AISTGNFVTLSNVSVASIAIATL 246

Db 185 FQEPDPAFLSLNNWMDLSRGVGSVQDTFPAVTLTRVNNQPIVDSLTHGSAVALATL 244

OY 247 FVC 249

Db 245 FVC 247

OY 247 FVC 249

Db 245 FVC 247

RESULT 6

S32430 abrin-b precursor - Indian licorice (fragment)

N/contains: rRNA N-glycosidase (EC 3.2.2.22)

C/species: Abrus precatorius (Indian licorice)

C/date: 30-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 20-Aug-1999

C/accession: S32430, S34408

R/mod: Biol 229, 263-267 1993

J/mol: Biol 229, 263-267 1993

A/title: Primary structure of three distinct isobabins determined by cDNA sequencing.

A/reference number: S32429; PMID:9132798; PMID:842313

A/accession: S32430

A/molecule type: mRNA

A/residues: 1-527 <HUN>

A/cross-references: GB:M98345; NID:9166296; PIDN:AAA32625.1; PID:9166297

A:Accession: S32429  
 A:Status: nucleic acid sequence not shown  
 A:Residues: 261-347, 'T', 349-351, 'A', 353-357, 'U', 359-528 <KTM>  
 A:Cross-references: GB:M8344; NID:q166294; PTDN:AAA2624.1; PID:q166295  
 A:Note: the coding region for the sequence shown is preceded by an ATG codon  
 A:Note: residues 1-8 were derived from the synthesized primer  
 R:Punatsu, G.; Taguchi, Y.; Kawasano, M.; Yanaka, M.  
 Agric. Biol. Chem. 52, 1095-1097, 1988  
 A>Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from  
 A:Reference number: J10202  
 A:Accession: J10202  
 A:Molecule type: protein  
 A:Residues: 261-347, 'T', 349-351, 'A', 353-357, 'U', 359-528 <KTM>  
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
 R:Punatsu, G.; Mathiesen, A.; Sundan, A.  
 J. Biol. Chem. 266, 6848-6852, 1991  
 A>Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
 A:Reference number: A39761; MUID:91201329; PMID:2016300  
 A:Accession: A39761  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 'E', '2-251 <EV2>  
 A:Cross-references: GB:M8344  
 A:Note: residues 1-8 were derived from the synthesized primer  
 R:Punatsu, G.; Mathiesen, A.; Sundan, A.  
 J. Biol. Chem. 266, 6848-6852, 1991  
 A>Title: The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic  
 A:Reference number: J1398; MUID:91201329; PMID:7763422  
 A:Contents: seeds  
 A:Accession: J1398  
 A:Molecule type: protein  
 A:Residues: 261-347, 'T', 349-351, 'A', 353-357, 'U', 359-528 <KTM>  
 A:Experimental source: seed  
 R:Evensen, G.; Mathiesen, A.; Sundan, A.  
 Submitted to the EMBL Data Library, October 1990  
 A:Description: Direct molecular cloning of two distinct abrin A-chains.  
 A:Accession: S14471  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 'ME', '2-251 <EV2>  
 A:Cross-references: EMBL:X54873; NID:q16090; PTDN:CAA38655.1; PID:q16091  
 R:Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, C.Y.  
 FEBS Lett. 309, 115-118, 1992  
 A>Title: The complete primary structure of abrin-a B chain.  
 A:Reference number: S24133; MUID:92371656; PMID:1505674  
 A:Accession: S24133  
 A:Molecule type: protein  
 A:Residues: 342-257, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'U', 484-528 <CHE>  
 R:Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.  
 Eur. J. Biochem. 240, 564-569, 1996  
 A>Title: Probing the domain structure of abrin-a by tryptic digestion.  
 A:Reference number: S74110; MUID:97008945; PMID:8856055  
 A:Accession: S74110  
 A:Molecule type: protein  
 A:Residues: 69-108, 154-172 <LIN>  
 A:Experimental source: seed  
 A:Accession: S74110  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 342-276, 'X', 278-280, 329-348, 369-388, 399-418 <LIN>  
 A:Experimental source: seed  
 C:Comment: Abtin-a is more toxic than ricin. The toxin consists of an A chain, which has  
 staining receptors on the cell surface. The A and B chains are linked by a single disulfide  
 C:Superfamily: ricin, rRNA N-glycosidase homology  
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyrrolidone acid  
 F/1-251/Product: abrin-a chain A #status experimental <ACH>  
 F/7-246/Domains: rRNA N-glycosidase homology experimental <ACH>  
 F/261-326/Product: abrin-a chain B #status experimental <ACH>  
 F/2/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F/74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F/164,167/Active site: Glu, Arg #status predicted

Query Match 37.08; Score 480; DB 1; Length 528;  
 Best Local Similarity 43.58; Evalue 2.2e-35;  
 Matches 110; Conservative 37; Mismatches 80; Indels 26; Gaps 6;  
 9 THGTTGDEYRFITLADYSSGSPNEIFILROETIPYSDAQRPVLYELRNQGDSDITL 68  
 9 TGAATSGYVQFTEALERTL-RGGLHDIVLPDPT-TLQERNKTYVELSDTESIEV 66  
 69 AIDVTAVVAVVAVQADGSGYFLRDPAPRAETHLFTGTRRSGLPTGSDYDLERYACH-R 127  
 67 GIDVTAVVAVVAVQADGSGYFLRDPAPRAETHLFTGTRRSGLPTGSDYDLERYACH-R 124  
 128 DQIFLQIQLQISGALRRPGSTRKORRSTILQIKWISAPRPNILMRRODINGS 187  
 125 QQLFLQIQLQISGALRRPGSTRKORRSTILQIKWISAPRPNILMRRODINGS 184  
 188 ELPPMVTGELRTSGQDQSTQVQGHSTGQVFNPPRLAISTGNFTVLSNVS----- 237  
 185 PDPALMTSLNNMNDLSRGVQESVQDIFPVQ-----VTLNIRNRPVYDSLH 234  
 238 -VINSALIMLPVC 249  
 235 PTVAVLALMLPVC 247  
 RESULT 3  
 C39761 (clone 7.2) precursor - Indian jicorice (fragment)  
 N:Contig: rRNA N-glycosidase (EC 3.2.2.22)  
 C:Species: Abiru preacocius (Indian jicorice)  
 C:Date: 21-Feb-1992 #sequence\_reversion 31-Dec-1993 #text\_change 20-Aug-1999  
 C:Accession: C39761; S14471  
 R:Evensen, G.; Mathiesen, A.; Sundan, A.  
 J. Biol. Chem. 266, 6848-6852, 1991  
 A>Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
 A:Reference number: A39761; MUID:91201329; PMID:2016300  
 A:Accession: C39761  
 A:Molecule type: DNA  
 A:Residues: 'E', '2-251 <EV2>  
 A:Cross-references: EMBL:X54873  
 A:Note: residues 1-8 were derived from the synthesized primer  
 R:Punatsu, G.; Mathiesen, A.; Sundan, A.  
 Submitted to the EMBL Data Library, October 1990  
 A:Description: Direct molecular cloning of two distinct abrin A-chains.  
 A:Reference number: S14471  
 A:Accession: S14471  
 A:Molecule type: DNA  
 A:Residues: 'W', '1-251 <EV2>  
 A:Cross-references: EMBL:X54873; NID:q16088; PTDN:CAA38654.1; PID:q16089  
 C:Superfamily: ricin, rRNA N-glycosidase homology  
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; toxin  
 F/1-246/Domains: rRNA N-glycosidase homology experimental <ACH>  
 F/7-246/Domains: rRNA N-glycosidase homology experimental <ACH>  
 F/74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F/164,167/Active site: Glu, Arg #status predicted  
 Query Match 35.6%; Score 462; DB 2; Length 251;  
 Best Local Similarity 44.9%; Evalue 3.2e-34;  
 Matches 109; Conservative 36; Mismatches 92; Indels 6; Gaps 5;  
 9 THGTTGDEYRFITLADYSSGSPNEIFILROETIPYSDAQRPVLYELRNQGDSDITL 68  
 9 TGAATSGYVQFTEALERTL-RGGLHDIVLPDPT-TLQERNKTYVELSDTESIEV 66  
 69 AIDVTAVVAVVAVQADGSGYFLRDPAPRAETHLFTGTRRSGLPTGSDYDLERYACH-R 127  
 67 GIDVTAVVAVVAVQADGSGYFLRDPAPRAETHLFTGTRRSGLPTGSDYDLERYACH-R 124  
 128 DQIFLQIQLQISGALRRPGSTRKORRSTILQIKWISAPRPNILMRRODINGS 187  
 125 QQLFLQIQLQISGALRRPGSTRKORRSTILQIKWISAPRPNILMRRODINGS 184  
 188 ELPPMVTGELRTSGQDQSTQVQGHSTGQVFNPPRLAISTGNFTVLSNVS----- 237  
 185 PDPALMTSLNNMNDLSRGVQESVQDIFPVQ-----VTLNIRNRPVYDSLH 234  
 238 -VINSALIMLPVC 249  
 235 PTVAVLALMLPVC 247



Thu Dec 11 16:09:47 2003

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Query Match 8.7%; Score 122.5; DB 2; Length 492;  
Best Local Similarity 32.4%; Pred. No. 0.00021;  
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;  
QY 22 VYRDDPHDNOQLMESKNNNDNQATIRNDGTRNSG-CITTYGTAGYTMFD 80  
DB 379 IDVKNATADGTOVLNDCHSS--NQWYTSSEFPRIENKCLDAGSSMGAVQYIS 436  
QY 81 CNTAVREKTIWQIMDNGTIIIPRSNIVLAASSGIGKTTITVQ 122  
DB 437 CWGSAWOK--WELRDGTVGVOSGICLDVAGSGTNGTRIQ 476

Search completed, December 11, 2003, 14:11:35  
JOB time : 10.1403 secs

Thu Dec 11 16:09:47 2003

us-09-601-667c-11.ra1

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Oy 7 ASEP-----TVAIVGNKRVYDDEDFHDSNQIOLMPKSNNDPVQMTIKRD 55  
Db 354 SSSPPXXXXXADGQIKGVG-SGRCLDVPDASTDGTOLMDCHSGT--NQOMATDA 410  
Oy 56 GTRISNG-SCLTGYGTAGVYVMI FDCNTAVREATTIQTIMQNGTTINPRSNLVLA--SS 112  
Db 411 GELRYGDKCLDAAGTSNGSKVQIYSCMGSDNGK--MRLNSDSVVGVSGLCLDAVNG 468  
Oy 113 GIKGTTLTVOITDVTYLGQGW 132  
Db 469 TANGTLIOLYTCSNGSNRW 488

RESULT 14  
US-09-770-621-8

Sequence 8, Application US/09770621  
US-09-770-621-8  
GENERAL INFORMATION:  
Applicant: M nyl, Arja  
Applicant: Vehmaaper, Jari  
Applicant: Federer m, Richard  
Applicant: Lantto, Raija  
Applicant: Palohelmo, Marja  
Applicant: Suominen, Piirko  
Applicant: Lantinen, Raija  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,621  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/590,563  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIORITY NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 493 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. 6506593 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: M64551  
US-09-770-621-8

Query Match 8.7%; Score 122.5; DB 4; Length 491;  
Best Local Similarity 28.6%; Pred. No. 0.00021;  
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;  
Oy 7 ASEP-----TVAIVGNKRVYDDEDFHDSNQIOLMPKSNNDPVQMTIKRD 55  
Db 354 SSSPPXXXXXADGQIKGVG-SGRCLDVPDASTDGTOLMDCHSGT--NQOMATDA 410  
Oy 56 GTRISNG-SCLTGYGTAGVYVMI FDCNTAVREATTIQTIMQNGTTINPRSNLVLA--SS 112  
Db 411 GELRYGDKCLDAAGTSNGSKVQIYSCMGSDNGK--MRLNSDSVVGVSGLCLDAVNG 468  
Oy 113 GIKGTTLTVOITDVTYLGQGW 132  
Db 469 TANGTLIOLYTCSNGSNRW 488

RESULT 15  
US-09-468-812-4

Sequence 4, Application US/09468812  
US-09-468-812-4  
Patient No. 5938836  
GENERAL INFORMATION:  
Applicant: Vehmaaper, Jari  
Applicant: M nyl, Arja  
Applicant: Federer m, Richard  
Applicant: Lantto, Raija  
Applicant: Palohelmo, Marja  
Applicant: Suominen, Piirko  
Applicant: Lantinen, Raija  
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/468,812  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIORITY NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Larry B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050.0340002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 493 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-468-812-4

Thu Dec 11 16:09:47 2003

us-09-601-667c-11.rat

Db 379 IDVPKNTADGTQVYKCHSSG--NOQTTSSGSEFFIKKCLDAGSGSNGAVVQIS 436  
Qy 81 CNTAVRENTIWOIWDNGTINPESNLYLAASGIKETTLVQ 122  
Db 437 CMGANOK--WEHRAADGTVGVSGCLDAGVGGTGNGFRLQ 476

RESULT 12

US-08-468-812-8  
Sequence 8, Application US/08468812  
Patent No. 5935836  
GENERAL INFORMATION:  
APPLICANT: Vahmanper, Carl  
APPLICANT: M nyl, Arja  
APPLICANT: Pegerstr m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Palohelmo, Marja  
APPLICANT: Suominen, Pirkko  
APPLICANT: Lantinen, Tarja  
APPLICANT: Kistio, Paula  
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods  
TITLE OF INVENTION: of Use  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 06-JUN-1995  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Larry B.  
REGISTRATION/DOCKET NUMBER: 35,086  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2640  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: M64551  
US-08-468-812-8

Query Match 8.7%; Score 122.5; DB 2; Length 491;  
Best Local Similarity 28.6%; Pred. No. 0.00021;  
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

Qy 7 ASEP-----TWIYGRNQMVDVDRDDPHDNGQIQWPSKSNDDPQWLTKRD 55  
Db 354 SSEPPXXXXXADGGQIKVGV-SRGCLDVPDASTSDOTQJWDCHSGT--NOQMAATDA 410

Qy 56 GTIRANG-SCLTGYGYAGVYVWIFDCNRAVENTIWOIWDNGTINPESNLYLA--SS 112  
Db 411 GELRYVDPKCLDAPAGTSGNSKVOIYSCM3DNOK--WEHNSDSYGVSGCLDAGVNG 468  
Qy 113 GIKGTVTVQTLIDVYLGQGM 132  
Db 469 TANGTLQTLTCSGSGNQM 488

RESULT 13

US-08-590-563-8  
Sequence 8, Application US/08590563  
Patent No. 6300114  
GENERAL INFORMATION:  
APPLICANT: Vahmanper, Carl  
APPLICANT: M nyl, Arja  
APPLICANT: Pegerstr m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Palohelmo, Marja  
APPLICANT: Suominen, Pirkko  
APPLICANT: Lantinen, Tarja  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 26-JAN-1996  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/468,812  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION/DOCKET NUMBER: 35,086  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2640  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: M64551  
US-08-590-563-8

Query Match 8.7%; Score 122.5; DB 4; Length 491;  
Best Local Similarity 28.6%; Pred. No. 0.00021;  
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

Qy 7 ASEP-----TWIYGRNQMVDVDRDDPHDNGQIQWPSKSNDDPQWLTKRD 55  
Db 354 SSEPPXXXXXADGGQIKVGV-SRGCLDVPDASTSDOTQJWDCHSGT--NOQMAATDA 410

Db 379 IDVENGNADGTVOYLIDCHSSG--NQOMTYTSSGGERIFGKCLDAGSSNCAVVOYIS 436  
Qy 81 CNTAVREATIMQIMDNGTILINRSNTVLASGIGKFTLLVQ 122  
Db 437 CWGANOK--WEIRADGTLIVGSGCLDAVGSIGTGRTLD 476

RESULT 10  
US-08-590-563-5  
Sequence 5, Application US/08590563  
Patent No. 6300114  
GENERAL INFORMATION:  
APPLICANT: M Nyl, Aija  
APPLICANT: Venmaaper, Jari  
APPLICANT: Fagerstam, Richard  
APPLICANT: Lantto, Ralf  
APPLICANT: Palohimo, Marja  
APPLICANT: Suominen, Pirkko  
APPLICANT: Lahtinen, Tarja  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,563  
FILING DATE: 26-JUN-1996  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 08/468,812  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050,0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2640  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 480 amino acids  
TYPE: amino acid  
STRANDNESS: acid relevant  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50  
US-08-590-563-5

Query Match 8.7%; Score 122.5; DB 4; Length 480;  
Best Local Similarity 32.4%; Pred. No. 0.0002;  
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;  
Qy 22 VDVARDDFHGNQIQLPKSKNDNPQMLTKRKDTIRNSG-CLTYGYTAQVYWMFD 80

Db 379 IDVENGNADGTVOYLIDCHSSG--NQOMTYTSSGGERIFGKCLDAGSSNCAVVOYIS 436  
Qy 81 CNTAVREATIMQIMDNGTILINRSNTVLASGIGKFTLLVQ 122  
Db 437 CWGANOK--WEIRADGTLIVGSGCLDAVGSIGTGRTLD 476

RESULT 11  
US-09-770-621-5  
Sequence 5, Application US/09770621  
Patent No. 6506593  
GENERAL INFORMATION:  
APPLICANT: M Nyl, Aija  
APPLICANT: Venmaaper, Jari  
APPLICANT: Fagerstam, Richard  
APPLICANT: Lantto, Ralf  
APPLICANT: Palohimo, Marja  
APPLICANT: Suominen, Pirkko  
APPLICANT: Lahtinen, Tarja  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,621  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
PRIOR APPLICATION NUMBER: 08/590,563  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050,0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2640  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 480 amino acids  
TYPE: amino acid  
STRANDNESS: Relevant  
MOLECULE TYPE: linear  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50  
US-09-770-621-5

Query Match 8.7%; Score 122.5; DB 4; Length 480;  
Best Local Similarity 32.4%; Pred. No. 0.0002;  
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;  
Qy 22 VDVARDDFHGNQIQLPKSKNDNPQMLTKRKDTIRNSG-CLTYGYTAQVYWMFD 80

Thu Dec 11 16:09:47 2003

us-09-601-667c-11.ra1

Page 4

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; APPLICANT: Hakler, Torben
; APPLICANT: Hedegard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159.106
; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15

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Query Match
Best Local Similarity 9.6%; Score 136; DB 3; Length 132;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;

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OY 18 NGNRVYRDDPHDNGIQIOLWPSKSNNDPNQMLTKRDGTIRNSGCLTYY--GYTAGY 75
DB 14 NGWCVDVFWADPFTGNVQVITGSGN--AAQWTGSGSDTVFALGKCLDVDSSTRGAA 71
OY 76 VMIPDONTAVREATIWMQW--DNGT--INPRSNLYLAASSGI--KQTLTVQGLDPTL 128
DB 72 VQWWTGN-----GTGAKQKAYIDAGSKALRNPQSGCLDNTGAGAPLNDGRLQWTWNGIT 126
OY 129 GQGM 132
DB 127 AQGM 130

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RESULT 8
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Dietter, Ivan
; APPLICANT: Hedegard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159.106
; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

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Query Match
Best Local Similarity 9.6%; Score 136; DB 3; Length 435;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;
OY 18 NGNRVYRDDPHDNGIQIOLWPSKSNNDPNQMLTKRDGTIRNSGCLTYY--GYTAGY 75
DB 317 NGWCVDVFWADPFTGNVQVITGSGN--AAQWTGSGSDTVFALGKCLDVDSSTRGAA 374

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OY 76 VMIPDONTAVREATIWMQW--DNGT--INPRSNLYLAASSGI--KQTLTVQGLDPTL 128
DB 14 NGWCVDVFWADPFTGNVQVITGSGN--AAQWTGSGSDTVFALGKCLDVDSSTRGAA 71
OY 129 GQGM 132
DB 127 AQGM 130

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RESULT 9
US-08-468-812-5
; Sequence 5, Application US/08468812
; Patent No. 5935836
; GENERAL INFORMATION:
; APPLICANT: Vermaander, Jari
; APPLICANT: M neyl, Arja
; APPLICANT: Fagerberg, Richard
; APPLICANT: Pajolahti, Marja
; APPLICANT: Pajolahti, Marja
; APPLICANT: Saarelainen, Pirkko
; APPLICANT: Laitinen, Tarja
; APPLICANT: Kristo, Paula
; TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.812
; FILING DATE: 06-08-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332.412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/282.001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BEGLISBY, Darryl S.
; REGISTRATION NUMBER: 310965
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2600
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; POSITION: 1-480
; POSITION/SEGMENT: AMS0
US-08-468-812-5

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Query Match
Best Local Similarity 8.7%; Score 122.5; DB 2; Length 480;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
OY 22 VVRDDPHDNGIQIOLWPSKSNNDPNQMLTKRDGTIRNSGCLTYYGYTAGYVWTFD 80

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Thu Dec 11 16:09:47 2003

us-09-601-667c-11.rat

Page 3

QY 5 CSASEPTVAIVGRNMGKRVDDDFHDGNOIQLPKSKNSNDPNQMTIKEDGTIRNSGSC 64  
DB 282 CMDEPFIIVGRNMGKRVDDDFHDGNOIQLPKSKNSNDPNQMTIKEDGTIRNSGSC 341  
QY 65 LITVGTAGVYVIMFPCNTAIRENTINQINDGTTINPSNUTLAASGCTITLITQTL 124  
DB 342 LITKSSPRQOVIYVNCSTAVQATRMQITMDRTILIPBSGVLALTSNGSTKLTQTN 401  
QY 125 DYTLGQGMAGNDTAPREVTIYGFEDLCMESNGSVVETCDSSQKQKALYQDGSIR 184  
DB 402 IYAVSOGMLPTNNTOPEFTIYVGLYGMCLQANSKVTLEDG-TSEKAEQMALYDGSIR 460  
QY 185 PRONODCLTSGRDSVSTVINIVSGSASGSRWFTNEGAILMLNLSLMDVYAOANPKL 244  
DB 461 PQNRNDCLTIDNINIKQIVKILSCGPASGSRWFTNEGAILMLNLSLMDVYAOANPKL 520  
QY 245 RRIITYPANKRQKMWLPVP 264  
DB 521 KQIVHPFHNLMQWLPVF 540

RESULT 5

US-08-485-286-77  
Sequence 77, Application US/08485286  
Patent No. 5646026 5646119  
GENERAL INFORMATION:  
APPLICANT: TERENCE A  
APPLICANT: HEY TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
TITLE OF INVENTION: USING  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ANDREA T. BORKUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485-286  
FILING DATE: 4/3  
PRIORITY DATE: 4/3  
PRIORITY APPLICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/378761  
FILING DATE: 26-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BORKUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-286-77

Query Match 54.3%; Score 777.5; DB 1; Length 540;  
Best Local Similarity 55.8%; Pred. No. 26-73;  
Matches 145; Conservative 42; Mismatches 72; Indels 1; Gaps 1;

QY 5 CSASEPTVAIVGRNMGKRVDDDFHDGNOIQLPKSKNSNDPNQMTIKEDGTIRNSGSC 64  
DB 282 CMDEPFIIVGRNMGKRVDDDFHDGNOIQLPKSKNSNDPNQMTIKEDGTIRNSGSC 341  
QY 65 LITVGTAGVYVIMFPCNTAIRENTINQINDGTTINPSNUTLAASGCTITLITQTL 124  
DB 342 LITKSSPRQOVIYVNCSTAVQATRMQITMDRTILIPBSGVLALTSNGSTKLTQTN 401  
QY 125 DYTLGQGMAGNDTAPREVTIYGFEDLCMESNGSVVETCDSSQKQKALYQDGSIR 184  
DB 402 IYAVSOGMLPTNNTOPEFTIYVGLYGMCLQANSKVTLEDG-TSEKAEQMALYDGSIR 460  
QY 185 PRONODCLTSGRDSVSTVINIVSGSASGSRWFTNEGAILMLNLSLMDVYAOANPKL 244  
DB 461 PQNRNDCLTIDNINIKQIVKILSCGPASGSRWFTNEGAILMLNLSLMDVYAOANPKL 520  
QY 245 RRIITYPANKRQKMWLPVP 264  
DB 521 KQIVHPFHNLMQWLPVF 540

RESULT 6

US-09-512-342-14  
Sequence 14, Application US/09512342  
Patent No. 638068  
GENERAL INFORMATION:  
APPLICANT: SATOH, SHINBU  
APPLICANT: SATOH, SHINBU  
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT  
TITLE OF INVENTION: INTERCELLULAR FLUID  
FILE REFERENCE: 081356/0142  
CURRENT APPLICATION NUMBER: US/09/512,342  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 14  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Cucumis sativus  
US-09-512-342-14

Query Match 13.1%; Score 185.5; DB 4; Length 293;  
Best Local Similarity 27.4%; Pred. No. 2,2e-11;  
Matches 66; Conservative 35; Mismatches 101; Indels 39; Gaps 10;

QY 14 IYGNMGRVDRDDDFHDGNOIQLPKSKNSNDPNQMTIKEDGTIRNSGSC 59  
DB 41 IYGNMGRVDRDDDFHDGNOIQLPKSKNSNDPNQMTIKEDGTIRNSGSC 89  
QY 60 SNQSCITLITVGTAGVYVIMFPCNTAIRENTINQINDGTTINPSNUTLAASGCTITLITQTL 116  
DB 90 SNQSCITLITVGTAGVYVIMFPCNTAIRENTINQINDGTTINPSNUTLAASGCTITLITQTL 145  
QY 117 TITVGTAGVYVIMFPCNTAIRENTINQINDGTTINPSNUTLAASGCTITLITQTL 174  
DB 146 TITVGTAGVYVIMFPCNTAIRENTINQINDGTTINPSNUTLAASGCTITLITQTL 202  
QY 175 WATVGSIRPKQNDCLTSGRDSVSTVINIVSGSASGSRWFTNEGAILMLNLSLMDVYAOANPKL 234  
DB 203 WATVGSIRPKQNDCLTSGRDSVSTVINIVSGSASGSRWFTNEGAILMLNLSLMDVYAOANPKL 260  
QY 235 V 235  
DB 261 V 261

RESULT 7

US-09-459-106-15  
Sequence 15, Application US/09159106  
Patent No. 6284509  
GENERAL INFORMATION:  
APPLICANT: FETTER, PAU  
APPLICANT: DIERS, IVAN

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us-09-601-667c-11.fai

Page 2

```
RESULT 2
US-08-776-059-33
Sequence 33, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
INVENTOR: LENTZEN, Hans
APPLICANT: BATE, Axel
APPLICANT: BATE, Axel
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EXAMINER APPLICATION NUMBER: 95109949.8
EXAMINER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
TYPE: PRT
ORGANISM: Vascum album

Query Match
Best Local Similarity 93.1%; Score 1318.5; DB 3; Length 264;
Matches 248; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 1 DVTGCSSEPTVAVGNGKGVVDDDDPDHNDGNOICLWFSKSNNDPQMLTKIKDGTIS 60
DB 2 DVTGCSSEPTVAVGNGKGVVDDDDPDHNDGNOICLWFSKSNNDPQMLTKIKDGTIS 61
QY 61 NSCLTGYGTAGVYVMEFDGNTAVRENTWQIMDNGTIINPSNLVLAASGIGKLTLL 120
DB 62 NSCLTGYGTAGVYVMEFDGNTAVRENTWQIMDNGTIINPSNLVLAASGIGKLTLL 121
QY 121 VQTLDTLGGMLAGNTAPREVTIIVSCSGSGSQGVFTNEGALINKSLAVTVQA 180
DB 122 VQTLDTLGGMLAGNTAPREVTIIVSCSGSGSQGVFTNEGALINKSLAVTVQA 180
QY 181 GSIRPKQNDCLTSGSDSVTVIVSCSGSGSQGVFTNEGALINKSLAVTVQA 240
DB 181 GSIRPKQNDCLTSGSDSVTVIVSCSGSGSQGVFTNEGALINKSLAVTVQA 240
QY 241 NPKLRRIIIPATGKQNMPLV 263
DB 241 NPKLRRIIIPATGKQNMPLV 263

RESULT 3
US-08-776-059-35
Sequence 35, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
INVENTOR: LENTZEN, Hans
APPLICANT: BATE, Axel
APPLICANT: BATE, Axel
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EXAMINER APPLICATION NUMBER: 95109949.8
EXAMINER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
TYPE: PRT
ORGANISM: Vascum album
```

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US-08-776-059-35
Query Match
Best Local Similarity 93.1%; Score 1318.5; DB 3; Length 564;
Matches 248; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 1 DVTGCSSEPTVAVGNGKGVVDDDDPDHNDGNOICLWFSKSNNDPQMLTKIKDGTIS 60
DB 2 DVTGCSSEPTVAVGNGKGVVDDDDPDHNDGNOICLWFSKSNNDPQMLTKIKDGTIS 61
QY 61 NSCLTGYGTAGVYVMEFDGNTAVRENTWQIMDNGTIINPSNLVLAASGIGKLTLL 120
DB 62 NSCLTGYGTAGVYVMEFDGNTAVRENTWQIMDNGTIINPSNLVLAASGIGKLTLL 121
QY 121 VQTLDTLGGMLAGNTAPREVTIIVSCSGSGSQGVFTNEGALINKSLAVTVQA 180
DB 122 VQTLDTLGGMLAGNTAPREVTIIVSCSGSGSQGVFTNEGALINKSLAVTVQA 180
QY 181 GSIRPKQNDCLTSGSDSVTVIVSCSGSGSQGVFTNEGALINKSLAVTVQA 240
DB 181 GSIRPKQNDCLTSGSDSVTVIVSCSGSGSQGVFTNEGALINKSLAVTVQA 240
QY 241 NPKLRRIIIPATGKQNMPLV 263
DB 241 NPKLRRIIIPATGKQNMPLV 563

RESULT 4
US-08-378-761A-77
Sequence 77, Application US/08378761A
Patent No. 5633984
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
INVENTOR: HEY, TIMOTHY D
APPLICANT: MORAN, ALICE E
INVENTOR: MORAN, ALICE E
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
ZIP: 46226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 08/378, 761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4848
FAX: (317) 337-4848
INVENTOR CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match
Best Local Similarity 54.8%; Score 777.5; DB 1; Length 540;
Matches 145; Conservative 42; Mismatches 72; Indels 1; Gaps 1;
```



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us-09-601-667c-11.rapb

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
APPLICATION INFORMATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
STRANDNESS: No. US20010024815A1 Relevant  
MOLECULE TYPE: linear  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: M64551  
US-09-770-621-8

Query Match 8.7% Score 122.5; DB 9; Length 491;  
Best Local Similarity 28.6%; Pred. No. 0.00075;  
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

QY 7 ASEP-----TVRIKGNMNVYRDDDFDQNGIQIPSSKNNDPNQLTKED 55  
DB 354 SSEPXXXXXXXXXADGQIRKVG-SRCLDVPASISDGRCDLMDCHST--NCOMALTA 410  
QY 56 CRTSNG-SCITTYGTHGIVYMIFDQCTNREACTIQIMDGIINPSNVLAA--SS 112  
DB 411 GELRVGKCKLDAAGTSMGSKVYSCVGGDNCK--WRINSDGSVGVGSLCLDAVNG 468  
QY 113 GKGTTLVVTOTLDYTLAQGW 132  
DB 469 TANGTLDIOLYTCNSGNSQRM 488

US09-770-621-4  
Sequence 4, Application US/09770621  
Patent No. US20010024815A1  
GENERAL INFORMATION:  
APPLICANT: M Ryt, Arja  
APPLICANT: Velmaamp, Jari  
APPLICANT: Fagerstr, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Paloheimo, Maria  
APPLICANT: Suominen, Eirkko  
APPLICANT: Suominen, Raija  
INVENTOR: Suominen, Raija  
INVENTOR: Suominen, Eirkko  
INVENTOR: Suominen, Raija  
INVENTOR: Suominen, Eirkko  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERN, KESSLER, GOLDBSTEIN & POX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM: 178; floppy disk  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,621  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/590,563  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
STRANDNESS: No. US20010024815A1 Relevant  
MOLECULE TYPE: linear  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: M64551  
US-09-770-621-4

Query Match 8.7% Score 122.5; DB 9; Length 492;  
Best Local Similarity 32.4%; Pred. No. 0.00076;  
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;

QY 22 VRRDDDFDQNGIQIPSSKNNDPNQLTKED 55  
DB 379 IDVPKGTLDIOLYTCNSGNSQRM 488  
QY 81 CNTAVRATIMQIWDGTTINPSNVLAASSGKGTTLVQ 122  
DB 437 CMCANOK--WELRADGITVGVGSLCLDAVNGTNGTFLQ 476

Search completed: December 11, 2003, 14:48:51  
Job time: 18.0129 secs

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GENERAL INFORMATION:
APPLICANT: OMORI, SATOSHI
APPLICANT: OMORI, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIWA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIORITY DATE: 2002-05-23
PRIORITY APPLICATION NUMBER: JP 2001-204089
PRIORITY FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: JP 2001-272697
PRIORITY FILING DATE: 2001-08-02
NUMBER OF SEQ. ID NOS.: 15109
SEQ. ID NO. 10246
LENGTH: 647
TYPE: PRT
ORGANISM: Streptomyces avermectilis
US-10-156-761-10246
Query Match
Best local similarity 8.5%; Score 126; DB 15; Length 647;
Matches 45; Conservative 20; Mismatches 60; Indels 46; Gaps 8;

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Db 9 EFTVALVGRNRKRVYVDDEPHGQIQIWPFSKANDPVOLATIRKDTIRNSGCT--T 66
520 DGTGSPVLGKGLDVAASSANGTAVOLY--DCNGSTAGWTVVADSVQAKKLDVT 577
Qy 67 TTYGTVAGVYVIFDQNTAVREATVQIWDNGTIIIPRSHLVLAASSGKTKTTLVQTLDY 126
578 SASITADGAKIQLDYDN---GTPAQKRWSTN-----ASTGVDVNTLADKLDV 620
Db 127 TLGGWGLAGNTAPREVTIYGFEDLCMESHSQSVWETCDSQKQKRAL 177
621 T-----GNSR-----NRRKQIWSG-IGANQ-SKEL 646

```

RESULT 13

```

US-09-770-621-5
Sequence 5, Application US/0970621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Velmamper, Jari
APPLICANT: Pagarster m, Richard
APPLICANT: Rantto, Raija
APPLICANT: Rantto, Raija
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:

```

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
COMPUTER READABLE FORM:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
TELEPHONE/DOCKET NUMBER: 1050,0340003
TELEPHONE: 202-571-2600
TELEFAX: 202-571-2600
INVENTOR: RANTTO, RAIJA
INVENTOR: SUOMINEN, PIIRKO
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-09-770-621-5
Query Match
Best local similarity 8.7%; Score 122.5; DB 9; Length 480;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;

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Qy 22 VVRDDPHFDHNGQIQMPFSKNDPNQIWKTRDPTIRNSG-CITTYGTVAGVYVIFD 80
379 IIVPRGKGTQDTQVQVLYDCHSGS--NQMTYSSGFPRFKKLDAGSSNGAVQIYS 436
Db 379 IIVPRGKGTQDTQVQVLYDCHSGS--NQMTYSSGFPRFKKLDAGSSNGAVQIYS 436
Qy 81 CNTAVREATVQIWDNGTIIIPRSHLVLAASSGKTKTTLVQ 122
437 CWGANQR--WEIRADGTIVQSGICLDLAVAGTGNGTQLQ 476
Db 437 CWGANQR--WEIRADGTIVQSGICLDLAVAGTGNGTQLQ 476

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RESULT 14

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US-09-770-621-8
Sequence 8, Application US/0970621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Velmamper, Jari
APPLICANT: Pagarster m, Richard
APPLICANT: Rantto, Raija
APPLICANT: Rantto, Raija
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:

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Page 4

;; PRIOR APPLICATION NUMBER: JP 2001-272697  
;; PRIOR FILING DATE: 2001-08-02  
;; NUMBER OF SEQ ID NOS: 15109  
;; SEQ ID NO 8170  
;; LENGTH: 536  
;; TYPE: PRT  
;; ORGANISM: Streptomyces avermectin  
us-10-156-761-8170

Query Match 9.5%; Score 134; DB 15; Length 536;  
Best Local Similarity 30.1%; Pred. No. 5.6e-05;  
Matches 40; Conservative 18; Mismatches 59; Indels 16; Gaps 6;

QY 14 IVGNRGR-VVDDDEHGNQIQLPSPKSNNDPQQLMTIKRQGTIRNSG--SCLTYY-- 68  
DB 409 LVGASNECLDYNNGTARPGTKETWDC--GGANQVYITTAAGSLRYGGTQCLDANDN 465  
QY 69 GYTAGVYVMTEDQNTAVREATIQTINDGTTINPSNLVLT-----AASSGKGTTLTVQ 122  
DB 466 GTTSGTKVQLYTCNGANQK--WSLNPNGVYGTQSLCLDVTGDDQSSNVTGTALEIM 523  
QY 123 TLDYTLGGWLAG 135  
DB 524 TONGANQQRRLD 536

RESULT 9

US-10-137-077-18  
;; Sequence 18, Application US/10137077  
;; Publication No. US20030092109A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Goldstein, Irwin J.  
;; APPLICANT: Wenger, Harry C.  
;; APPLICANT: Moser, Robert C.  
;; TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin  
;; FILE REFERENCE: US-071924  
;; CURRENT APPLICATION NUMBER: US/10/137,077  
;; CURRENT FILING DATE: 2002-05-02  
;; PRIOR APPLICATION NUMBER: 60/288,596  
;; PRIOR FILING DATE: 2001-05-03  
;; PRIOR APPLICATION NUMBER: 60/354,322  
;; PRIOR FILING DATE: 2002-02-04  
;; NUMBER OF SEQ ID NOS: 32  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 18  
;; SEQ ID NO 48  
;; TYPE: PRT  
;; ORGANISM: Ruminus communis  
us-10-137-077-18

Query Match 9.0%; Score 127; DB 15; Length 41;  
Best Local Similarity 53.7%; Pred. No. 8.6e-06;  
Matches 22; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 224 GATLNKSKLMVDVQAQNPFLKRIITTPATGKFNQWMLPYF 264  
DB 1 GTLNKSKLMVDVQAQNPFLKRIITTPATGKFNQWMLPYF 41

RESULT 10

US-09-973-457-5  
;; Sequence 5, Application US/09973457  
;; Patent No. US20020164746A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Kapeller-Liberman, Rosana  
;; TITLE OF INVENTION: 4,11,6,8 NOVEL HUMAN GLYCOSYLTRANSFERASE  
;; TITLE OF INVENTION: AND USE THEREOF  
;; FILE REFERENCE: 10448-099001  
;; CURRENT APPLICATION NUMBER: US/09/973,457  
;; CURRENT FILING DATE: 2001-10-09  
;; PRIOR APPLICATION NUMBER: 60/238,849  
;; PRIOR FILING DATE: 2000-10-06  
;; NUMBER OF SEQ ID NOS: 6

;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 5  
;; LENGTH: 135  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; OTHER INFORMATION: Consensus sequence  
us-09-973-457-5

Query Match 9.0%; Score 127; DB 10; Length 135;  
Best Local Similarity 25.7%; Pred. No. 4.4e-05;  
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNRGRVYV--RDDPHGNQIQLPSPKSNNDPQQLMTI---KRDGTIRNSG--CLTT 67  
DB 7 IGSVNGCLDYNNGSBSKSDGNPQQLMDCHGG--NQLMTLVESDGLKINSIDCLTV 64  
QY 68 YGTAGVYVMTEDQNTAVR--EATIQIWDGTTINPSNLVLAASSGKGTTLTVQ 125  
DB 65 NG-----TVTISQDGTDRKNGNQKQKPVKQGTIRNR--SKKKGYDSG----- 106  
QY 126 YTLGGWLAGNDTARPRVYITGFRDLQNE--SNGSVYVETCCSSQKQKRN 175  
DB 107 -----LCDVQDNKTVQLMTQNGSDANQKN 132

RESULT 11

US-10-074-527-6  
;; Sequence 6, Application US/10074527  
;; Publication No. US2002014246A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Olanic, Peter J.  
;; APPLICANT: Moser, Robert C.  
;; APPLICANT: Galvin, Katherine A.  
;; TITLE OF INVENTION: 33945, A Human Glycosyltransferase and  
;; TITLE OF INVENTION: Uses Therefor  
;; FILE REFERENCE: WPI2001-018P/KCP1(W)  
;; CURRENT APPLICATION NUMBER: US/10/074,527  
;; CURRENT FILING DATE: 2002-02-12  
;; PRIOR APPLICATION NUMBER: 60/269202  
;; PRIOR FILING DATE: 2000-02-15  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 135  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: consensus  
us-10-074-527-6

Query Match 9.0%; Score 127; DB 14; Length 135;  
Best Local Similarity 25.7%; Pred. No. 4.4e-05;  
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNRGRVYV--RDDPHGNQIQLPSPKSNNDPQQLMTI---KRDGTIRNSG--CLTT 67  
DB 7 IGSVNGCLDYNNGSBSKSDGNPQQLMDCHGG--NQLMTLVESDGLKINSIDCLTV 64  
QY 68 YGTAGVYVMTEDQNTAVR--EATIQIWDGTTINPSNLVLAASSGKGTTLTVQ 125  
DB 65 NG-----TVTISQDGTDRKNGNQKQKPVKQGTIRNR--SKKKGYDSG----- 106  
QY 126 YTLGGWLAGNDTARPRVYITGFRDLQNE--SNGSVYVETCCSSQKQKRN 175  
DB 107 -----LCDVQDNKTVQLMTQNGSDANQKN 132

RESULT 12

US-10-156-761-10246  
;; Sequence 10246, Application US/10156761  
;; Publication No. US20030119018A1

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Page 3

Publication No. US20020142426A1  
GENERAL INFORMATION:  
APPLICANT: Olander, Peter J.  
INVENTOR: Meyer, Rachel E.  
APPLICANT: Meyer, Rachel E.  
APPLICANT: Millen, Katherine A.  
TITLE OF INVENTION: 3345. A Human Glycosyltransferase and  
TITLE OF INVENTION: Uses Thereof  
FILE REFERENCE: MP12001-018P1C01(M)  
CURRENT APPLICATION NUMBER: US/10/074,527  
PRIOR FILING DATE: 2001-02-12  
CURRENT APPLICATION NUMBER: 60/269202  
PRIOR FILING DATE: 2001-02-15  
OTHER SEQ ID NOS: 9  
SEQUENCE: PstCSeq for Windows Version 4.0  
SEQ ID NO: 5  
LENGTH: 145  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: consensus  
US-10-074-527-5

Query Match 12.1%; Score 171; DB 14; Length 145;  
Best Local Similarity 32.8%; Pred. No. 1.5e-09;  
Matches 45; Conservative 20; Mismatches 58; Indels 14; Gaps 4;

QY 11 TTRVGRNRYVRRDDPHQVQOLMPSKNDPVQMT---KROGTIR---NSGC 64  
DB 7 TTVVNGSGRCIDVNSSESISNQVQVQVNGCHNPGNQMLTYDBDSGLSYVNNKC 66  
QY 65 LTVGVYGVYVMTFPCNTAVREATTIOWINDGTTIRP-----RSNVLV--ASSGKIG 116  
DB 67 LTVNANSFGEVLYQCDSATSDNQKMLNNGILNKLINLVMTGLVLDVKGSPDTORG 126  
QY 117 TTVVQVLDYTLGGGM 133  
DB 127 TKLILYCSGGNQML 143

RESULT 6

US-10-156-761-14970  
Sequence 14970, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
INVENTOR: IKEDA, HARUO  
APPLICANT: IKEDA, HARUO  
INVENTOR: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
INVENTOR: SHIBA, TADAYOSHI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
PRIOR FILING DATE: 2002-05-29  
CURRENT APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
OTHER SEQ ID NOS: 15109  
SEQUENCE: PstCSeq for Windows Version 4.0  
SEQ ID NO: 420  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-14970

Query Match 10.3%; Score 155; DB 15; Length 420;  
Best Local Similarity 31.2%; Pred. No. 2.8e-07;  
Matches 44; Conservative 19; Mismatches 68; Indels 10; Gaps 5;  
QY 1 DD-VTCSASEFTVATVGNMRYVYDDDFHGNQIQMPSKSNNDPVQMTIKKDGCTI 58

DB 284 DWRKVTYDSSGAPITGLAKCVDVAGSSSANGAPVQLY--DCNGTQAKWVYASDGT 341  
QY 59 RNSGCI--TVYGVYGVYVMTFPCNTAVREATTIOWINDGTTIRP---LVLAASSGI 114  
DB 342 RALGKCIDVTENSTMGSTVQVMDGGSANOK--WVYLAAGDIWPAKCKLDVTGNSA 399  
QY 115 KETITVQVLDYTLGGGM 135  
DB 400 NGRMQVNSCGAANQKRGK 420

RESULT 7

US-10-156-761-9724  
Sequence 9724, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
INVENTOR: IKEDA, HARUO  
APPLICANT: IKEDA, HARUO  
INVENTOR: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
INVENTOR: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
PRIOR FILING DATE: 2002-05-29  
CURRENT APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
OTHER SEQ ID NOS: 15109  
SEQUENCE: PstCSeq for Windows Version 4.0  
SEQ ID NO: 9724  
LENGTH: 658  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-9724

Query Match 9.8%; Score 138.5; DB 15; Length 658;  
Best Local Similarity 32.1%; Pred. No. 2.6e-05;  
Matches 44; Conservative 17; Mismatches 57; Indels 19; Gaps 7;

QY 11 TTRVGRNRYVRRDDPHQVQOLMPSKNDPVQMT---KROGTIR 59  
DB 523 TTRVGRNRYVRRDDPHQVQOLMPSKNDPVQMT---KROGTIR 580  
QY 60 SNAGCITTY--GYTAGVYVMTFPCNTAVREATTIOWINDGTTIRP---SSGK 115  
DB 581 YQNKCDANIGTNGTYVIMDNGQANOK--WVNSDGTITVYVAGCDAVYATAN 638  
QY 116 GTTIVQVLDYTLGGGM 132  
DB 639 GTSILVMSGTCGDNQK 655

RESULT 8

US-10-156-761-8170  
Sequence 8170, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
INVENTOR: IKEDA, HARUO  
APPLICANT: IKEDA, HARUO  
INVENTOR: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
INVENTOR: SHIBA, TADAYOSHI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
PRIOR FILING DATE: 2002-05-29  
CURRENT APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30

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Page 2

QY 121 VOTLDYTLGGWLAGNDTAPREVTIYGFPRDLCSNCSGQWVFETCSSQKQKQKALYGD 180  
DB 121 VOTLDYTLGGWLAGNDTAPREVTIYGFPRDLCSNCSGQWVFETCSSQKQKQKALYGD 179  
QY 181 GSIRPRONODQCLTSGRDSVSTVINIVSCGASGSGQWVFETCSQKQKQKALYGD 240  
DB 180 GSIRPRONODQCLTSGRDSVSTVINIVSCGASGSGQWVFETCSQKQKQKALYGD 239  
QY 241 NPKLRRIIIPATKPKQWMLPV 263  
DB 240 NPKLRRIIIPATKPKQWMLPV 262

RESULT 2  
US-09-347-064-4  
Sequence 4, Application US/09347064A  
Patent No. US2002045209A1  
GENERAL INFORMATION:  
APPLICANT: Beck, Jürgen  
INVENTOR: Schmidt, Arno  
TITLE OF INVENTION: Ribosome-Inactivating Fusion Proteins Based on  
TITLE OF INVENTION: album  
FILE REFERENCE: 09282-5  
CURRENT APPLICATION NUMBER: US/09/347,064A  
EARLIER FILING DATE: 1999-07-02  
EARLIER APPLICATION NUMBER: PCT/EP98/00009  
EARLIER FILING DATE: 1998-01-02  
EARLIER APPLICATION NUMBER: EP 97 10 0012.0  
EARLIER FILING DATE: 1997-01-02  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn ver. 2.1  
LENGTH: 267  
TYPE: PRF  
ORGANISM: Viscum album  
US-09-347-064-4

Query Match 93.1%; Score 1318.5; DB 9; Length 267;  
Best Local Similarity 94.3%; Pred. No. 8.5e-127;  
Matches 248; Conservative 3; Mismatches 11; Indels 1; Gaps 1;  
QY 1 DDTGASSEPTVIVGNKGRVDRDDDFRDNQCLMPKSKNDNDQCLTIRGDTIS 60  
DB 1 DDTGASSEPTVIVGNKGRVDRDDDFRDNQCLMPKSKNDNDQCLTIRGDTIS 60  
QY 61 NSGCTTGYTAGVYVMIPECKIVBEATIMQIMNGTIIINPRSNIVLAASGIGTIT 120  
DB 61 NSGCTTGYTAGVYVMIPECKIVBEATIMQIMNGTIIINPRSNIVLAASGIGTIT 120  
QY 121 VOTLDYTLGGWLAGNDTAPREVTIYGFPRDLCSNCSGQWVFETCSSQKQKQKALYGD 180  
DB 121 VOTLDYTLGGWLAGNDTAPREVTIYGFPRDLCSNCSGQWVFETCSSQKQKQKALYGD 179  
QY 181 GSIRPRONODQCLTSGRDSVSTVINIVSCGASGSGQWVFETCSQKQKQKALYGD 240  
DB 180 GSIRPRONODQCLTSGRDSVSTVINIVSCGASGSGQWVFETCSQKQKQKALYGD 239  
QY 241 NPKLRRIIIPATKPKQWMLPV 263  
DB 240 NPKLRRIIIPATKPKQWMLPV 262

RESULT 3  
US-10-083-336A-1  
Sequence 3, Application US/10083336A  
Patent No. US2003018165A1  
GENERAL INFORMATION:  
APPLICANT: Olson, Mark A  
INVENTOR: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Mannemacher, Robert W

QY 121 VOTLDYTLGGWLAGNDTAPREVTIYGFPRDLCSNCSGQWVFETCSSQKQKQKALYGD 180  
DB 121 VOTLDYTLGGWLAGNDTAPREVTIYGFPRDLCSNCSGQWVFETCSSQKQKQKALYGD 179  
QY 181 GSIRPRONODQCLTSGRDSVSTVINIVSCGASGSGQWVFETCSQKQKQKALYGD 240  
DB 180 GSIRPRONODQCLTSGRDSVSTVINIVSCGASGSGQWVFETCSQKQKQKALYGD 239  
QY 241 NPKLRRIIIPATKPKQWMLPV 263  
DB 240 NPKLRRIIIPATKPKQWMLPV 262

RESULT 4  
US-10-137-077-17  
Sequence 17, Application US/10137077  
Patent No. US2003092109A1  
GENERAL INFORMATION:  
APPLICANT: Kinner, Robert P.  
INVENTOR: Kinner, Robert P.  
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin  
FILE REFERENCE: US-07124  
CURRENT APPLICATION NUMBER: US/10/137,077  
EARLIER FILING DATE: 2002-05-02  
EARLIER APPLICATION NUMBER: 60/288,596  
EARLIER FILING DATE: 2001-05-03  
EARLIER APPLICATION NUMBER: 60/354,322  
SOFTWARE: PatentIn version 3.1  
LENGTH: 44  
TYPE: PRF  
ORGANISM: Ricinus communis  
US-10-137-077-17

Query Match 13.1%; Score 186; DB 15; Length 44;  
Best Local Similarity 77.3%; Pred. No. 8.5e-12;  
Matches 34; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 121 VOTLDYTLGGWLAGNDTAPREVTIYGFPRDLCSNCSGQWVFETCSSQKQKQKALYGD 180  
DB 121 VOTLDYTLGGWLAGNDTAPREVTIYGFPRDLCSNCSGQWVFETCSSQKQKQKALYGD 179  
QY 181 GSIRPRONODQCLTSGRDSVSTVINIVSCGASGSGQWVFETCSQKQKQKALYGD 240  
DB 180 GSIRPRONODQCLTSGRDSVSTVINIVSCGASGSGQWVFETCSQKQKQKALYGD 239  
QY 241 NPKLRRIIIPATKPKQWMLPV 263  
DB 240 NPKLRRIIIPATKPKQWMLPV 262

RESULT 5  
US-10-074-527-5  
Sequence 5, Application US/10074527







CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (1) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains. In many different isoforms  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC are used to treat cancer and other diseases. The method allows  
 CC free from toxins present in natural mistletoe extracts. The sequence  
 CC represents a fragment of a mistletoe lectin I protein variant.

XX Sequence 532 AA;

Query Match 93.5%; Score 1324.5; DB 20; Length 532;

Best Local Similarity 94.7%; Pred. No. 6, 2e-119;

Matches 249; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

DB 1 DDTGSAEPTVAVVGNNGNVDYDDPFDGNGQIQAQMSKNDPQMTTKRDTGRS 60

DB 269 DDTGSAEPTVAVVGNNGNVDYDDPFDGNGQIQAQMSKNDPQMTTKRDTGRS 328

DB 61 NSGCLTYGTAGVYVWIPDCNVAEATVWQIDNGRTIPRSNVLVAASGIGKGTILT 120

DB 329 NSGCLTYGTAGVYVWIPDCNVAEATVWQIDNGRTIPRSNVLVAASGIGKGTILT 388

DB 121 VQTLDTYTGGMAGNUTAPREVITYGPRDLCESNGSSVWETCDSSQNGKALYGD 180

DB 389 VQTLDTYTGGMAGNUTAPREVITYGPRDLCESNGSSVWETCDSSQNGKALYGD 447

DB 181 GSIRPKONQDCLTSGDSVSTVINVSCGASGSGQWVFNAGAILNLKSLWVYDQA 240

DB 448 GSIRPKONQDCLTSGDSVSTVINVSCGASGSGQWVFNAGAILNLKSLWVYDQA 507

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

XX Nucleic acid encoding fusion protein containing mistletoe lectin A  
 PT chain - useful for treatment of proliferative and autoimmune  
 PT diseases, allergies and tumours

XX Disclosure, Fig 11b', 115p; German.

XX This sequence represents a variant mistletoe lectin B-chain, rMB. This  
 XX sequence can be used in the construction of a fusion protein which  
 XX comprises an effector module that is cytotoxic intracellularly, a  
 XX processing module covalently bonded to the effector module and  
 XX containing a protease recognition sequence, and a targeting module  
 XX covalently bonded to the processing module, able to bind specifically to  
 XX the surface of a cell so as to mediate internalisation of the fusion  
 XX protein. Such a fusion protein can be used for treating disorders  
 XX involving proliferation and/or elevated activation of cells, especially  
 XX autoimmune disease, allergy and tumours. The proteins are administered  
 XX as a solution, e.g. in a buffer, or as a solid, e.g. in a dry form.  
 XX A solution may be used for ex vivo use at 1 pg to 500 ng/ml.  
 XX A solid may be used for in vivo use at 1 pg to 500 ng/ml.  
 XX Fusion proteins can develop toxic activity in a wide range of target  
 XX cells. The processing module prevents extracellular dissociation, and  
 XX fusion proteins based on mistletoe lectin A-chain are far more active  
 XX than those based on ricin and do have the associated problems of  
 XX non-specific toxicity. The protein may be expressed in a non-glycosylated  
 XX form that does not bind to sugar receptors in the liver, and which has a  
 XX long half-life in the blood. Where the mistletoe lectin B-chain is used,  
 XX it actively assists in translocation of the M-A-chain from the  
 XX endoplasmic reticulum to the cytoplasm.

XX Sequence 263 AA;

Query Match 93.1%; Score 118.5; DB 19; Length 263;

Best Local Similarity 94.3%; Pred. No. 8, 8e-119;

Matches 248; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

DB 1 DDTGSAEPTVAVVGNNGNVDYDDPFDGNGQIQAQMSKNDPQMTTKRDTGRS 60

DB 269 DDTGSAEPTVAVVGNNGNVDYDDPFDGNGQIQAQMSKNDPQMTTKRDTGRS 328

DB 61 NSGCLTYGTAGVYVWIPDCNVAEATVWQIDNGRTIPRSNVLVAASGIGKGTILT 120

DB 329 NSGCLTYGTAGVYVWIPDCNVAEATVWQIDNGRTIPRSNVLVAASGIGKGTILT 388

DB 121 VQTLDTYTGGMAGNUTAPREVITYGPRDLCESNGSSVWETCDSSQNGKALYGD 180

DB 389 VQTLDTYTGGMAGNUTAPREVITYGPRDLCESNGSSVWETCDSSQNGKALYGD 447

DB 181 GSIRPKONQDCLTSGDSVSTVINVSCGASGSGQWVFNAGAILNLKSLWVYDQA 240

DB 448 GSIRPKONQDCLTSGDSVSTVINVSCGASGSGQWVFNAGAILNLKSLWVYDQA 507

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

DB 508 NPKLRILIIYPATGKPNQMTLTV 530

DB 241 NPKLRILIIYPATGKPNQMTLTV 263

Search completed: December 11, 2003, 14:07:46  
 Job time : 27.0864 secs

XX Sequence 264 AA;  
 SQ Query Match 93.5%; Score 1324.5; DB 20; Length 264;  
 Best Local Similarity 94.7%; Pred. No. 2.3e-119;  
 Matches 249; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DDTCSASEPTVAVIRGNKRVVDVDDPHDQNOIQLPFSKSNDDPQMLTKIKDGTIRS 60  
 DB 1 DDTCSASEPTVAVIRGNKRVVDVDDPHDQNOIQLPFSKSNDDPQMLTKIKDGTIRS 60  
 QY 61 NSCLITVYAGVYVWIFPCNTAVREATTIWOIMNGTIIINRSNLVLAASSGKGTTLT 120  
 DB 61 NSCLITVYAGVYVWIFPCNTAVREATTIWOIMNGTIIINRSNLVLAASSGKGTTLT 120  
 QY 121 VQTLDTYTLGGWLAGNDTAPREVITYGPRDLCMSNGSVMWETCVSSQONO-RMALYGD 180  
 DB 121 VQTLDTYTLGGWLAGNDTAPREVITYGPRDLCMSNGSVMWETCVSSQONO-RMALYGD 179  
 QY 121 VQTLDTYTLGGWLAGNDTAPREVITYGPRDLCMSNGSVMWETCVSSQONO-RMALYGD 179  
 DB 121 VQTLDTYTLGGWLAGNDTAPREVITYGPRDLCMSNGSVMWETCVSSQONO-RMALYGD 179  
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTFEGAILINKSLMWVVAQA 240  
 DB 180 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTFEGAILINKSLMWVVAQA 239  
 QY 241 NPKLRRIITIVATGKNQMLPV 263  
 DB 240 NPKLRRIITIVATGKNQMLPV 262

RESULT 13  
 AAY25979  
 ID AAY25979 standard; Protein; 531 AA.  
 XX AAY25979;  
 AC 18-OCT-1999 (first entry)  
 XX DT Mistletoe lectin I protein fragment.  
 XX DE Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 XX KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin I.  
 XX OS Viscum album.  
 XX PN DE19804210-A1.  
 XX PD 12-AUG-1999.  
 XX PS 03-FEB-1998; 98DE-1004210.  
 XX PR 03-FEB-1998; 98DE-1004210.  
 XX PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX PI Morris P, Stiefel T, Voelter W, Welters P.  
 XX DR MPI, 1999-445335/38.  
 XX N-PSDB; AA209103.  
 XX PT Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX Claim 7; Fig 1B; 78pp; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to increase the strength of the antigenic response,  
 CC and they increase cytotoxicity to increase the strength of the  
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a mistletoe lectin I protein fragment.  
 XX  
 SQ Sequence 531 AA;  
 Query Match 93.5%; Score 1324.5; DB 20; Length 531;  
 Best Local Similarity 94.7%; Pred. No. 6.2e-119;  
 Matches 249; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DDTCSASEPTVAVIRGNKRVVDVDDPHDQNOIQLPFSKSNDDPQMLTKIKDGTIRS 60  
 DB 269 DDTCSASEPTVAVIRGNKRVVDVDDPHDQNOIQLPFSKSNDDPQMLTKIKDGTIRS 328  
 QY 61 NSCLITVYAGVYVWIFPCNTAVREATTIWOIMNGTIIINRSNLVLAASSGKGTTLT 120  
 DB 329 NSCLITVYAGVYVWIFPCNTAVREATTIWOIMNGTIIINRSNLVLAASSGKGTTLT 268  
 QY 121 VQTLDTYTLGGWLAGNDTAPREVITYGPRDLCMSNGSVMWETCVSSQONO-RMALYGD 180  
 DB 389 VQTLDTYTLGGWLAGNDTAPREVITYGPRDLCMSNGSVMWETCVSSQONO-RMALYGD 447  
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTFEGAILINKSLMWVVAQA 240  
 DB 448 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTFEGAILINKSLMWVVAQA 507

RESULT 14  
 AAY25982  
 ID AAY25982 standard; Protein; 532 AA.  
 XX AAY25982;  
 AC 18-OCT-1999 (first entry)  
 XX DT Mistletoe lectin I (variant) protein fragment.  
 XX DE Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 XX KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin I.  
 XX OS Viscum album.  
 XX PN DE19804210-A1.  
 XX PD 12-AUG-1999.  
 XX PS 03-FEB-1998; 98DE-1004210.  
 XX PR 03-FEB-1998; 98DE-1004210.  
 XX PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX PI Morris P, Stiefel T, Voelter W, Welters P.  
 XX DR MPI, 1999-445335/38.  
 XX N-PSDB; AA209106.  
 XX PT Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX Disclosure; Fig 4B; 78pp; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of

QY 61 NSGCLTGYGTAGYVWIMPCNTAVREATTIWOIMDNGTIINFRSNLWLAASSGIKGTTLT 120  
 DB 61 NSGCLTGYGTAGYVWIMPCNTAVREATTIWOIMDNGTIINFRSNLWLAASSGIKGTTLT 120  
 QY 121 VQTLDTYTLGCGMLAGNDTAPRETTIYGFRLCRESNGSGVWETCTCSQCKRAIYGD 180  
 DB 121 VQTLDTYTLGCGMLAGNDTAPRETTIYGFRLCRESNGSGVWETCTCSQCKRAIYGD 180  
 QY 181 GSIRPKRONODCLTSGRDSVSTVINIVSCGASGSGQRFVFNKALINKSLMVDVAQA 240  
 DB 181 GSIRPKRONODCLTSGRDSVSTVINIVSCGASGSGQRFVFNKALINKSLMVDVAQA 240  
 QY 241 NPTLRRIITTPATKRNOMLPEV 264  
 DB 241 NPTLRRIITTPATKRNOMLPEV 264

## RESULT 11

ID AAY25985 standard; Protein; 263 AA.  
 XX AAY25985;

DT 18-OCT-1999 (first entry)  
 XX AAY25985;

DE Mistletoe lectin B protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KM ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
 XX cancer; cytotoxicity; antigen; isoform; lectin B.

XX Viscum album.

XX DB19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Welters P;

XX WPI; 1999-445335/38.

XX N-PSDB; AA209109.

XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants

XX Claim 9; Fig 7B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancer) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response. (I) is particularly useful as a co-administered antigen  
 CC (tumour-associated antigen) in a vaccine. The method allows production of  
 CC mistletoe lectin, and its individual chains, in recombinant systems  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a mistletoe lectin B protein.

XX Sequence 263 AA;

XX Query Match 93.5%; Score 1324.5; DB 20; Length 263;  
 XX Best Local Similarity 94.7%; Pred. No. 2,3e-119.

Matches 249; Conservative 3; Mismatches 10; Indels 1; Gaps 1;  
 QY 1 DVTCSASEPTVRIVGRNGKRVDRDDDPHQNQQLMPKSKNDPQMLTIKDGRTS 60  
 DB 1 DVTCSASEPTVRIVGRNGKRVDRDDDPHQNQQLMPKSKNDPQMLTIKDGRTS 60  
 QY 61 NSGCLTGYGTAGYVWIMPCNTAVREATTIWOIMDNGTIINFRSNLWLAASSGIKGTTLT 120  
 DB 61 NSGCLTGYGTAGYVWIMPCNTAVREATTIWOIMDNGTIINFRSNLWLAASSGIKGTTLT 120  
 QY 121 VQTLDTYTLGCGMLAGNDTAPRETTIYGFRLCRESNGSGVWETCTCSQCKRAIYGD 180  
 DB 121 VQTLDTYTLGCGMLAGNDTAPRETTIYGFRLCRESNGSGVWETCTCSQCKRAIYGD 180  
 QY 181 GSIRPKRONODCLTSGRDSVSTVINIVSCGASGSGQRFVFNKALINKSLMVDVAQA 240  
 DB 181 GSIRPKRONODCLTSGRDSVSTVINIVSCGASGSGQRFVFNKALINKSLMVDVAQA 240  
 QY 241 NPTLRRIITTPATKRNOMLPEV 263  
 DB 241 NPTLRRIITTPATKRNOMLPEV 262

## RESULT 12

ID AAY25991 standard; Protein; 264 AA.  
 XX AAY25991;

DT 18-OCT-1999 (first entry)  
 XX AAY25991;

DE Mistletoe lectin B variant protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KM ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
 XX cancer; cytotoxicity; antigen; isoform; lectin B.

XX Viscum album.

XX DB19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Welters P;

XX WPI; 1999-445335/38.

XX N-PSDB; AA209115.

XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 13B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancer) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response. (I) is particularly useful as a co-administered antigen  
 CC (tumour-associated antigen) in a vaccine. The method allows production of  
 CC mistletoe lectin, and its individual chains, in recombinant systems  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a variant mistletoe lectin B protein.

Db 181 GSIRPRKQNDCLTSGRDSVSTVINIVSCGASGSGRWFTNEBAILNKSGPMDVQA 240  
QY 241 NPKLRRIIIVPATGKPNQWMLPVF 264  
Db 241 NPKLRRIIIVPATGKPNQWMLPVF 264

## RESULT 9

AAZ25987  
ID AAZ25987 standard; Protein; 264 AA.  
XX  
XX AAZ25987;  
XX  
XX 18-OCT-1999 (first entry)  
XX  
XX Mistletoe lectin B2 protein fragment.  
DE  
XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MAb; immunity;  
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
XX cancer; cytotoxicity; antigen; isoform; lectin B2.  
OS  
XX Viscum album.  
XX  
XX DE19804210-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
XX  
XX Morris P, Stiefel T, Voelter W, Walters P;  
XX WPI; 1999-445335/38.  
XX N-PDB; AA209111.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Claim 9; Fig 9B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (MA)  
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
XX fragments are used to treat uncontrolled cell growth (particularly  
XX cancers) and if they lack cytotoxicity, to increase the strength of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX recombinant products, in particular in yeast, in which different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a mistletoe lectin B2 protein.

Sequence 264 AA;

Query Match 96.3%; Score 1364; DB 20; Length 264;  
Best Local Similarity 96.6%; Pred. No. 3,6e-123;  
Matches 255; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DDTGASAPPTVIRVGRGKRVADDDPHDQNOIQLPKSKNDPNQWMLTKKDGITIS 60  
Db 1 DDTGASAPPTVIRVGRGKRVADDDPHDQNOIQLPKSKNDPNQWMLTKKDGITIS 60  
QY 61 NSGCLTYGTAGYVWIFDCNPAVEATIMQWNGTINPRSNVLAASGIGKTTT 120  
Db 61 NSGCLTYGTAGYVWIFDCNPAVEATIMQWNGTINPRSNVLAASGIGKTTT 120

QY 121 VQTLDTYTLGGQMLAGNDPAFREVTIVGFRDLCEMSNGSGSYWETCDSSQKQKQVAYCD 180  
Db 121 VQTLDTYTLGGQMLAGNDPAFREVTIVGFRDLCEMSNGSGSYWETCDSSQKQKQVAYCD 180  
QY 181 GSIRPRKQNDCLTSGRDSVSTVINIVSCGASGSGRWFTNEBAILNKSGPMDVQA 240  
Db 181 GSIRPRKQNDCLTSGRDSVSTVINIVSCGASGSGRWFTNEBAILNKSGPMDVQA 240  
QY 241 NPKLRRIIIVPATGKPNQWMLPVF 264  
Db 241 NPKLRRIIIVPATGKPNQWMLPVF 264

## RESULT 10

AAZ25993  
ID AAZ25993 standard; Protein; 265 AA.  
XX  
XX AAZ25993;  
XX  
XX 18-OCT-1999 (first entry)  
XX  
XX Mistletoe lectin B2 variant protein fragment.  
DE  
XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MAb; immunity;  
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
XX cancer; cytotoxicity; antigen; isoform; lectin B2.  
OS  
XX Viscum album.  
XX  
XX DE19804210-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
XX  
XX Morris P, Stiefel T, Voelter W, Walters P;  
XX WPI; 1999-445335/38.  
XX N-PDB; AA209111.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure; Fig 15B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (MA)  
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its  
XX fragments are used to treat uncontrolled cell growth (particularly  
XX cancers) and if they lack cytotoxicity, to increase the strength of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX recombinant products, in particular in yeast, in which different isoforms  
XX of mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a variant mistletoe lectin B2 protein.

Sequence 265 AA;

Query Match 96.3%; Score 1364; DB 20; Length 265;  
Best Local Similarity 96.6%; Pred. No. 3,6e-123;  
Matches 255; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DDTGASAPPTVIRVGRGKRVADDDPHDQNOIQLPKSKNDPNQWMLTKKDGITIS 60  
Db 1 DDTGASAPPTVIRVGRGKRVADDDPHDQNOIQLPKSKNDPNQWMLTKKDGITIS 60

ID AAY25995 standard; Protein: 264 AA.  
 XX  
 AC AAY25995;  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Mistletoe lectin B4 protein fragment.  
 XX  
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;  
 XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 XX cancer; cytotoxicity; antigen; isoform; lectin B4.  
 XX  
 OS Viscum album.  
 XX  
 XX DE19804210-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 XX WPI: 1999-445335/38.  
 XX N-PSDB; AA209113.  
 XX  
 PT Preparation of mistletoe lectin in heterologous systems,  
 particularly for use as anticancer agents and immunostimulants  
 XX  
 PS Claim 9; Fig 11B; 78pp; German.  
 XX  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumor and immunostimulatory activity. The A-chain (MHA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumor-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a mistletoe lectin B4 protein.  
 XX  
 SQ Sequence 264 AA;  
 XX  
 Query Match 98.24; Score 1390; DB 20; Length 264;  
 Best Local Similarity 98.14; Pred. No. 1,1e-125;  
 Matches 259; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTTCGASEPTVRIYGNMGAVYVDDPHDQNOIQLPMSKSNNDPQLMTIKKDGITRS 60  
 DB 1 DVTTCGASEPTVRIYGNMGAVYVDDPHDQNOIQLPMSKSNNDPQLMTIKKDGITRS 60  
 QY 61 NGSCLTGYTAGYVWIFDQCNARREKTIWQIMDNGTIIPRSMVLAAASGKIGTTLT 120  
 DB 61 NGSCLTGYTAGYVWIFDQCNARREKTIWQIMDNGTIIPRSMVLAAASGKIGTTLT 120  
 QY 121 VQTLIDYTLGGQMLAGNTAPREVTIYGRDLQMSNGSVWETCDSSQNGKMLAYGD 180  
 DB 121 VQTLIDYTLGGQMLAGNTAPREVTIYGRDLQMSNGSVWETCDSSQNGKMLAYGD 180  
 QY 122 VQTLIDYTLGGQMLAGNTAPREVTIYGRDLQMSNGSVWETCDSSQNGKMLAYGD 180  
 DB 122 VQTLIDYTLGGQMLAGNTAPREVTIYGRDLQMSNGSVWETCDSSQNGKMLAYGD 180  
 QY 181 GSIRPKNQOGLTSGDSVSTYININSCGASGSGWFTNBSGAILMLKSPNDVQA 240  
 DB 181 GSIRPKNQOGLTSGDSVSTYININSCGASGSGWFTNBSGAILMLKSPNDVQA 240  
 QY 241 NPKLRITITPATGKGNOMLPVF 264  
 DB 241 NPKLRITITPATGKGNOMLPVF 264

DB 241 NPKLRITITPATGKGNOMLPVF 264  
 RESULT 8  
 ID AAY25995 standard; Protein: 265 AA.  
 XX  
 AC AAY25995;  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Mistletoe lectin B4 variant protein fragment.  
 XX  
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;  
 XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 XX cancer; cytotoxicity; antigen; isoform; lectin B4.  
 XX  
 OS Viscum album.  
 XX  
 XX DE19804210-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX 03-FEB-1998; 98DE-1004210.  
 XX  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 XX WPI: 1999-445335/38.  
 XX N-PSDB; AA209119.  
 XX  
 PT Preparation of mistletoe lectin in heterologous systems,  
 particularly for use as anticancer agents and immunostimulants  
 XX  
 PS Disclosure; Fig 17B; 78pp; German.  
 XX  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumor and immunostimulatory activity. The A-chain (MHA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumor-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a variant mistletoe lectin B4 protein.  
 XX  
 SQ Sequence 265 AA;  
 XX  
 Query Match 98.24; Score 1390; DB 20; Length 265;  
 Best Local Similarity 98.14; Pred. No. 1,1e-125;  
 Matches 259; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTTCGASEPTVRIYGNMGAVYVDDPHDQNOIQLPMSKSNNDPQLMTIKKDGITRS 60  
 DB 1 DVTTCGASEPTVRIYGNMGAVYVDDPHDQNOIQLPMSKSNNDPQLMTIKKDGITRS 60  
 QY 61 NGSCLTGYTAGYVWIFDQCNARREKTIWQIMDNGTIIPRSMVLAAASGKIGTTLT 120  
 DB 61 NGSCLTGYTAGYVWIFDQCNARREKTIWQIMDNGTIIPRSMVLAAASGKIGTTLT 120  
 QY 121 VQTLIDYTLGGQMLAGNTAPREVTIYGRDLQMSNGSVWETCDSSQNGKMLAYGD 180  
 DB 121 VQTLIDYTLGGQMLAGNTAPREVTIYGRDLQMSNGSVWETCDSSQNGKMLAYGD 180  
 QY 122 VQTLIDYTLGGQMLAGNTAPREVTIYGRDLQMSNGSVWETCDSSQNGKMLAYGD 180  
 DB 122 VQTLIDYTLGGQMLAGNTAPREVTIYGRDLQMSNGSVWETCDSSQNGKMLAYGD 180  
 QY 181 GSIRPKNQOGLTSGDSVSTYININSCGASGSGWFTNBSGAILMLKSPNDVQA 240  
 DB 181 GSIRPKNQOGLTSGDSVSTYININSCGASGSGWFTNBSGAILMLKSPNDVQA 240

KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin B3.  
XX  
XX Viscum album.  
XX  
XX DE19804210-A1.  
XX  
XX  
XX  
XX 12-AUG-1999.  
XX  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
XX  
XX Morris P, Stiefel T, Voelter W, Welters P;  
XX WPI: 1999-44535/38.  
XX N-PSDB; AA209112.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Claim 9; Fig 10B; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (MAA)  
XX of the mistletoe lectin binds to, and inactivates, the A subunit of  
XX ribosomes. Non-cytotoxic forms of the mistletoe lectin (I) and its  
XX fragments produced to treat uncontrolled cell growth (particularly  
XX lymphoma) are used to increase the strength of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a mistletoe lectin B3 protein.  
XX  
XX Sequence 264 AA:  
SQ  
Query Match 98.7%; Score 1397; DB 20; Length 264;  
Best Local Similarity 98.5%; Pred. No. 2,4e-126;  
Matches 260; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
OY 1 DVTYCSASEPTVRIYVGNKGMVNDVDDPDHGNQIQIOWPKSKNDPNQIATKIDGTIRS 60  
DB 1 DVTYCSASEPTVRIYVGNKGMVNDVDDPDHGNQIQIOWPKSKNDPNQIATKIDGTIRS 60  
OY 61 NSGCLITGTYGAGVYVMEFCQNTNREKATIQIOWMNGTITNRSNVLAAASGIKGTLT 120  
DB 61 NSGCLITGTYGAGVYVMEFCQNTNREKATIQIOWMNGTITNRSNVLAAASGIKGTLT 120  
OY 121 VQTLDTLTGGWLAGNDVAPREVTIYGFRLDQMSNGSGVWATCDSSQNGKMAIYGD 180  
DB 121 VQTLDTLTGGWLAGNDVAPREVTIYGFRLDQMSNGSGVWATCDSSQNGKMAIYGD 180  
OY 122 VQTLDTLTGGWLAGNDVAPREVTIYGFRLDQMSNGSGVWATCDSSQNGKMAIYGD 180  
DB 122 VQTLDTLTGGWLAGNDVAPREVTIYGFRLDQMSNGSGVWATCDSSQNGKMAIYGD 180  
OY 181 GSIRPKONQDCLTSGRDSVSTIVNIVSCGASGSGRWFTNKGALINLKNLWTVYQA 240  
DB 181 GSIRPKONQDCLTSGRDSVSTIVNIVSCGASGSGRWFTNKGALINLKNLWTVYQA 240  
OY 241 NPKLRRIITIPATGKGNQMLPWF 264  
DB 241 NPKLRRIITIPATGKGNQMLPWF 264  
RESULT 6  
AAV25994  
ID AAV25994 standard; Protein; 265 AA.  
XX  
XX AAV25994;  
AC  
XX  
XX 18-OCT-1999 (first entry)  
DT

XX  
XX Mistletoe lectin B3 variant protein fragment.  
XX  
XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MAA; immunity;  
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin B3.  
XX  
XX Viscum album.  
XX  
XX DE19804210-A1.  
XX  
XX  
XX  
XX 12-AUG-1999.  
XX  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
XX  
XX Morris P, Stiefel T, Voelter W, Welters P;  
XX WPI: 1999-44535/38.  
XX N-PSDB; AA209118.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure; Fig 16B; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (MAA)  
XX of the mistletoe lectin binds to, and inactivates, the A subunit of  
XX ribosomes. Non-cytotoxic forms of the mistletoe lectin (I) and its  
XX fragments produced to treat uncontrolled cell growth (particularly  
XX lymphoma) are used to increase the strength of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a variant mistletoe lectin B3 protein.  
XX  
XX Sequence 265 AA:  
SQ  
Query Match 98.7%; Score 1397; DB 20; Length 265;  
Best Local Similarity 98.5%; Pred. No. 2,4e-126;  
Matches 260; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
OY 1 DVTYCSASEPTVRIYVGNKGMVNDVDDPDHGNQIQIOWPKSKNDPNQIATKIDGTIRS 60  
DB 1 DVTYCSASEPTVRIYVGNKGMVNDVDDPDHGNQIQIOWPKSKNDPNQIATKIDGTIRS 60  
OY 61 NSGCLITGTYGAGVYVMEFCQNTNREKATIQIOWMNGTITNRSNVLAAASGIKGTLT 120  
DB 61 NSGCLITGTYGAGVYVMEFCQNTNREKATIQIOWMNGTITNRSNVLAAASGIKGTLT 120  
OY 121 VQTLDTLTGGWLAGNDVAPREVTIYGFRLDQMSNGSGVWATCDSSQNGKMAIYGD 180  
DB 121 VQTLDTLTGGWLAGNDVAPREVTIYGFRLDQMSNGSGVWATCDSSQNGKMAIYGD 180  
OY 122 VQTLDTLTGGWLAGNDVAPREVTIYGFRLDQMSNGSGVWATCDSSQNGKMAIYGD 180  
DB 122 VQTLDTLTGGWLAGNDVAPREVTIYGFRLDQMSNGSGVWATCDSSQNGKMAIYGD 180  
OY 181 GSIRPKONQDCLTSGRDSVSTIVNIVSCGASGSGRWFTNKGALINLKNLWTVYQA 240  
DB 181 GSIRPKONQDCLTSGRDSVSTIVNIVSCGASGSGRWFTNKGALINLKNLWTVYQA 240  
OY 241 NPKLRRIITIPATGKGNQMLPWF 264  
DB 241 NPKLRRIITIPATGKGNQMLPWF 264  
RESULT 7  
AAV25989  
DT



XX 03-FEB-1998; 98DE-1004210.  
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 PA Morris P, Stiefel T, Voelter W, Welters P;  
 XX WPI: 1999-44535/38.  
 XX N-PSDB; A4209110.  
 XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX Claim 9, Fig 8B; 78DP; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumour and immunostimulatory activity. The A-chain (WLA)  
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly of  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX and on a large scale, at any time of the year. Recombinant products are  
 XX used as adjuvants in vaccines, if they lack cytotoxicity. This sequence  
 XX represents a fragment of a mistletoe lectin B1 protein.  
 XX Sequence 264 AA;  
 SO  
 Query Match 99.1%; Score 1403; DB 20; Length 264;  
 Best Local Similarity 98.9%; Pred. No. 6.3e-127;  
 Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DDTTCASSEPPTVRIYVGNAGNVDRDDPFHDGNOQLMPKSKNNDPNQLWTIKKIDGTRIS 60  
 DB 1 DDTTCASSEPPTVRIYVGNAGNVDRDDPFHDGNOQLMPKSKNNDPNQLWTIKKIDGTRIS 60  
 QY 61 NSCLTGYGTAGVYVWIPDCNRAVEATWQIMDKGTTINPSKLVLAASGKIGTTLT 120  
 DB 61 NSCLTGYGTAGVYVWIPDCNRAVEATWQIMDKGTTINPSKLVLAASGKIGTTLT 120  
 QY 121 VQTLDTLGGQMLAGNDTAPFEVYIYGRPLCMESNGSVWVEETCDSSQKQKALYGD 180  
 DB 121 VQTLDTLGGQMLAGNDTAPFEVYIYGRPLCMESNGSVWVEETCDSSQKQKALYGD 180  
 QY 181 GSIRPKQNOQCLTSGSDSVSTVINVCASGSGSRVNFBNBALINLKNGLANVDAQ 240  
 DB 181 GSIRPKQNOQCLTSGSDSVSTVINVCASGSGSRVNFBNBALINLKNGLANVDAQ 240  
 QY 241 NPKLRRIIIPATGKQKQMLPVF 264  
 DB 241 NPKLRRIIIPATGKQKQMLPVF 264

RESULT 4  
 ID AAY25992 standard; Protein; 265 AA.  
 AC AAY25992;  
 DT 18-OCT-1999 (first entry)  
 DE Mistletoe lectin B1 variant protein fragment.  
 KM ribzyme 28S subunit; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B1.

XX Viscum album.

PN DE19804210-A1.  
 XX 12-AUG-1999.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 PA Morris P, Stiefel T, Voelter W, Welters P;  
 XX WPI: 1999-44535/38.  
 XX N-PSDB; A4209116.  
 XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX Disclosure; Fig 14B; 78DP; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumour and immunostimulatory activity. The A-chain (WLA)  
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly of  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX and on a large scale, at any time of the year. Recombinant products are  
 XX free from toxins present in natural mistletoe extracts. This sequence  
 XX represents a fragment of a variant mistletoe lectin B1 protein.  
 XX Sequence 265 AA;  
 SO  
 Query Match 99.1%; Score 1403; DB 20; Length 265;  
 Best Local Similarity 98.9%; Pred. No. 6.3e-127;  
 Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DDTTCASSEPPTVRIYVGNAGNVDRDDPFHDGNOQLMPKSKNNDPNQLWTIKKIDGTRIS 60  
 DB 1 DDTTCASSEPPTVRIYVGNAGNVDRDDPFHDGNOQLMPKSKNNDPNQLWTIKKIDGTRIS 60  
 QY 61 NSCLTGYGTAGVYVWIPDCNRAVEATWQIMDKGTTINPSKLVLAASGKIGTTLT 120  
 DB 61 NSCLTGYGTAGVYVWIPDCNRAVEATWQIMDKGTTINPSKLVLAASGKIGTTLT 120  
 QY 121 VQTLDTLGGQMLAGNDTAPFEVYIYGRPLCMESNGSVWVEETCDSSQKQKALYGD 180  
 DB 121 VQTLDTLGGQMLAGNDTAPFEVYIYGRPLCMESNGSVWVEETCDSSQKQKALYGD 180  
 QY 181 GSIRPKQNOQCLTSGSDSVSTVINVCASGSGSRVNFBNBALINLKNGLANVDAQ 240  
 DB 181 GSIRPKQNOQCLTSGSDSVSTVINVCASGSGSRVNFBNBALINLKNGLANVDAQ 240  
 QY 241 NPKLRRIIIPATGKQKQMLPVF 264  
 DB 241 NPKLRRIIIPATGKQKQMLPVF 264

RESULT 5  
 ID AAY25988 standard; Protein; 264 AA.  
 AC AAY25988;  
 DT 18-OCT-1999 (first entry)  
 DE Mistletoe lectin B3 protein fragment.  
 KM ribzyme 28S subunit; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KW cancer; cytotoxicity; T-cell activation; immune response;

PT Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Claim 9; Fig 12b; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its  
CC fragments are used to treat uncontrolled cell growth (particularly  
CC cancers) and if they lack cytotoxicity, to increase the strength of the  
CC immune response, particularly to a co-administered antigen  
CC (tumour-associated, bacterial or viral). The method allows production of  
CC mistletoe lectin, and its individual chains, in many different isoforms  
CC and on a large scale, at any time of the year. Recombinant products are  
CC free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a mistletoe lectin B5 protein.  
XX  
SQ Sequence 264 AA;  
Query Match 100.0%; Score 1416; DB 20; Length 264;  
Blast Local Similarity 100.0%; Pred. No. 3.5e-128;  
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DVTCSASEPTVRIYVGNKGVYVDDPDHNDQIQIMPSKSNNDPNCQITIKEDGTRIS 60  
DB 1 DVTCSASEPTVRIYVGNKGVYVDDPDHNDQIQIMPSKSNNDPNCQITIKEDGTRIS 60  
OY 61 NSGCLITVGYTAGVYVMPDCTAVRENTIWIQINDGTTINRSNVLAASSGIKGTTLT 120  
DB 61 NSGCLITVGYTAGVYVMPDCTAVRENTIWIQINDGTTINRSNVLAASSGIKGTTLT 120  
OY 121 VQILDYTLQGGWLAGNDTAREVYVIGFEDLCMBNSGSGYVWETCDSSQDQGNALYGD 180  
DB 121 VQILDYTLQGGWLAGNDTAREVYVIGFEDLCMBNSGSGYVWETCDSSQDQGNALYGD 180  
OY 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINLNSIMWVDAQ 240  
DB 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINLNSIMWVDAQ 240  
OY 241 NPKLRRIIYPATGKNQMLPEVF 264  
DB 241 NPKLRRIIYPATGKNQMLPEVF 264  
RESULT 2  
AAZ5996 ID AAZ5996 standard; Protein; 265 AA.  
XX  
XX AAZ5996;  
XX 18-OCT-1999 (first entry)  
XX Mistletoe lectin B5 variant protein fragment.  
XX  
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin B5.  
XX  
XX Viscum album.  
XX  
XX DEL19804210-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
XX

PI Morris P, Stiefel T, Woelker M, Welters P;  
XX  
XX WPI; 1999-445336/38.  
XX  
XX N-PSDB; AA03120.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
PT particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure; Fig 18b; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
CC fragments are used to treat uncontrolled cell growth (particularly  
CC cancers) and if they lack cytotoxicity, to increase the strength of the  
CC immune response, particularly to a co-administered antigen  
CC (tumour-associated, bacterial or viral). The method allows production of  
CC mistletoe lectin, and its individual chains, in many different isoforms  
CC and on a large scale, at any time of the year. Recombinant products are  
CC free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a variant mistletoe lectin B5 protein.  
XX  
SQ Sequence 265 AA;  
Query Match 100.0%; Score 1416; DB 20; Length 265;  
Blast Local Similarity 100.0%; Pred. No. 3.5e-128;  
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DVTCSASEPTVRIYVGNKGVYVDDPDHNDQIQIMPSKSNNDPNCQITIKEDGTRIS 60  
DB 1 DVTCSASEPTVRIYVGNKGVYVDDPDHNDQIQIMPSKSNNDPNCQITIKEDGTRIS 60  
OY 61 NSGCLITVGYTAGVYVMPDCTAVRENTIWIQINDGTTINRSNVLAASSGIKGTTLT 120  
DB 61 NSGCLITVGYTAGVYVMPDCTAVRENTIWIQINDGTTINRSNVLAASSGIKGTTLT 120  
OY 121 VQILDYTLQGGWLAGNDTAREVYVIGFEDLCMBNSGSGYVWETCDSSQDQGNALYGD 180  
DB 121 VQILDYTLQGGWLAGNDTAREVYVIGFEDLCMBNSGSGYVWETCDSSQDQGNALYGD 180  
OY 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINLNSIMWVDAQ 240  
DB 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRWFTNEGALINLNSIMWVDAQ 240  
OY 241 NPKLRRIIYPATGKNQMLPEVF 264  
DB 241 NPKLRRIIYPATGKNQMLPEVF 264  
RESULT 3  
AAZ5986 ID AAZ5986 standard; Protein; 264 AA.  
XX  
XX AAZ5986;  
XX 18-OCT-1999 (first entry)  
XX Mistletoe lectin B1 protein fragment.  
XX  
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin B1.  
XX  
XX Viscum album.  
XX  
XX DEL19804210-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX

Thu Dec 11 16:09:47 2003

us-09-601-667c-11.reg

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 : Search time 26.0864 Seconds  
(without alignments)  
1506.345 Million cell updates/sec

Title: US-09-601-667C-11

Perfect score: 1416  
Sequence: 1 DVTGCSASEPTVAVHNMK.....RRIIVPAGKPNQWMLPVE 264

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1415	100.0	264	20	AAV25990
2	1415	100.0	264	20	AAV25996
3	1403	99.1	264	20	AAV25986
4	1403	99.1	264	20	AAV25992
5	1397	98.7	264	20	AAV25988
6	1397	98.7	264	20	AAV25994
7	1390	98.2	264	20	AAV25985
8	1390	98.2	264	20	AAV25995
9	1384	96.3	264	20	AAV25987

10	1364	96.3	265	20	AAV25993	Mistletoe lectin B
11	1324.5	93.5	263	20	AAV25985	Mistletoe lectin B
12	1324.5	93.5	264	20	AAV25991	Mistletoe lectin B
13	1324.5	93.5	531	20	AAV25979	Mistletoe lectin I
14	1324.5	93.5	532	20	AAV25982	Mistletoe lectin I
15	1318.5	93.1	263	19	AAV64662	Mistletoe rMLB var
16	1318.5	93.1	264	20	AAV10023	Prepro mistletoe I
17	1318.5	93.1	263	20	AAV90126	Mistletoe rMLB pro
18	1318.5	93.1	264	20	AAV90126	Mistletoe rMLB pro
19	1318.5	93.1	564	20	AAV90127	Mistletoe lectin I
20	1318.5	93.1	564	20	AAV90127	Mistletoe lectin I
21	1290	91.1	264	20	AAV25978	Mistletoe lectin B
22	1290	91.1	264	20	AAV25972	Mistletoe lectin B
23	1290	91.1	264	20	AAV25975	Mistletoe lectin B
24	1290	91.1	533	20	AAV25970	Mistletoe lectin P
25	1290	91.1	533	20	AAV25973	Mistletoe lectin P
26	1242.5	87.8	267	19	AAV4667	Mistletoe rMLB pro
27	1242.5	87.8	267	19	AAV4667	Mistletoe rMLB pro
28	1184.5	76.9	263	20	AAV17085	B-chain isoform fo
29	1085.5	74.1	581	25	AAV7925	B-chain isoform fo
30	1049.5	70.4	266	22	AAV84703	Sequence of B-prepro
31	997	63.8	565	6	AAV50166	Sequence of B-prepro
32	903.5	63.8	565	22	AAV78300	Sequence of B-prepro
33	903.5	63.8	565	22	AAV78304	Sequence of B-prepro
34	901.5	63.7	574	8	AAV70325	Sequence of B-prepro
35	901.5	63.7	574	8	AAV70325	Sequence of B-prepro
36	901.5	63.7	576	18	AAV25787	Caenorhin ricin
37	901.5	63.7	576	18	AAV25787	Caenorhin ricin
38	901.5	63.7	576	21	AAV55882	Ricinus communis r
39	901.5	63.7	576	21	AAV55882	Ricinus communis r
40	901.5	63.7	576	22	AAV78302	Caenorhin ricin
41	891.5	63.3	565	7	AAV60240	Caenorhin ricin
42	891.5	63.3	565	7	AAV60240	Caenorhin ricin
43	895.5	63.2	262	10	AAV90200	B chain of ricin D
44	892.5	63.0	262	10	AAV90200	B chain of ricin D
45	885.5	62.5	576	8	AAV70326	Sequence of Ricin

ALIGNMENTS

PROTEIN 1  
ID AAV25990  
AAV25990 standard; Protein, 264 AA.

AC AAV25990;  
18-OCT-1999 (first entry)

DE Mistletoe lectin B5 protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
KX riboprotein 28S subunit; non-cytotoxic; T-cell activation; immune response;  
KX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
KX cancer; cytotoxicity; antigen; isoform; lectin B5.

OS Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.





"Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomol proteins and study of their expression patterns.";  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: AY03801; AK02458.1; Ricin\_B\_lectin.  
DR InterPro: IPR001574; RIP.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00652; Ricin\_B\_lectin; 5.  
DR PRINTS: PR00396; SHIGARICIN.  
DR SMART: SM00458; RICIN; 2.  
DR PROSITE: PS50231; RICIN\_B\_LECTIN; 2.  
KV Hydrolase; Signal; Toxin.  
FT SIGNAL 1 32 POTENTIAL.  
FT CHAIN 1 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN  
SQ SEQUENCE 581 AA; 64215 MW; 6859388FBA1D196 CRC64;  
Query Match 58.0%; Score 821.5; DB 10; Length 581;  
Best Local Similarity 59.2%; Pred. No. 2.9e-61;  
Matches 157; Conservative 34; Mismatches 71; Indels 3; Gaps 2;  
OY 1 DVTCSASEPTVAVGKNGKRVVDDDPDQNGQIQLPKSKNDPQQLMTIKEDGTTIS 60  
DB 317 NDDTCADPEPTVIRISRMNLCVVDKRNKNGNFIQWPKCKNSDVMQMLTMRDGLRS 376  
OY 61 NSGCLTYGTAAGVYVMTFCNTAVRENTIQTWNGTIIIPRSNYLAASSGIGKTTIVQT 120  
DB 377 NGKCLTNGISMDIYVLDKRTPTVRSIQFPAHQIIPGSAVLVLSRSGPPTILF 436  
OY 121 VQTLDTLGGQGLAGNDTAPREVTIYGFRLCMSGSGSVVETGSSQNGKMAIYGD 180  
DB 377 NGKCLTNGISMDIYVLDKRTPTVRSIQFPAHQIIPGSAVLVLSRSGPPTILF 436  
OY 437 VQNTIYASRQGLAGNDTAPREVTIYGFRLCMSGSGSVVETGSSQNGKMAIYGD 495  
DB 181 GSIRPKQND--QCLTSGRDSVTVINIVSCGASGQRFVFNRAIMIKSLMTDVA 238  
OY 496 GSIRPKQND--QCLTSGRDSVTVINIVSCGASGQRFVFNRAIMIKSLMTDVA 238  
DB 496 GSIRPKQND--QCLTSGRDSVTVINIVSCGASGQRFVFNRAIMIKSLMTDVA 238  
OY 239 GNPTRRIITYPANGKPMQWLPV 263  
DB 556 GSNPSHIIIMPRKGNHMMPL 580  
RESULT 12  
OQ06076 PRELIMINARY; FRT; 528 AA.  
AC OQ06076;  
DT 01-NOV-1996 (TRENDEL. 01, Created)  
DT 01-NOV-1996 (TRENDEL. 01, Last sequence update)  
DT 01-MAR-2003 (TRENDEL. 23, Last annotation update)  
DT 01-MAR-2003 (TRENDEL. 23, Last sequence update)  
OS Abrus precatorius (Indian licorice) (Crab's eye).  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
CC eucosids; Fabales; Fabaceae; Papilionoideae; Abrusae; Abrus.  
OX NCBI\_TaxID:3816;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:313758; PubMed:642133;  
RA HUNG C.-H., Lee N.-C., Lee C.-H., distinct isoforms determined by cDNA  
RA sequencing; conservation and significance.";  
RT J. Mol. Biol. 229:263-267 (1993).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: M9346; AAA3262.1; -.  
DR HSRP; P1140; IABR.  
DR InterPro: IPR000772; Ricin\_B\_lectin.  
DR InterPro: IPR001574; RIP.

DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
DR PRINTS: PR00396; SHIGARICIN.  
DR SMART: SM00458; RICIN; 2.  
DR PROSITE: PS50231; RICIN\_B\_LECTIN; 2.  
DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
KV Hydrolase; Toxin.  
FT SIGNAL 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 528 AA; 58870 MW; 62BD42FB8F60F8 CRC64;  
Query Match 53.8%; Score 762; DB 10; Length 528;  
Best Local Similarity 54.4%; Pred. No. 2.8e-56;  
Matches 142; Conservative 47; Mismatches 90; Indels 2; Gaps 2;  
OY 5 CASL-EPVAVIRGRKRVVDDDPDQNGQIQLPKSKNDPQQLMTIKEDGTTIS 63  
DB 269 CASREPTVIRISRMNLCVVDKRNKNGNFIQWPKCKNSDVMQMLTMRDGLRS 328  
OY 64 CLTYGTAAGVYVMTFCNTAVRENTIQTWNGTIIIPRSNYLAASSGIGKTTIVQT 123  
DB 329 CLTTEGIVAGVYVMTFCNTAVRENTIQTWNGTIIIPRSNYLAASSGIGKTTIVQT 386  
OY 124 LDYTLGGQGLAGNDTAPREVTIYGFRLCMSGSGSVVETGSSQNGKMAIYGD 183  
DB 329 CLTTEGIVAGVYVMTFCNTAVRENTIQTWNGTIIIPRSNYLAASSGIGKTTIVQT 386  
OY 184 RKQNDQCLTSGRDSVTVINIVSCGASGQRFVFNRAIMIKSLMTDVAQAMP 243  
DB 448 RKQNDQCLTSGRDSVTVINIVSCGASGQRFVFNRAIMIKSLMTDVAQAMP 243  
OY 244 LRKIIITYPATKQPMQWLPV 264  
DB 508 LRKIIITYPATKQPMQWLPV 264  
RESULT 13  
OQ89A43 PRELIMINARY; FRT; 382 AA.  
AC OQ89A43;  
DT 01-JUN-2002 (TRENDEL. 21, Created)  
DT 01-JUN-2002 (TRENDEL. 21, Last sequence update)  
DT 01-MAR-2003 (TRENDEL. 23, Last annotation update)  
DE Abrin isoform G (BC 3.2.2.22) (RNA N-glycosidase)  
CC (Fragment).  
OS Abrus precatorius (Indian licorice) (Crab's eye).  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
CC eucosids; Fabales; Fabaceae; Papilionoideae; Abrusae; Abrus.  
OX NCBI\_TaxID:3816;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE:leaf;  
RA Cook J.P., Roberts L.N., Lord M.;  
RA "New isoform of abrin - abrin G.";  
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: AF49626; AL77434.1;  
DR InterPro: IPR000772; Ricin\_B\_lectin.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
DR SMART: SM00458; RICIN; 2.  
DR PROSITE: PS50231; RICIN\_B\_LECTIN; 2.  
DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
KV Hydrolase; Toxin.  
FT NON\_TER 1 1  
FT CHAIN 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 382 AA; 42743 MW; B0B8B341813AD2BE CRC64;

DB 496 GSIRPHODRCLSTNDHSCSTIISSCSFSSGSRVFWNDSTILNKGVLWVNG 555  
 QY 240 ANPKRLRIIYPATGPKQWMLPV 263  
 DB 556 SNPSHQLIIMPATGKPNQWMLPL 579

## RESULT 9

Q94BM3 PRELIMINARY; PRT; 580 AA.  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Type 2 ribosome-inactivating protein cinnamonin III precursor  
 DE EC 3.2.2.22 (rRNA N-glycosidase).  
 OS Cinnamomum camphora (Camphor tree).  
 OC Embryophyta; Viridiplantae; Streptophyta; Eukaryota; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 NCBI\_TaxID=33429;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Yang Q., Gong Z.Z., Liu W.Y.;  
 RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamonin precursors and study of their expression  
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases  
 RL -1- CATALYTIC ACTIVITY: ENDOPHYLOSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; AY039803; AAK82460.1; -.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
 DR PIRam; PR00161; RIP; 1.  
 DR SMART; SM00458; RIB2; 2.  
 DR PROSITE; PS5031; Ricin\_B\_lectin; 2.  
 KW Hydroxylase; Signal; Toxin.  
 FT SIGNAL 1 32 POTENTIAL.  
 FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN  
 FT PT CINNAMOMIN III.  
 SQ SEQUENCE 580 AA; 64421 MW; 940D10F0LE7B55 CRC64;

Query Match 50.7% Score 860; DB 10; Length 580;  
 Best Local Similarity 52.1%; Pos. No. 1,68-61;  
 Matches 164; Conservative 35; Mismatches 63; Indels 2; Gaps 2;

QY 1 DVTCSASEPTVIVGKNGKVDVDDPHQNDQLPCKSNNDPQWLTIKGGTIR 60  
 DB 317 NBDTCADPEFTVIRISRNGLCDVDDGKNNKNPQLMPCKNSPVQWLTIKGGTIR 376  
 QY 61 NSCLITVGTAGVYVWIPDCAVREATIWMQINDGTLINPSNVLTAASSIGKTTLT 120  
 DB 377 NSCLITVGTAGVYVWIPDCAVREATIWMQINDGTLINPSNVLTAASSIGKTTLT 436  
 QY 121 VQTLDTYLLQGLNAGNDTPREVTIVGPDLCNENSGSVVETCGSSQKQKXWALYGD 180  
 DB 437 VQADIVASRGVLAGNNEPFTSVIGFNDLCQANQAGAMVVEETSSAAQ-QWALYGD 495  
 QY 181 GSIRPKQNOQCLTS-GSDVSVIVINIVSCSAGSGQVWFNEDALINLKSSIMVDAQ 239  
 DB 496 GSIRPHODRCLSTNDHSCSTIISSCSFSSGSRVFWNDSTILNKGVLWVNG 555  
 QY 240 ANPKRLRIIYPATGPKQWMLPV 263  
 DB 556 SNPSHQLIIMPATGKPNQWMLPL 579

RESULT 10  
 Q94BM3 PRELIMINARY; PRT; 549 AA.  
 DT 09FV22

AC 09FV22;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Type II ribosome-inactivating protein cinnamonin IEC 3.2.2.22 (rRNA N-glycosidase) (Fragment).  
 OS Cinnamomum camphora (Camphor tree).  
 OC Embryophyta; Viridiplantae; Streptophyta; Eukaryota; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 NCBI\_TaxID=33429;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Xie L., Liu W.-Y., Wang E.-D.;  
 RT Molecular cloning of cinnamonin A-, B-chain and the expression, purification, characterization and mutagenesis of the A-chain";  
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RL -1- CATALYTIC ACTIVITY: ENDOPHYLOSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; AF259548; AAF68378.2; -.  
 DR HSPB; P02879; 2A1.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 5.  
 DR PIRam; PR00161; RIP; 1.  
 DR SMART; SM00458; RIB2; 2.  
 DR PROSITE; PS5031; Ricin\_B\_lectin; 2.  
 KW Hydroxylase; Toxin.  
 FT SIGNAL 1  
 FT CHAIN 1  
 FT PT NOV TER  
 SQ SEQUENCE 549 AA; 60648 MW; 02607P607CA480 CRC64;

Query Match 58.0% Score 821.5; DB 10; Length 549;  
 Best Local Similarity 59.2%; Pos. No. 2,76-61;  
 Matches 157; Conservative 34; Mismatches 71; Indels 3; Gaps 2;

QY 1 DVTCSASEPTVIVGKNGKVDVDDPHQNDQLPCKSNNDPQWLTIKGGTIR 60  
 DB 285 NBDTCADPEFTVIRISRNGLCDVDDGKNNKNPQLMPCKNSPVQWLTIKGGTIR 344  
 QY 61 NSCLITVGTAGVYVWIPDCAVREATIWMQINDGTLINPSNVLTAASSIGKTTLT 120  
 DB 345 NSCLITVGTAGVYVWIPDCAVREATIWMQINDGTLINPSNVLTAASSIGKTTLT 404  
 QY 121 VQTLDTYLLQGLNAGNDTPREVTIVGPDLCNENSGSVVETCGSSQKQKXWALYGD 180  
 DB 405 VQADIVASRGVLAGNNEPFTSVIGFNDLCQANQAGAMVVEETSSAAQ-QWALYGD 463  
 QY 181 GSIRPKQNOQCLTS-GSDVSVIVINIVSCSAGSGQVWFNEDALINLKSSIMVDAQ 238  
 DB 464 GSIRPHODRCLSTNDHSCSTIISSCSFSSGSRVFWNDSTILNKGVLWVNG 523  
 QY 239 ANPKRLRIIYPATGPKQWMLPV 263  
 DB 524 SNPSHQLIIMPATGKPNQWMLPL 548

RESULT 11  
 Q94BM3 PRELIMINARY; PRT; 581 AA.  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Type 2 ribosome-inactivating protein cinnamonin I precursor  
 DE EC 3.2.2.22 (rRNA N-glycosidase).  
 OS Cinnamomum camphora (Camphor tree).  
 OC Embryophyta; Viridiplantae; Streptophyta; Eukaryota; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 NCBI\_TaxID=33429;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Yang Q., Gong Z.Z., Liu W.Y.;

DR PFAM: P000161; R1P; 1.  
DR PRINTS: P000396; SHIGARICIN.  
DR SMART: SM00458; RICIN; 2.  
DR PROSITE: PS00231; RICIN\_B\_LECTIN; 2.  
DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
DR PROSITE: PS00338; SOMATOTROPIN\_2; 1.  
DR Hydrolase; Toxin.  
FT NON\_TER 1  
SQ SEQUENCE 541 AA; 60281 MW; 28782CDSEFLFE29D9 CRC64;  
Query Match 63.8%; Score 903.5; DB 10; Length 541;  
Best Local Similarity 63.5%; Pred. No. 36-68;  
Matches 165; Conservative 35; Mismatches 59; Indels 1; Gaps 1;

OY 5 CSASEPTVRIYVGNKGVVDVDDDFDGNQIQIUMPSKSNNDPNQIWKIKDGTIRSGSC 64  
DB 283 CMDEPIYRIYVGNGLCVDRGRFHNGNAILQMFCKSNYDANQIWLTKNDTIRSGKC 342  
OY 65 LITVGYTAGVYVWIFDCNTAVBAATWQINDGTINPESNLVLAASSGKRTLVQTL 124  
DB 343 LITVGSPEVYVWITDNTATDTRWQINDGTINPESNLVLAASSGKRTLVQTN 402  
OY 125 DYTLCQMTLNDTAREVITVIGFRDLCSNSGSVWETCCSQKQKRALYDGSIR 184  
DB 403 IYVSGQMLPTNNTPFVTTIVGLYGCILQANSQVWLEDC-TSEKABQQALYDGSIR 461  
OY 185 PRONODCLTSGSDSVSTVINIVSCGASGQRFWETNSGAILNKLNSLAWDAQANPL 244  
DB 462 PQRNDICLTIDNMGVTVKLSGCVASGQRFWETNDITLNLVGLVYDVRSDPS 521  
OY 245 LRRTIYPATGKPNQMTLPV 264  
DB 522 KQIIVHPEHGNLQIMLPF 541

## RESULT 7

OY Q41143 PRELIMINARY; PRT; 263 AA.  
AC Q41143  
DT 01-NOV-1996 (TRENBERL 01, Created)  
DT 01-NOV-1996 (TRENBERL 01, Last sequence update)  
DT 01-MAR-2003 (TRENBERL 23, Last annotation update)  
DE RICIN B beta chain (Fragment).  
DR 01-NOV-1996 (TRENBERL 01, Created)  
DR 01-MAR-2003 (TRENBERL 23, Last annotation update)  
OS Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eudicots I; Malpighiales; Euphorbiales; Ricinus.  
OX NCBI\_Taxid:3988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ladin B.F., Murray E.E., Halling A.C., Halling K.C., Tlikaratne N.,  
RA Long G.L., Houston L.L., Weaver R.F.;  
RT "Characterization of a cDNA encoding ricin E, a hybrid ricin-Ricinus  
RT communis agglutinin gene from the castor plant Ricinus communis";  
RT EMBL: M1631; J058953 (1987).  
DR HESP; P02879; 2AA1.  
DR InterPro; IPR000772; Ricin\_B\_Lectin.  
DR InterPro; IPR01400; Somatotropin.  
DR Pfam; PF00652; Ricin\_B\_Lectin; 6.  
DR SMART; SM00458; RICIN; 2.  
DR PROSITE; PS00231; RICIN\_B\_LECTIN; 2.  
DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
FT NON\_TER 1  
SQ SEQUENCE 263 AA; 29134 MW; A880FDDIDDE14 CRC64;

Query Match 61.5%; Score 871; DB 10; Length 263;  
Best Local Similarity 61.3%; Pred. No. 6-66;  
Matches 160; Conservative 38; Mismatches 61; Indels 2; Gaps 2;  
OY 5 CSASEPTVRIYVGNKGVVDVDDDFDGNQIQIUMPSKSNNDPNQIWKIKDGTIRSGSC 64

DB 4 CMDEPIYRIYVGNGLCVDRGRFHNGNAILQMFCKSNYDANQIWLTKNDTIRSGKC 63  
OY 65 LITVGYTAGVYVWIFDCNTAVBAATWQINDGTINPESNLVLAASSGKRTLVQTL 124  
DB 343 LITVGSPEVYVWITDNTATDTRWQINDGTINPESNLVLAASSGKRTLVQTN 123  
OY 125 DYTLCQMTLNDTAREVITVIGFRDLCSNSGSVWETCCSQKQKRALYDGSIR 184  
DB 403 IYVSGQMLPTNNTPFVTTIVGLYGCILQANSQVWLEDC-TSEKABQQALYDGSIR 182  
OY 185 PRONODCLTSGSDSVSTVINIVSCGASGQRFWETNSGAILNKLNSLAWDAQANP-K 243  
DB 462 PQRNDICLTIDNMGVTVKLSGCVASGQRFWETNDITLNLVGLVYDVRSDPS 242  
OY 244 LRRTIYPATGKPNQMTLPV 264  
DB 243 KQIIVHPEHGNLQIMLPF 263

## RESULT 8

OY Q94BWA PRELIMINARY; PRT; 580 AA.  
AC Q94BWA  
DT 01-DEC-2001 (TRENBERL 19, Created)  
DT 01-DEC-2001 (TRENBERL 19, Last sequence update)  
DT 01-MAR-2003 (TRENBERL 23, Last annotation update)  
DE Type 2 ribosome-inactivating protein cinnamomoin II precursor  
DE (EC 3.2.2.22) (rRNA N-glycosidase).  
OS Cinnamomum camphora (Camphor tree).  
OS Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
OX NCBI\_Taxid:13429;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yeung Q. Gong Z.Z., Lin W.Y.;  
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)  
RT genes encoding cinnamomoin proteins and study of their expression  
RT patterns";  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL; AF039802; AK82459; 1.  
DR InterPro; IPR000172; Ricin\_B\_Lectin.  
DR InterPro; IPR00652; Ricin\_B\_Lectin; 6.  
DR Pfam; P000161; R1P; 1.  
DR PRINTS; P000396; SHIGARICIN.  
DR SMART; SM00458; RICIN; 2.  
DR PROSITE; PS00231; RICIN\_B\_LECTIN; 2.  
DR Hydrolase; Signal; Toxin.  
FT SIGNAL 1  
FT CHAIN 33 580  
SQ SEQUENCE 580 AA; 64265 MW; 37544289CECECF CRC64;

Query Match 61.2%; Score 867; DB 10; Length 580;  
Best Local Similarity 62.5%; Pred. No. 48-65;  
Matches 165; Conservative 34; Mismatches 63; Indels 2; Gaps 2;

OY 1 DDTGSCSEPTVRIYVGNKGVVDVDDDFDGNQIQIUMPSKSNNDPNQIWKIKDGTIRSG 60  
DB 317 CMDEPIYRIYVGNGLCVDRGRFHNGNAILQMFCKSNYDANQIWLTKNDTIRSGKC 376  
OY 61 NSCITITVGYTAGVYVWIFDCNTAVBAATWQINDGTINPESNLVLAASSGKRTLVQTL 120  
DB 377 NSCITITVGYTAGVYVWIFDCNTAVBAATWQINDGTINPESNLVLAASSGKRTLVQTN 120  
OY 121 VQDLYTLCQMTLNDTAREVITVIGFRDLCSNSGSVWETCCSQKQKRALYDGSIR 180  
DB 437 VQDLYTLCQMTLNDTAREVITVIGFRDLCSNSGSVWETCCSQKQKRALYDGSIR 180  
OY 437 VQDLYTLCQMTLNDTAREVITVIGFRDLCSNSGSVWETCCSQKQKRALYDGSIR 180  
DB 181 GSIRPRONODCLTSGSDSVSTVINIVSCGASGQRFWETNSGAILNKLNSLAWDAQAN 239



AC GBLK01;  
 DT 01-OCT-2002 (TRENBERL. 22, Created)  
 DT 01-OCT-2002 (TRENBERL. 23, Last sequence update)  
 DT 01-MAR-2003 (TRENBERL. 23, Last annotation update)  
 DE Lectin chain B isoform 3 (Fragment).  
 OS Viscum album subsp. coloratum  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Santalales; Viscaceae; Viscum.  
 NCBI\_TaxID=159976;  
 RX SEQUENCE FROM N.A.  
 MEDLINE=2156752; PubMed=11710524;  
 RA Do M.-S., Song S.K.;  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RA "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RL Mol. Cells 12:215-220(2001).  
 (2)  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RA Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 RA EMBL: AF508917; AM46935.1; -;  
 DR InterPro: IPR000772; Rictin\_B\_lectin.  
 DR Pfam: PF00652; Rictin\_B\_lectin; 6.  
 DR SMART: SM00458; Rictin\_2; Rictin\_2\_lectin; 6.  
 DR PROSITE: PS50231; RICTIN\_B\_LECTIN; 2.  
 DR NON\_TER 1 1  
 FT NON\_TER 263 263  
 FT SEQUENCE 263 AA; 29071 MW; 3F9C4DA860F061D CRC64;  
 SQ  
 Query Match 76.7%; Score 1085.5; DB 10; Length 263;  
 Best Local Similarity 77.2%; Pred. No. 4.6e-84;  
 Matches 203; Conservative 23; Mismatches 36; Indels 1; Gaps 1;  
 QY 1 DVTGASAPPTVAVGNKGVVDVDDPDHNOIQIMFSSKNDPQWLTKEDGTTIS 60  
 DB 1 DDTCTSPPTVAVGNKGVVDVDDPDHNOIQIMFSSKNDPQWLTKEDGTTIS 60  
 QY 61 NSCLTITGTAAGVAVFPCNTAVREAVTQIMDNGTIPRSNLVLAASGKGT 120  
 DB 61 NSCLTITGTAAGVAVFPCNTAVREAVTQIMDNGTIPRSNLVLAASGKGT 120  
 QY 121 VOTLQVLSGGWLAGNDTAPREVTIYGRDLCEMSNGSVVETCDSSQKNGWALYGD 180  
 DB 121 VOTLQVLSGGWLAGNDTAPREVTIYGRDLCEMSNGSVVETCDSSQKNGWALYGD 180  
 QY 181 GSTREKQNDQCTISGSDVSIVINIVCSGASGQWVFTNEGALINLKSIVAVDAQ 240  
 DB 181 GSTREKQNDQCTISGSDVSIVINIVCSGASGQWVFTNEGALINLKSIVAVDAQ 240  
 QY 241 NPKLRIRIIPATKPNQWMLPV 263  
 DB 241 NPKLRIRIIPATKPNQWMLPV 263  
 QY 240 NPKLRIRIIPATKPNQWMLPV 262  
 DB 240 NPKLRIRIIPATKPNQWMLPV 262  
 RESULT 5  
 GBLK03  
 AC GBLK03;  
 DT 01-OCT-2002 (TRENBERL. 22, Created)  
 DT 01-OCT-2002 (TRENBERL. 23, Last sequence update)  
 DT 01-MAR-2003 (TRENBERL. 23, Last annotation update)  
 DE Lectin chain B isoform 1 (Fragment).  
 OS Viscum album subsp. coloratum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Santalales; Viscaceae; Viscum.  
 NCBI\_TaxID=159976;  
 RX SEQUENCE FROM N.A.  
 MEDLINE=2156752; PubMed=11710524;

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RA "cDNA cloning and sequence analysis of the lectin genes of the Korean  
 RT mistletoe (Viscum album coloratum).";  
 RL Mol. Cells 12:215-220(2001).  
 (1)  
 RP SEQUENCE FROM N.A.  
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,  
 RA Do M.-S., Song S.K.;  
 RA Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 RA EMBL: AF508917; AM46935.1; -;  
 DR InterPro: IPR000772; Rictin\_B\_lectin.  
 DR Pfam: PF00652; Rictin\_B\_lectin; 5.  
 DR SMART: SM00458; Rictin\_2; Rictin\_2\_lectin; 2.  
 DR PROSITE: PS50231; RICTIN\_B\_LECTIN; 2.  
 DR NON\_TER 1 1  
 FT NON\_TER 266 266  
 FT SEQUENCE 266 AA; 29537 MW; 4A51472C37B94C73 CRC64;  
 SQ  
 Query Match 70.4%; Score 997; DB 10; Length 266;  
 Best Local Similarity 69.2%; Pred. No. 1.5e-76;  
 Matches 184; Conservative 32; Mismatches 46; Indels 4; Gaps 2;  
 QY 1 DVTGASAPPTVAVGNKGVVDVDDPDHNOIQIMFSSKNDPQWLTKEDGTTIS 60  
 DB 1 DVTGASAPPTVAVGNKGVVDVDDPDHNOIQIMFSSKNDPQWLTKEDGTTIS 60  
 QY 61 NSCLTITGTAAGVAVFPCNTAVREAVTQIMDNGTIPRSNLVLAASGKGT 117  
 DB 61 NSCLTITGTAAGVAVFPCNTAVREAVTQIMDNGTIPRSNLVLAASGKGT 117  
 QY 118 TLTQVLTGTAAGVAVFPCNTAVREAVTQIMDNGTIPRSNLVLAASGKGT 177  
 DB 118 TLTQVLTGTAAGVAVFPCNTAVREAVTQIMDNGTIPRSNLVLAASGKGT 177  
 QY 179 YGSGIIPKQNDQCTISGSDVSIVINIVCSGASGQWVFTNEGALINLKSIVAVDAQ 237  
 DB 179 YGSGIIPKQNDQCTISGSDVSIVINIVCSGASGQWVFTNEGALINLKSIVAVDAQ 237  
 QY 238 AANPKLRIRIIPATKPNQWMLPV 263  
 DB 238 AANPKLRIRIIPATKPNQWMLPV 263  
 QY 240 AANPKLRIRIIPATKPNQWMLPV 265  
 DB 240 AANPKLRIRIIPATKPNQWMLPV 265  
 RESULT 6  
 Q41174  
 ID Q41174;  
 AC Q41174;  
 DT 01-NOV-1996 (TRENBERL. 01, Created)  
 DT 01-NOV-1996 (TRENBERL. 01, Last sequence update)  
 DT 01-MAR-2003 (TRENBERL. 23, Last annotation update)  
 DE Rhoctin A chain (EC 3.2.2.22) (RNA-N-glycosylase)  
 OS Viscum album subsp. coloratum  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Santalales; Viscaceae; Viscum.  
 NCBI\_TaxID=159976;  
 RX SEQUENCE FROM N.A.  
 MEDLINE=2338377; PubMed=163311;  
 RA Roberts L.W., Regear J.M., Lord J.M.;  
 RA "Molecular cloning of rhoctin A chain (EC 3.2.2.22) (RNA-N-glycosylase) from Viscum album subsp. coloratum";  
 CC -1- SIMILARITY: BELONGS TO THE RHOCTIN INACTIVATING PROTEIN FAMILY.  
 DR EMBL: AF0879; 1886.  
 DR HSSP: P02879; 1886.  
 DR InterPro: IPR000772; Rictin\_B\_lectin.  
 DR InterPro: IPR001574; RIP.  
 DR InterPro: IPR001400; Somatotropin.  
 DR Pfam: PF00652; Rictin\_B\_lectin; 6.

Matches 244; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 1 DDTGASAEPTVAVKNGKAVDVDDPHDQNLQLPKSKNDPNQMTIKKDGITRS 60  
DB 269 DDTGASAEPTVAVKNGKAVDVDDPHDQNLQLPKSKNDPNQMTIKKDGITRS 328  
QY 61 NSGCLTYGTAGYVWIFDCNNAVEKATITWQIMNGTIIIPRSNLVLAASSGIGTIT 120  
DB 329 NSGCLTYGTAGYVWIFDCNNAVEKATITWQIMNGTIIIPRSNLVLAASSGIGTIT 368  
QY 121 VQTLDTLGGGLAGNDTAPREVTIYGFRLQCMNSGSSVWETCVSSQNGQ-RNALYGD 180  
DB 389 VQTLDTLGGGLAGNDTAPREVTIYGFRLQCMNSGSSVWETCVSSQNGQ-RNALYGD 447  
QY 181 GSIRPKONODCLTSGDSVSTVINIVSCGASGSGQWFTNEGALINLKNGLMVDVQA 240  
DB 448 GSIRPKONODCLTSGDSVSTVINIVSCGASGSGQWFTNEGALINLKNGLMVDVQA 507  
QY 241 NPKLRILITTPATGKPNQWMLPV 263  
DB 508 NPKLRILITTPATGKPNQWMLPV 530

RESULT 2

ID Q8LK02 PRELIMINARY; PRT; 263 AA.

AC Q8LK02;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Lactin chain B isoform 2 (fragment).  
OS Vascum album subsp. coloratum.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
NCBI TaxID:159976; Viscum.  
RN [1]\_TaxID:159976;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2156752; PubMed=11710524;  
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,  
Do M.-S., Song S.K.;  
RT "cDNA cloning and sequence analysis of the lactin genes of the Korean  
mistletoe (Vascum album coloratum).";  
RT Mol. Cells 12:215-220(2001).  
RN [1]\_Source: FROM N.A.  
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,  
Do M.-S., Song S.K.;  
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF069318; AA046936.1;  
DR InterPro; IPR000772; Ricin\_B\_lectin.  
DR Pfam; PF00652; Ricin\_B\_lectin; 5.  
DR SMART; SM00458; RICIN\_2.  
DR PROSITE; PS00231; RICIN\_B\_LECTIN; 2.  
FT NON-ITER 1  
FT NON-ITER 263  
FT SEQUENCE 263 AA; 22150 MW; B685ECB7C4C9D1F CRC64;

Query Match 78.8%; Score 116.5; DB 10; Length 263;  
Best Local Similarity 78.7%; Pred. No. 1,le-86;  
Matches 207; Conservative 23; Mismatches 32; Indels 1; Gaps 1;

QY 1 DDTGASAEPTVAVKNGKAVDVDDPHDQNLQLPKSKNDPNQMTIKKDGITRS 60  
DB 269 DDTGASAEPTVAVKNGKAVDVDDPHDQNLQLPKSKNDPNQMTIKKDGITRS 328  
QY 61 NSGCLTYGTAGYVWIFDCNNAVEKATITWQIMNGTIIIPRSNLVLAASSGIGTIT 120  
DB 329 NSGCLTYGTAGYVWIFDCNNAVEKATITWQIMNGTIIIPRSNLVLAASSGIGTIT 368  
QY 121 VQTLDTLGGGLAGNDTAPREVTIYGFRLQCMNSGSSVWETCVSSQNGQ-RNALYGD 180  
DB 389 VQTLDTLGGGLAGNDTAPREVTIYGFRLQCMNSGSSVWETCVSSQNGQ-RNALYGD 447  
QY 181 GSIRPKONODCLTSGDSVSTVINIVSCGASGSGQWFTNEGALINLKNGLMVDVQA 240  
DB 448 GSIRPKONODCLTSGDSVSTVINIVSCGASGSGQWFTNEGALINLKNGLMVDVQA 507  
QY 241 NPKLRILITTPATGKPNQWMLPV 263  
DB 508 NPKLRILITTPATGKPNQWMLPV 530

Matches 240; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 181 GSIRPKONODCLTSGDSVSTVINIVSCGASGSGQWFTNEGALINLKNGLMVDVQA 240  
DB 180 GSIRPKONODCLTSGDSVSTVINIVSCGASGSGQWFTNEGALINLKNGLMVDVQA 239  
QY 241 NPKLRILITTPATGKPNQWMLPV 263  
DB 240 NPKLRILITTPATGKPNQWMLPV 262

RESULT 3

ID Q8W243 PRELIMINARY; PRT; 565 AA.

AC Q8W243;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE VCA precursor (BC 3.2.2.22) (tRNA N-glycosylase).  
OS Vascum album subsp. coloratum.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
NCBI TaxID:159976; Viscum.  
RN [1]\_TaxID:159976;  
RP SEQUENCE FROM N.A.  
RA Park W.-B., Lyu S.;  
RT "Cloning of Vascum album subsp. coloratum (Korean mistletoe).";  
RT Biochem. Biophys. Res. Commun. 0:0(2002).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL; AF069318; AA046936.1;  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
DR PRINTS; PR00396; SHIGARICIN.  
DR SMART; SM00458; RICIN\_2.  
DR PROSITE; PS00231; RICIN\_B\_LECTIN; 2.  
KV Hydrolyase; Signal; Toxin.  
FT SIGNAL 1  
FT SIGNAL 22  
FT CHAIN 23  
FT CHAIN 273  
FT CHAIN 309  
FT SEQUENCE 565 AA; 62401 MW; 991E394D005F11 CRC64;

Query Match 77.9%; Score 110.5; DB 10; Length 565;  
Best Local Similarity 79.8%; Pred. No. 3,6e-85;  
Matches 210; Conservative 17; Mismatches 31; Indels 5; Gaps 2;

QY 1 DDTGASAEPTVAVKNGKAVDVDDPHDQNLQLPKSKNDPNQMTIKKDGITRS 60  
DB 307 DDTGASAEPTVAVKNGKAVDVDDPHDQNLQLPKSKNDPNQMTIKKDGITRS 362  
QY 61 NSGCLTYGTAGYVWIFDCNNAVEKATITWQIMNGTIIIPRSNLVLAASSGIGTIT 120  
DB 363 NSGCLTYGTAGYVWIFDCNNAVEKATITWQIMNGTIIIPRSNLVLAASSGIGTIT 422  
QY 121 VQTLDTLGGGLAGNDTAPREVTIYGFRLQCMNSGSSVWETCVSSQNGQ-RNALYGD 180  
DB 422 VQTLDTLGGGLAGNDTAPREVTIYGFRLQCMNSGSSVWETCVSSQNGQ-RNALYGD 481  
QY 181 GSIRPKONODCLTSGDSVSTVINIVSCGASGSGQWFTNEGALINLKNGLMVDVQA 240  
DB 482 GSIRPKONODCLTSGDSVSTVINIVSCGASGSGQWFTNEGALINLKNGLMVDVQA 541  
QY 241 NPKLRILITTPATGKPNQWMLPV 263  
DB 542 NPKLRILITTPATGKPNQWMLPV 564

RESULT 4

ID Q8LK01 PRELIMINARY; PRT; 263 AA.





Thu Dec 11 16:09:48 2003

us-09-601-667c-11.rmp

Page 13

FT CARBOHYD 131 131 N-LINKED (GLCNAc. . .) (POTENTIAL).  
FT CARBOHYD 211 211 N-LINKED (GLCNAc. . .) (POTENTIAL).  
FT CARBOHYD 343 343 N-LINKED (GLCNAc. . .) (POTENTIAL).  
FT CARBOHYD 444 444 N-LINKED (GLCNAc. . .) (POTENTIAL).  
SQ SEQUENCE 545 AA, 60148 MW, 2DCSA710CE9D59C CRC64,

Query Match 6.7%; Score 94.5; DB 1; Length 545;  
Best Local Similarity 19.5%; Pred. No. 1.1;  
Matches 45; Conservative 43; Mismatches 98; Indels 45; Gaps 8;

OY 22 VDVRRDDDFHGGNQLQMPKSNNDPNQWTKRKGITRNSCLTYGYTA-----72  
DB 342 LDIITRSIANGDRRLVTVINKNR-----IVTRDIPVQWGLTEYDCTTAEDLMDGKTQ 395  
OY 73 ---GVYVMIEDCNTAVREATIQ-----INDGIIIPRSNULIASSGIXKITLTYQT 124  
DB 396 KISDHKIELASHATVFRSLPQGSSEVPTGLVPTASGNLTNA--NSVAFQSC 452  
OY 125 DYTLGGGLAGNDTPAPREVTYIGFRLQMESNGSVWETCDSSQKQKMAIYGDGSR 184  
DB 453 NGFTSCIVWTPSSGIVFVS--QTTQCLADGNLYELQACDSTDSQDKATYPTGSLK 509  
OY 185 PRONQOCLTSGDSVSIVINIVCSGSGSQRWFTNEGAIIINKSLNV 235  
DB 510 -NKTGGLTSS-----VQKMSC-----LYRDKGVRLPSGVOL 544

Search completed: December 11, 2003, 14:09:07  
Job time : 4.6201 secs

Oy	148	FBDJLONSN----	QGSVWATSDSQQNDGMAVLGVGDSSFRKQNOPOOCLINSR-DVSVF	202
Db	432	PFEKVYTKKKGGQAPEPDA	CHAGAGNDA-MELTKEER--SDTLSSSHVYGSG	547
Oy	203	VINVSGSGASGSGORMT--	NESGLTNLSNLMPDYADAPFLRLITTYPATGRKNR	259
Db	546	EKLKERSTSVKINVTAVDDQ	AGSLFKTRKTCVTDGCVTLDECC--GLADNDQ	603
Oy	260	M 260		
Db	604	M 604		
RESTART 15				
OC	ZGBL_ASPMG	STRANDAD,	PRT,	545 AA.
OC	ASPNG			
AC	01-DEC-1992 [Rel. 24, Created]			
DT	01-DEC-1992 [Rel. 24, Last sequence update]			
DT	16-OCT-2001 [Rel. 40, Last annotation update]			
DN	Alpha-galactosidase A precursor [EC 3.2.1.22] (Melibiose)			
OC	AGLA.			
OC	Aspergillus niger.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; maltosporic Trichocomaceae; Aspergillus.			
OC	KCPL_TextID=5061;			
BP	SEQUENCE FROM N.A., AND SEQUENCE OF 32-59.			
RX	STRAINS=ATCC 9089 / M402;			
RX	MEDLINE=92318893; PubMed=12010186;			
RA	van den Herder I.F., Rosell J.A.M.M., van Zullen C.M., Punt P.J.,			
ZA	"Cloning and expression of a member of the Aspergillus niger gene			
FT	family encoding alpha-galactosidase."			
FT	Mol. Gen. Genec. 233:404-410(1992).			
CC	-!- ACTIVITY IN A NIGER A MINOR EXTRACELLULAR ALPHA-GALACTOSIDASE			
CC	-!- CATALYTIC ACTIVITY: Melibiose + H <sub>2</sub> O = galactose + glucose.			
CC	-!- PTM: A C-TERMINAL SER-/THR-RICH REGION MAY PROVIDE POSSIBLE SITES			
CC	FOR O-GLYCOSYLATION.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 27 OF GLYCOSYL HYDROLASES.			
CC	-!- SIMILARITY: Contains 1 rich B-type lectin domain.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-9 IS THE INITIATOR.			
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CC	EMBL; X63348; CAA44950.1 ;			
DR	PIR; G33582; S23582.			
DR	IYPSCULDEB; Y002931.			
DR	IYPSCULDEB; Y002931.			
DR	Interpro; IR000111; Glyco_Hydro_GHD.			
DR	Interpro; IR000772; Richn_B_Lectin			
DR	Pfam; PF002065; Melibiase_1.			
DR	Pfam; PF00562; Richn_B_Lectin_3.			
DR	PRINTS; PR00740; GHYDRLSD27.			
DR	PRODOM; PD002572; Glyco_Hydro_GHD_1.			
DR	SMART; SM00489; RICHN_1			
DR	PROSITE; PS00512; ALPHA_GALACTOSIDASE; 1.			
DR	PROSITE; PS00531; ALPHA_LECTIN_1			
FM	SYMBOLase; Glycosylase; Signal; Glycoprotein; Lectin.			
FT	CHAIN	32	545	
FT	DOMAIN	421	518	ALPHA-GALACTOSIDASE A.
FT	ACT SITE	327	337	POTENTIAL.
FT	CARDHOWD	57	95	N-LINKED (GLNAC. .) (POTENTIAL).
FT	CARDHOWD	95	95	N-LINKED (GLNAC. .) (POTENTIAL).
FT	CARDHOWD	101	101	N-LINKED (GLNAC. .) (POTENTIAL).

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CC -----
CC EMBL: M4551, accession: M4551, version: 62,
CC InterPro: IPR000772, Ricin_B_lectin.
CC InterPro: IPR000772, Ricin_B_lectin.
CC Pfam: PF00664, Glyco_hydrol_62.1.
CC SMART: SM00458, Ricin_B_lectin; 1.
CC PROSITE: PS50231, Ricin_B_lectin; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal; lectin.
CC SIGNAL 1 37
CC FT CHAIN 38 475 ALPHA-L-ARABINOFURANOSIDASE.
CC DOMAIN 38 16369 MM; GCCEIHERH95MD CRC64;
CC SEQUENCE 475 AA; 50369 MM;
CC -----
Query Match 7.9%; Score 112.5; DB 1; Length 475;
Best Local Similarity 24.1%; Pred. No. 0.026;
Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;
QY 6 SASEPTVAVICNRCVVRDDPDHNDQOLQWPSKSNNDPQWLTKRQGTIRSN-SC 64
DB 37 AASGALNGAGNRCLDVLGSGQDGLALQYDQWQ3T--NQQTSTDTGALTVYGDRC 93
QY 65 LITVGYTA--GVYVWIFDGNVAVKATVQINDGTTINPSNVLV-AASSGI-KGTLT 120
DB 94 LDVPGHATPGRVQVWISGSGNRQC--WVNSDGVGVESGLCLEAGAGTPNGTAVQ 151
QY 121 VQTLIDYTLGGQWLANDTAPRPT-----LYGRDLMSNGSIVWETCD-SGQNRCK 174
DB 152 LMTGNGGNGKWTGLTGFPTDTCALPSTYMSSTGVLAQPSVVALDCTIVYHNR 211
QY 175 WALYDGS-----IRPKQVQDCLTSGDSVS 201
DB 212 HLYVGSSTSGSSGVSWFSPFTWSDMASQGNAN 247
-----
RESULT 13
SPL_PAPPA STANDARD; PRT; 525 AA.
ID SPL_PAPPA
AC 005308;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Serine protease I precursor (EC 3.4.21.-) (Rpt).
OS Rarobacter faecitabidus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Rarobacteraceae; Rarobacter.
OX NCBI_TaxID=13243;
PI SOURCE: FROM N. A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.
RX MEDLINE=93094226; PubMed=1339445;
RA Shimoi H., Iimura Y., Obara T., Tadenuma M.;
RT "Molecular structure of Rarobacter faecitabidus protease I, A yeast-
RT lytic serine protease having mannose-binding activity.";
RL J. Biol. Chem. 267:25189-25195 (1992).
(2)
RZ SEQUENCE OF 212-247.
RX MEDLINE=9128668; PubMed=1779983;
RZ SEQUENCE OF 212-247.
RZ SEQUENCE OF 212-247.
RT "Characterization of Rarobacter faecitabidus protease I, a
RT yeast-lytic serine protease having mannose-binding activity.";
RL J. Biochem. 110:608-613 (1991).
-1- FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD
CC LIVING YEAST CELLS. SIMILAR TO ELIASINE IN ITS SUBSTRATE
CC SPECIFICITY AND HAS A LECTIN-LIKE AFFINITY FOR MANNOSE.
CC MANNOPROTEINS MAY BE THE NATIVE SUBSTRATE FOR RPI.
-1- SUBCELLULAR LOCATION: secreted.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 82A.
CC -1- SIMILARITY: BELONGS TO LECTIN B-TYPE LECTIN domain.
CC -----
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CC -----
CC EMBL: P10753, accession: P10753, version: 1.
CC InterPro: IPR004236, AL protease.
CC InterPro: IPR001316, Endoprotease2.
CC InterPro: IPR000772, Ricin_B_lectin.
CC InterPro: IPR001254, Ser_protease_Try.
CC Pfam: PF02993, AL protease; 1.
CC Pfam: PF00852, Ricin_B_lectin; 3.
CC Pfam: PF00852, Ricin_B_lectin; 1.
CC SMART: SM00458, Ricin_B_lectin; 1.
CC PROSITE: PS00134, TRYPSIN_HIS. 1.
CC PROSITE: PS00134, TRYPSIN_SER. 1.
CC PROSITE: PS50231, Ricin_B_lectin; 1.
CC HYDROLASE; Serine protease; Mannose-binding; Signal; Zymogen;
CC LECTIN.
CC SIGNAL 1 32
CC FT PROPEP 33 211 SERINE PROTEASE 1.
CC FT CHAIN 33 525 RICIN B-TYPE LECTIN.
CC FT DOMAIN 336 525 ESSENTIAL FOR THE LYTIC ACTIVITY, BUT NOT
CC FT DOMAIN 401 525 FOR CATALYTIC FUNCTION.
CC DISULFID 223 239
CC DISULFID 310 320 BY SIMILARITY.
CC DISULFID 346 376 BY SIMILARITY.
CC DISULFID 412 431 BY SIMILARITY.
CC DISULFID 453 472 BY SIMILARITY.
CC DISULFID 496 514 BY SIMILARITY.
CC ACT SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC ACT SITE 270 270 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC ACT SITE 352 352
CC SEQUENCE 525 AA; 55654 MM; DABCFYD30EBB61 CRC64;
CC -----
Query Match 7.9%; Score 111; DB 1; Length 525;
Best Local Similarity 31.1%; Pred. No. 0.04;
Matches 33; Conservative 17; Mismatches 44; Indels 12; Gaps 5;
QY 2 DVTCSASEPTVAVICNRCVVRDDPDHNDQOLQWPSKSNNDPQWLTKRQGTIRSN 64
DB 399 DVT-----TSYVQYQNNCTIVPSPFDKQOLQWVWNCN--AQKVSHPDGLRI 150
QY 62 GSCLITVYKTAAGYVWIFDGNVAVKATVQINDGTTINPSNVLV-AASSGI-KGTLT 120
DB 451 GSKLDARWATHNGTETVQWLNCKGHI--AQKFTLNAGDVLWVHAN 494
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RESULT 14
PAG3_CABEL STANDARD; PRT; 612 AA.
ID PAG3_CABEL
AC P34678; G91003;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE POLYPEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 3 (EC 2.4.1.41)
DE N-ACETYLGLUCOSAMINYLTRANSFERASE (NAG-6-T) (EC 2.4.1.41)
DE N-ACETYLGLUCOSAMINYLTRANSFERASE (NAG-6-T) (EC 2.4.1.41)
DE GUY-3 OR 22689/8
OS Caenorhabditis elegans.
OC Caenorhabditidae; Ctenophora; Ctenophoridae; Ctenophorales;
OC Eukaryota; Metazoa; Chordata; Chordata; Chordata; Chordata;
OC Rhabditidae; Pelodieridae; Caenorhabditidae.
OX NCBI_TaxID=6239;
PI SOURCE: FROM N. A.
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DR Pfam: PF00652; Ricin B lectin; 3.
DR SMART: SMO0456; RICIN-1.
DR PROSITE: PS0031; RICIN B LECTIN: 1.
DR HYDROLASE; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
PT SIGNAL 37 548 POTENTIAL.
PT CHAIN 1 36 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.
PT DOMAIN 422 540 RICIN B-TYPE LECTIN.
PT DOMAIN 37 430 POSSIBLE BETA-GLUCANASE ACTIVITY, BUT IS
PT DOMAIN 472 548 UNABLE TO DISRUPT CELLS
PT DOMAIN 472 548 FOR THE BETA-GLUCANASE FUNCTION.
SQ SEQUENCE 548 AA; 58088 MW; 412B54AA24C04BD CRES4;
OY Best Match
OY Query Similarity 81.1%; Score 114; DB 1; Length 548;
OY Matches 4; Conservative 18; Mismatches 52; Indels 20; Gaps 7;
OY 16 GERNKY-----DVEDDFHDSNQLGLMPSKSNDEPNGLMTIRKDGITRNSNCSL--TT 67
OY 422 GTHAKRGVSTCLADYVMDPTDPLDVG--ATGSNAAAGQNRGTGDIYALAKLCLDPAK 479
OY 68 YGTAGAGVYVTPPCN-TVNEVETQWQMNQST--IINPSNLYVLAASGI---KRTLLY 121
OY DB 480 STADGAGVAVVYCNQNTAQKPT---YDSATVLAIRPQSGKCDLADGAGLADGAGKVL 535
OY 122 QTLDTLYLGGQW 132
OY DB 536 WTCNQTEADQW 546
RN RESULT 12
RN ABBP_STRLI STANDARD; PRT; 475 AA.
ID ABBP_STRLI
AC P96463;
AC 15-DEC-1998 (Rel. 37, Created)
AC 15-DEC-1998 (Rel. 37, Last sequence update)
AC 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
DE Streptococcus lividans.
DE Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
DE Streptomyces; Streptomycesetaceae; Streptococci.
OC NCBI_TaxID:1916;
RN [1]
RN DB SEQUENCE FROM N.A.
RN STRAIN=66 / 1326;
RN MEDLINE=97220396; PubMed=9148739;
RN Kinetic P., Shareck F., Dubont C., Morosoli R., Klempfner D.;
RN cloning and DNA sequence of the aB5 gene and characterization of the
RN enzyme";
RN L. Biochem. J. 322:845-852(1997).
RN [2]
RN REVIEWS.
RN STRAIN=66 / 1326;
RN Shareck F.;
RN Shumaker (CUT-1998) to the EMBL/Genbank/ODDB databases.
RN -1- XYLANASE FROM STRAIN 66 OF THE SPECIES A. B5 WITH AN ACTIVITY ON
RN BUNDLES OF XYLANS. THIS SPECIES IS CLOSELY RELATED WITH THE XYLANASES AND
RN IT LIBERATES ARABINOSE AND, AFTER PROLONGED INCUBATION, THE
RN PURIFIED ENZYME EXHIBITS SOME XYLANOXYLYTIC ACTIVITY AS WELL.
RN -1- CARBOLYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-D-
RN arabinofuranoside residues in alpha-L-arabinosides.
RN -1- PATHWAY: Xylan degradation.
RN -1- SUBCELLULAR LOCATION: Secreted.
RN -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
RN -1- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
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InterPro: IPR000772; Ricin B lectin.  
 Pfam: PF00652; Ricin B lectin. 3.  
 PRINTS: PR00134; GHYDRLASH10.  
 DR SMART: SM00458; R1CIN.1.  
 DR PROSITE: PS00591; GLYCOSYL\_HYDROL\_F10.1.  
 DR PROSITE: PS50231; R1CIN\_B\_LECTIN.1.  
 KX Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;  
 KX Xylan structure. 1  
 FT SIGNAL 1 41  
 FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.  
 FT DOMAIN 361 477 R1CIN\_B-TYPE LECTIN.  
 FT ACT SITE 169 169 PROTON DONOR.  
 FT ACT SITE 277 277 NUCLEOPHILE.  
 SQ SEQUENCE 477 AA; 51162 MW; 81497E37BD66CC CRC64;  
 Query Match 8.9%; Score 125.5; DB 1; Length 477;  
 Best Local Similarity 23.9%; Pred. No. 0.002; 61; Indels 13; Gaps 6;  
 Matches 40; Conservative 20; Mismatches 61; Indels 13; Gaps 6;  
 QY 7 ASPP-----TVRTVGNNGRVDVDDPDHGNQIOIWPESKSNNDPQMLTKEDGTRISN 61  
 DB 346 SSEPPADGQIKVQ-SFPCIDVPDSTSPGQIQIMDCSGGT--NCPAANDAGSLVY 402  
 QY 62 G-SCLTYGTAGTYMIFDCNTVBAETIWMQIMNTIIPRSMVLA--SSGIKQT 118  
 DB 403 GPKCLDAGTMSKSTVSTISCGAGDNQ--WELNSDSYVQSSCLDVGNTAKET 460  
 QY 119 LTVQTLDTYLGQW 132  
 DB 461 TQLYTCSNGSNQW 474  
 RESULT 9  
 AFBP STRCO STANDARD; PRT; 475 AA.  
 ID AFBP STRCO  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).  
 GN AFBP OR SC05932 OR SCTH.02.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomyces; Streptomyces; Streptomyces.  
 KX NCBI\_TaxID:1502;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: A3(2) / M45;  
 RX MEDLINE: 21996410; PubMed: 1200953;  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Klee H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chan C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Horvath S.,  
 RA Huang C.-H., Klee H., Klee H., Lurie D., Murphy D., Oliver K.,  
 RA Rasmussen S., Rasmussen S., Rasmussen S., Rasmussen S.,  
 RA Seeger K., Saunders D., Sharp S., Squares S., Squares S.,  
 RA Warren T., Wietzorek A., Woodward J., Barrett B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomyces Streptomyces  
 coelicolor A3(2).";  
 RL Nature 417:141-147(2002).  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-  
 arabinofuranoside residues in alpha-L-arabinosides.  
 CC -1- SIMILARITY: Belongs to family 62 of GLYCOSYL\_HYDROLASES.  
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.  
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 CC  
 DR EMBL: AL039125; CHA16189.1; .  
 DR PIR: T35697; T35697.  
 DR InterPro: IPR005193; Glyco\_hydro\_62.  
 DR InterPro: IPR000772; Ricin B lectin.  
 DR Pfam: PF00652; Ricin B lectin. 3.  
 DR SMART: SM00458; R1CIN.1.  
 DR PROSITE: PS50231; R1CIN\_B\_LECTIN.1.  
 KX Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;  
 KX Complete proteome.  
 FT SIGNAL 1 37  
 FT CHAIN 38 475 ALPHA-L-ARABINOFURANOSIDASE.  
 FT DOMAIN 361 475 R1CIN\_B-TYPE LECTIN.  
 FT ACT SITE 169 169 PROTON DONOR.  
 FT ACT SITE 277 277 NUCLEOPHILE.  
 SQ SEQUENCE 475 AA; 50045 MW; 47307E353C6A0D CRC64;  
 Query Match 8.2%; Score 115.5; DB 1; Length 475;  
 Best Local Similarity 24.1%; Pred. No. 0.014;  
 Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;  
 QY 6 SASEPPIRVGNNGRVDVDDPDHGNQIOIWPESKSNNDPQMLTKEDGTRISN-SC 64  
 DB 37 PASESALKSGSNK-LVLAGSQDDALDLDICSGGT--NCPSTSTSLVYSGK 93  
 QY 65 LTVYGTN--GYVMTFPCNTVBAETIWMQIMNTIIPRSMVLA--SSGIKQT 120  
 DB 140 GPKCLDAGTMSKSTVSTISCGAGDNQ--WELNSDSYVQSSCLDVGNTAKET 460  
 QY 121 VQTLDTYLGQW 132  
 DB 461 TQLYTCSNGSNQW 474  
 QY 175 WNLNGSG-----IRFQNGQCLTSGNDVS 201  
 DB 212 HVIYGTSSGSSYSQSWPTPTMDSMA-SKGNM 247  
 RESULT 10  
 E13B ARTSP STANDARD; PRT; 548 AA.  
 ID E13B ARTSP  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-OCT-2003 (Rel. 41, Last annotation update)  
 DE Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) (1->3)-beta-  
 DE glucan endohydrolase ((1->3)-beta-glucanase).  
 GN GUCI.  
 OS Athrobacter sp. (strain YCMB).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococcales; Micrococcales; Athrobacter.  
 KX NCBI\_TaxID:167;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: YCMB;  
 RX PubMed: 1200953;  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Klee H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chan C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Horvath S.,  
 RA Huang C.-H., Klee H., Klee H., Lurie D., Murphy D., Oliver K.,  
 RA Rasmussen S., Rasmussen S., Rasmussen S., Rasmussen S.,  
 RA Seeger K., Saunders D., Sharp S., Squares S., Squares S.,  
 RA Warren T., Wietzorek A., Woodward J., Barrett B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomyces Streptomyces  
 coelicolor A3(2).";  
 RL Nature 417:141-147(2002).  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages  
 CC in 1,3-beta-D-glucans; periplasmic (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (by similarity).  
 CC -1- SIMILARITY: Belongs to family 62 of GLYCOSYL\_HYDROLASES.  
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
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Cc		SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES TRANSLATION.
Cc	-1-	CATALYTIC ACTIVITY: Endo- $\alpha$ -mannosidase of the N-glycosidic bond at one specific asparagine on the 28S rRNA.
Cc	-1-	SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
Cc	-1-	SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
Cc	-1-	SIMILARITY: Contains 2 ricin B-type lectin domains.
Cc		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at Heidelberg. European institutions are allowed to make unrestricted use by non-profit institutions as long as the credit goes to the source modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
Cc		EMBL; U41299; ABAB3475.1; -
Dc	PIR; S37382; S37382.	Ricin B lectin.
Dc	Inferno; PR000772;	Ricin B lectin.
Dc	Pfam; PF00652;	Ricin B lectin. 6.
Dc	Pfam; PF00161; RLP_1	lectin. 6.
Dc	DR PRINTS; P000366;	SHIACRICN.
Dc	DR SMART; SMO0458;	RICIN; 2.
Dc	DR PROSITE; PS00275;	SHIGA_RICIN; 1.
Dc	DR PROSITE; PS50231;	RICIN_B_Lectin; 2.
Kw		Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Ricin B chain; Ricin B type 2; Ricin B protein; Ricin B subunit; Ricin B domain; Ricin B repeat; Ricin B signal.
Ft	CHAIN	26 297.
Ft	CHAIN	298 563.
Ft	DOMAIN	305 431.
Ft	DOMAIN	434 559.
Ft	REPEAT	316 356.
Ft	REPEAT	357 397.
Ft	REPEAT	398 432.
Ft	REPEAT	433 465.
Ft	REPEAT	466 527.
Ft	REPEAT	528 554.
Ft	ACT_SITES	188 188.
Ft	DISULFID	274 302.
Ft	DISULFID	319 338.
Ft	DISULFID	360 377.
Ft	DISULFID	448 463.
Ft	DISULFID	464 506.
Ft	DISULFID	507 525.
Ft	CARBOND	368 368.
Ft	CARBOND	376 376.
Ft	CARBOND	483 483.
Ft	CARBOND	537 537.
Ft	CONFLICT	39 39.
Sc	SEQUENCE	563 AA; 62300 MW; F250CHEZ4621BP14 CMC64; K->V (IN REF. 2).
Query Match	Similarity	37.28; Score 526.5; DB.1; Length 563;
B	Matches	108; Conservative 94; Identical 108; Indels 7; Gaps 5
Oy	1	DVTGSAEPEYTR-IVRNGKRGVDVDDDPHGQNIQLPWKSNDPVOIAMTIKSDGTIR 59
Db	298	DGDTGLRTLSFRNIVGRGKCDVNRVPLTGFLQLMVGQR--NQGMFFSDPTIR 356
Oy	356	SNQCCLTVYAGVYVLPDPCFAVEATLRQIWDGIIIPRSNTLVLAASSIKETTL 119
Db	356	SMKCNCTWLNKNSNVIVPMQCIKENHAIKNKEPVDSIIINSQSVNAPRAASSTLL 415
Oy	120	TVOELDTLTLAGQMLANGDAFRVETLYEPDFDCHESSG--GSVTFPSGSGQNGKML 177
Db	416	LLEBDVIYAACQMTVNRRVFIVASIVGVEMCLOSISGNNGNWMEDEKTSIQ--CWAL 474
Db	416	LEBDDIYAAQCMVTNNRRVFIVASIVGVEMCLOSISGNNGNWMEDEKTSIQ--CWAL 474

Qy	178 YDDSGTSPKPOQOCLTSBMSDSVSTVINVCSSGASGSQGRWTFNFGALILTKNSJAVD
Dd	475 YDDTLTRVMSRQLCTVTNNYSKDILLIKLQGLP-SGRMPFNSQIALVPXSRHVD
Qy	238 AOANPKLRRIITLYPATGCKPMWL 261
Dd	534 RASNVSLEKIIITFPATSNQQMW 557
CC	RESULT 8
DR	XVYA_STRLI
ID	P26514; P96464;
AC	01-AUG-1992 (Rel. 23, Created)
DT	30-MAY-2000 (Rel. 35, Last sequence update)
DE	15-SEP-2003 (Rel. 45, Last annotation update)
DE	Enco-1,4-beta-xylanase A precursor [EC 5.2.1.8] (Xylanase A)
GN	XNA_beta-D-xylan xylohydrolase A.
OS	Streptomyces lividans.
OC	Bacteria; Actinobacteria; Actinomycetales; Streptomyces.
OX	NCBI_TaxID=1916;
EN	[1]
RC	SEQUENCE FROM N.A., AND SEQUENCE OF 42-92.
RC	STRAIN=66 / 1326;
RX	MEDLINE=2007433; PubMed=1743521;
PT	"Molecular cloning of the gene encoding Enco-1,4-beta-xylanase A"
RT	"Sequences of three genes specifying xylanases in Streptomyces lividans."
RL	Gene 107:75-82(1991).
PN	[2]
RP	REVISIONS TO 20 AND 140-141.
RC	SHRAIN=66 / 1326;
RA	Shareck F.;
RU	Submitted (JUL-1998) to the EMBL/Genbank/DDJJ databases.
RU	X-YLA CRYSTALLINOGRAPHY (2.6 ANGSTROMS) OR 42-340.
RX	MEDLINE=9434233; PubMed=80631693
RA	Dereveda U., Swenson L., Green R., Wei Y.Y., Morcosli R., Shareck F., Kluepfel D., Dereveda Z.S.;
RT	"Crystal structure, at 2.6-A resolution, of the Streptomyces lividans XylAmanase A, a member of the F family of beta-1,4-D-glycanases.";
RL	J. Biol. Chem. 269:20811-20814(1994).
CC	-1- FUNCTION: Contributes to hydrolyze hemicellulose, the major component of plant cell-walls. XLHA and XLHB seem to act sequentially or cooperatively on the substrate to yield xylobiose and xylose
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
CC	-1- PATHWAY: Xylan degradation.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL HYDROLASES).
CC	-1- SIMILARITY: Contains 1 rich B-type lectin domain.
CC	--
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CC	--
DR	EMBL; M6451; AAC6525.1; .
DR	FIR; J05059; J05059.
DR	PDB; 1BOV; 25-MAY-01.
DR	PDB; 1BOW; 25-MAY-01.
DR	PDB; 1KOL; 19-JUN-02.
DR	PDB; 1KNM; 19-JUN-02.
DR	PDB; 1WC9; 11-SEP-02.
DR	InterPro: IPR001000; Glyco hydrol 10.

[illegible][illegible]

DR EMBL; M98345; AAA32625.1; .  
DR PIR; S32430; S32430.  
DR HSPB; P1140; 1ABR.  
DR InterPro; IPR000772; R1cin\_B\_lectin.  
DR InterPro; IPR001574; R1P\_1.  
DR Pfam; PF00652; R1cin\_B\_lectin; 6.  
DR Pfam; PF00161; R1P; 1.  
DR PRINTS; PR00386; SHGARICIN.  
DR SMART; SMO0458; R1CIN; 2.  
DR PROSITE; PSS0231; R1CIN\_B\_LECTIN; 2.  
DR PROSITE; PSS0275; SHGA\_R1CIN; 1.  
KW Plant defense, Hydrolyase, Protein synthesis inhibitor, Toxin, Repeat,  
KW Glycoprotein, Lectin, Pyroglutamate carboxylic acid.  
KW CHAIN 1 250 AERIN-B A CHAIN.  
FT PEPTIDE 251 LINKER PEPTIDE.  
FT CHAIN 251 527 AERIN-B B CHAIN.  
FT DOMAIN 272 399 R1CIN-B TYPE LECTIN 1.  
FT DOMAIN 402 526 R1CIN-B-TYPE LECTIN 2.  
FT 527

PT	REPEAT	368	400	1-GAMA.
PT	REPEAT	413	448	2-ALPHA.
PT	REPEAT	452	491	2-BETA.
PT	REPEAT	461	501	2-GAMA.

FT	ACT SITE	163	BY SIMILARITY.
FT	ACT SITE	163	BY SIMILARITY.
FT	DISULFID	268	INTEGRAL (BY SIMILARITY).
FT	DISULFID	268	INTEGRAL (BY SIMILARITY).
FT	DISULFID	338	BY SIMILARITY.
FT	DISULFID	345	BY SIMILARITY.
FT	DISULFID	416	BY SIMILARITY.
FT	DISULFID	455	BY SIMILARITY.
FT	DISULFID	472	BY SIMILARITY.
FT	MOD_RES	1	CARBOXYLIC ACID (BY SIMILARITY).
FT	MOD_RES	1	CARBOXYLIC ACID (BY SIMILARITY).
FT	CARBONHD	110	N-LINKED (GLUCNA. . .) (POTENTIAL).
FT	CARBONHD	110	N-LINKED (GLUCNA. . .) (POTENTIAL).
FT	CARBONHD	360	N-LINKED (GLUCNA. . .) (POTENTIAL).
FT	CARBONHD	360	N-LINKED (GLUCNA. . .) (POTENTIAL).
FT	CARBONHD	360	N-LINKED (GLUCNA. . .) (POTENTIAL).
FT	CARBONHD	360	N-LINKED (GLUCNA. . .) (POTENTIAL).

FT	CONFLICT	282	282	N -> D (IN REB. 2.)
FT	CONFLICT	281	291	D -> N (IN REB. 2.)
FT	CONFLICT	350	351	AE -> PO (IN REP. 2.)
FT	CONFLICT	378	378	S -> N (IN REB. 2.)
FT	CONFLICT	426	426	T -> M (IN REB. 2.)
FT	CONFLICT	428	428	T -> D (IN REB. 2.)

Query Match	Score	DB 1	Length
Best Query Similarity	51.8%	Pred: No. 8.9e-59	527
FT	CONFLECT	484	R -> K (IN REP. 2)
FT	CONFLECT	491	N -> S (IN REP. 2)
FT	CONFLECT	493	R -> Y (IN REP. 2)
FT	CONFLECT	502	R -> G (IN REP. 2)
FT	CONFLECT	503	H -> M (IN REP. 2)
FT	CONFLECT	516	H -> T (IN REP. 2)
SEQUENCE	527 AA; 5914 MW; 3283AF90CE9454A CRC64;		

Oy 5 CAGS-EETRTVIGNMGVYIPEDDPDNDNOIOLAPSSKSNNDNDLTIRPGRITSSNS 63  
 Db 266 CSRRSEPTPIAGSNMGCAVDYDHDYNGNRIRIMZCKDRIENEDLTWIKSKPIISNRK 123  
 Oy 6 GTTGTGTGATGATIPEDNINRABETWQINQNTIPSNLYKASSGICITLYOT 353  
 Db 328 CTTGGVAGRNWYIDPCTSAVKEATWEMQNTIIPKSAIVYLAASSSGGILVOT 387  
 Oy 124 IDPTLGGGMAMNTPETRTVIGFRLCMESNGSSWVETDISSQNGOKALYADGS1 183

[illegible]







FT VARIANT 231 231 N -> S OR T.  
 FT VARIANT 231 233 NGI -> KSP.  
 FT VARIANT 232 235 GLAM -> SLAM.  
 SQ SEQUENCE 264 AA; 28981 MW; 7DDDC326CCEFF5A4 CRC64;  
 Query Match 99.1%; Score 1403; DB 1; Length 264;  
 Best Local Similarity 99.9%; Pred. No. 9,9e-114;  
 Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVTCSASBPFTVIVGNKRVVADDDPHDQNIQIOLPSSKNDPQOLMTIKEDITRS 60  
 DB 1 DVTCSASBPFTVIVGNKRVVADDDPHDQNIQIOLPSSKNDPQOLMTIKEDITRS 60  
 QY 61 NSGCLTGYGTAQYVWTFPCNANREKATINQINQINPSNIVLAASGIGKTTLT 120  
 DB 61 NSGCLTGYGTAQYVWTFPCNANREKATINQINQINPSNIVLAASGIGKTTLT 120  
 QY 121 VOTLPTLGGWLNAGNDPAPREVTYGFPHLCMESNGSVVETCDSSQKQWALYGD 180  
 DB 121 VOTLPTLGGWLNAGNDPAPREVTYGFPHLCMESNGSVVETCDSSQKQWALYGD 180  
 QY 121 VOTLPTLGGWLNAGNDPAPREVTYGFPHLCMESNGSVVETCDSSQKQWALYGD 180  
 DB 121 VOTLPTLGGWLNAGNDPAPREVTYGFPHLCMESNGSVVETCDSSQKQWALYGD 180  
 QY 181 GSIRPKQNDQCLTSGRDSVSTVIVSCGASGSGQWTFNEGALINLQSLMTVVAQA 240  
 DB 181 GSIRPKQNDQCLTSGRDSVSTVIVSCGASGSGQWTFNEGALINLQSLMTVVAQA 240  
 QY 241 NPTLRITIIYPAKGRNOMLPPF 264  
 DB 241 NPTLRITIIYPAKGRNOMLPPF 264  
 QY 241 NPTLRITIIYPAKGRNOMLPPF 264  
 DB 241 NPTLRITIIYPAKGRNOMLPPF 264

RESULT 2  
 RICI RICCO STANDARD; PRT; 576 AA.  
 AC P02879; P02880;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-APR-1987 (Rel. 05, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE RICI precursor (contains: Ricin A chain (traA N-glycosidase)  
 EC 3.2.2.21)  
 OS Ricinus communis (Castor bean)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucoside I; Malpighiales; Euphorbiaceae; Ricinus.  
 OX NCBI\_TaxID:3988;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=86067214; PubMed=2999712;  
 RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,  
 RA Weaver R.F.,  
 RA "Genomic cloning and characterization of a ricin gene from Ricinus  
 RT communis"  
 RT Nucleic Acids Res. 13:8019-8033(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=9163016; PubMed=1371405;  
 RA Tregear J.W., Roberts L.M.;  
 RA "The lectin gene family of Ricinus communis: cloning of a functional  
 RT ricin gene and three lectin pseudogenes."  
 RT Plant Mol. Biol. 18:515-525(1992).  
 RN [3]  
 RP SEQUENCE OF 12-576 FROM N.A.  
 RA MEDLINE=85179479; PubMed=3839723;  
 RA Lamb A., Roberts L.M., Lord J.M.;  
 RA "Nucleotide sequence of cloned cDNA coding for preproricin."  
 RT Eur. J. Biochem. 148:265-270(1985).  
 RN [4]  
 RP SEQUENCE OF 36-302.  
 RA Yoshitake S., Punatsu G., Punatsu M.;  
 RA "Isolation and sequences of peptic peptides, and the complete  
 RT sequence of the chain of ricin-D."  
 RT Agric. Biol. Chem. 42:1267-1274(1978).  
 RN [5]  
 RP SEQUENCE OF 315-576.

RA Punatsu G., Kimura M., Punatsu M.;  
 RA "Primary structure of A1a chain of ricin D."  
 RT Agric. Biol. Chem. 43:2221-2224(1979).  
 RN [6]  
 RP SEQUENCE OF 1-1000.  
 RA MEDLINE=90146223; PubMed=136817;  
 RA Kimura Y., Kusnoku H., Tada M., Takagi S., Punatsu G.;  
 RA "Structural analyses of sugar chains from ricin A-chain variant."  
 RT Agric. Biol. Chem. 54:157-162(1990).  
 RN [7]  
 RP REVIEW.  
 RA MEDLINE=21480122; PubMed=11595634;  
 RA Olsnes S., Kozlov D.V.;  
 RA "Ricin." 39:1723-1728(2001).  
 RN [8]  
 RP TOXICOLOGY.  
 RA MEDLINE=9152004; PubMed=1881881;  
 RA Katzin B.U., Collins E.J., Robertus J.D.;  
 RA "Structure of ricin A-chain at 2.5 A."  
 RT Proteins 10:251-259(1991).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
 RA MEDLINE=9152004; PubMed=1881881;  
 RA Katzin B.U., Collins E.J., Robertus J.D.;  
 RA "Structure of ricin A-chain at 2.5 A."  
 RT Proteins 10:251-259(1991).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.  
 RA MEDLINE=9152005; PubMed=1881882;  
 RA Rutember E., Robertus J.D.;  
 RA "Structure of ricin B-chain at 2.5-A resolution."  
 RT Proteins 10:260-269(1991).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.  
 RA MEDLINE=95082010; PubMed=7991030;  
 RA Weston S.A., Tucker A.D., Thatchar D.R., Deshpande D.T.,  
 RA "Crystal structure of recombinant ricin A-chain at 1.8-A resolution."  
 RT J. Mol. Biol. 244:410-422(1994).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.  
 RA MEDLINE=96374222; PubMed=8780513;  
 RA Day P.J., Ernst S.R., Frankel A.B., Monzingo A.F., Pascal J.M.,  
 RA Molina-Svane M.C., Robertus J.D.;  
 RA "Structure and activity of an active site substitution of ricin A  
 RT chain."  
 RT Biochemistry 35:11098-11103(1996).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
 RA MEDLINE=97240820; PubMed=9086280;  
 RA Yan X., Rojils T., Svane M., Day P., Monzingo A.F., Milne G.W.,  
 RA Robertus J.D.;  
 RA "Structure-based identification of a ricin inhibitor."  
 RT J. Mol. Biol. 266:1043-1049(1997).  
 RN [14]  
 RP MUTAGENESIS.  
 RA MEDLINE=9165632; PubMed=1287657;  
 RA Kim Y., Robertus J.D.;  
 RA "Analysis of several key active site residues of ricin A chain by  
 RT mutagenesis."  
 RT Protein Eng. 5:775-779(1992).  
 RN [15]  
 RP FUNCTION.  
 RA "Ricin is highly toxic to animal cells and to a less  
 CC extent to plant cells. The A chain is responsible for inhibiting  
 CC protein synthesis through the catalytic inactivation of 60S  
 CC ribosomal subunits. It acts as a glycosidase that removes a  
 CC specific adenine residue from an exposed loop of 28S ribosomal  
 CC RNA. As this loop is involved in the binding of elongation  
 CC factors, the modified ribosomes are unable to support protein  
 CC synthesis. The A chain can inactivate a few thousand ribosomes  
 CC per minute, thus inactivating them faster than the cell can make  
 CC new ones. A single A-chain molecule can therefore kill an animal



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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 4.53677 Seconds

2736.539 million cell updates/sec

Title: US-09-601-667C-11  
Docket# 1412

Sequence: 1 DVTCSASEPTVRIVGRNGM.....RRIITYPATGKPNQMWLPVF 264

Scoring table: BLOSUM62

Gapor 1.0.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

1st time first 43

Database : SwissProt 41:\*

Database : Sw1ssProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	94.00	89.7	256	1	MEZ_VISAL	P81890 VISUM album
2	94.00	89.7	256	1	MEZ_VISAL	P81890 VISUM album
3	94.00	89.7	256	1	MEZ_VISAL	P81890 VISUM album
4	77.5	55.0	54.4	1	ABRI_ABRIC	P11140 abricus com
5	75.9	54.0	54.4	1	ABRI_ABRIC	P06750 abricus com
6	75.9	54.0	54.4	1	ABRI_ABRIC	P06750 abricus com
7	52.5	37.2	56.3	1	NIGB_SAMI	P28590 abrus precac
8	12.5	8.9	47.7	1	NIGB_SAMI	P3143 seminus albe
9	11.5	8.2	47.5	1	ABRI_STRO	P26545 streptococcy
10	11.5	8.2	47.5	1	ABRI_STRO	O51611 streptococcy
11	11.4	8.1	48.1	1	ABRI_STRO	O51611 streptococcy
12	11.5	7.9	49.5	1	ABRI_STRI	P36463 streptococcy
13	11.1	7.8	49.5	1	ABRI_STRI	O06308 streptococcy
14	9.8	6.9	61.2	1	PAG3_CHEE	P34678 caenorhabdit
15	9.5	6.9	61.2	1	PAG3_CHEE	P34678 caenorhabdit
16	9.2	6.5	40.74	1	PERD_HUMAN	P28351 aspergillusni
17	9.2	6.5	40.74	1	PERD_HUMAN	O87c9c homo sapien
18	9.2	6.5	40.74	1	PERD_HUMAN	O87c9c homo sapien
19	9.1	6.6	80.0	1	CAOF_XENLA	P33148 xenopus laevis
20	9.1	6.6	80.0	1	CAOF_XENLA	O99832 xenopus laevis
21	9.0	6.4	123.1	1	PMOC_CULIN	P19631 culicampyla p
22	89.5	6.3	115.7	1	XNBA_THESA	P19517 thesia
23	89.5	6.3	125.5	1	RPOD_CYAPA	P48100 cyamopsis
24	88.5	6.2	157.7	1	HLVA_PROMI	P14566 proteus mirab
25	87.5	6.2	156.6	1	Y1Y6_AMAPA	O91911 anabaena sp
26	86.5	6.1	126.1	1	Y2Z3_ZANSA	O60282 methanococci
27	86.6	6.1	256	1	ELTA_FAT	P00773 xelutis moyi
28	85.2	6.0	152.1	1	FUDR_SALTY	P18972 salinella
29	85.2	6.0	152.1	1	FUDR_SALTY	P18972 salinella
30	84.5	6.0	230.1	1	FLID_ECOLI	O13225 bacillus th
31	84.5	6.0	230.1	1	FLID_ECOLI	P75936 escherichia
32	84.5	6.0	230.1	1	FLID_ECOLI	P14539 escherichia
33	83.5	5.9	169.3	1	PAB2_AYATH	P42751 arabidopsis
34	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
35	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
36	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
37	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
38	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
39	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
40	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
41	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
42	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
43	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
44	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
45	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
46	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
47	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
48	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
49	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
50	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
51	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
52	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
53	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
54	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
55	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
56	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
57	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
58	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
59	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
60	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
61	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
62	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
63	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
64	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
65	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
66	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
67	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
68	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
69	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
70	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
71	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
72	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
73	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
74	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
75	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
76	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
77	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
78	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
79	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
80	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
81	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
82	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
83	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
84	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
85	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
86	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
87	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
88	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
89	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
90	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
91	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
92	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
93	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
94	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
95	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
96	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
97	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
98	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
99	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus
100	83.5	5.9	169.3	1	Y1Y3_STNY3	O55553 synecoccus

## ALIGNMENTS

RESULT 1			
ID	MIB_VISUAL	STANDARD:	PRT: 264 AA.
D1	28-RB-2003 (Ref. 41, Created)		
D7	28-RB-2003 (Ref. 41, last sequence update)		
D7	28-RB-2003 (Ref. 41, last annotation update)		
D7	15-SBP-2003 (Ref. 42, last annotation update)		
D5	Galactose specific lectin I B chain (MUB) (ML-I-B).		
D5	Viscum album (European mistletoe).		
OC	Ephemeroptera; Veliidae; Planidae; Streptoptycha; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Santalales; Santalaceae; Viscum.		
RX	NBFI_Taxid39372;		
RX	SEQUENCE		
RX	MBDLINE=982895975; PubMed=9618255;		
AT	Soler M.H., Scola S., Voelter W.;		
AT	"Complete amino acid sequence of the B chain of mistletoe lectin I."		
RL	Biochem. Biophys. Res. Commun. 246:156-161(1998).		
CC	-I- FUNCTION: The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits by removing adenine from position 4,324 of 28S rRNA. The B chain binds to cell receptors and probably facilitates the entry of the whole molecule into the cell nucleus. Both chains are also responsible for cell agglutination (lectin activity).		
CC	-II- SIGNIFI: Disulfide-linked dimer of A and B chains.		
CC	-I- PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.		
CC	-I- MISCELLANEOUS: Several isoforms of MUB exist.		
CC	Similarity: Contains 2 ricin B-type lectin domains.		
DR	PDB: 1CE7; 2O-VAR-00.		
DR	PDB: 2MLT; 2O-VAR-00.		
DR	InterPro: IPRO001772; Ricin B lectin.		
DR	Pfam: PF00652; Ricin B lectin; 6.		
DR	SMART: SM00458; Ricin B lectin; 2.		
KM	Plant defense; Glycoprotein; Lectin; Repeat; 3D-structure.		
FM	DOMAIN		
FM	DOMAIN 1	136	135
FM	DOMAIN 2	136	135
FT	BINDING	236	238
FT	BINDING	5	5
FT	DISULFID	64	64
FT	DISULFID	152	165
FT	DISULFID	192	209
FT	CARBOND	61	61
FT	CARBOND	136	136
FT	VARIANT	18	18
FT	VARIANT	56	56
FT	VARIANT	157	157
FT	VARIANT	195	195
FT	VARIANT	224	224
G -> Y.			

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DB 309 GDCGLDAGTNGSNVQIVSCMGNDK--WHLSSGSGVYVSGSLGLDANVGNNTKNTL 366  
QY 119 LTVQTLIDYVIGQM 132  
DB 367 IOLYTCNSGNSGEM 380

RESULT 14  
T35697  
arabinofuranosidase - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 03-Dec-1999  
C/Accession: T35697  
R/Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1998  
A/Reference number: T35697  
A/Accession: T35697  
A/Status: preliminary; translated from GB/EMBL/DDB  
A/Molecule type: DNA  
A/Residues: 1-475 <MIR>  
A/Cross-references: EMBL:AL021411; PDB:CAL6183.1; GSPDB:GN00070; SCSDB:SC7H1.02  
A/Experimental source: strain A3(2)  
C/Genetics:  
A/Genes: abf; SCSDB:SC7H1.02

Query Match 8.28; Score 115.5; DB 2; Length 475;  
Best local similarity 24.18; Fred No. 0.054;  
Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;  
QY 6 SASPEPTVIVGNKGRVDDPDHGNOLMPSKSNDDNQLWTIKDGTIRSKG-SC 64  
DB 37 AAGSGALRGAGSNRC-LDVLGSGQDGLALQLYDCMGCT--NOCWTSTDTGALVYGDKC 93  
QY 65 LTVGYTAA--GYVWIPDGNTRAVENTWQINDWETINPSNLY-AASGC-IKGTTLT 120  
DB 94 LDVGGHAPETRVQVWISGSGANQ--WRNSDGVGVESGLRAGAGATNTAVQ 151  
QY 121 VQTLIDYVIGQMAGNTPAREVT-----LYGPRDLCSNGSGVWETCD-SQGNCK 174  
DB 152 LMTONGGNGQVWGLNTPPTDGTALPPTVANSSTGVLAQPSGVALKDKPTTYHGR 211  
QY 175 WALYDGS-----IRKONODCTSGRDSVS 201  
DB 212 HLYVGTSSSSSYGKVFSPFTNWDMAAGQNNRN 247

RESULT 15  
T35943  
probable hydrolytic protein - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C/Accession: T35943  
R/Seeger, K.J.; Hartle, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1999  
A/Reference number: T35943  
A/Accession: T35943  
A/Status: preliminary; translated from GB/EMBL/DDB  
A/Molecule type: DNA  
A/Residues: 1-464 <SEB>  
A/Cross-references: EMBL:AL035206; PDB:CAA22765.1; GSPDB:GN00070; SCSDB:SC9B5.23c  
A/Experimental source: strain A3(2)  
C/Genetics:  
A/Genes: SCSDB:SC9B5.23c

Query Match 8.13; Score 114; DB 2; Length 464;  
Best local similarity 28.13; Fred No. 0.07;  
Matches 38; Conservative 27; Mismatches 52; Indels 18; Gaps 8;  
QY 139 APREV---TVGF-RDLCSNGSGVW-----VETCSQKQKQWALYVDSGIRPKN 186  
DB 332 AEPVAPGVITVYGHNSRCIEV--AGHKVRDGAFLQIDCTGRKWKQVDFPDGTR--S 387  
QY 189 QPQCL--TSRDSVSTVIVVSGSGSGSQRWFTNBNALNLSLMDVA--QANPKLR 245

DB 388 LGLDNDATNGSTANGTVQVAVCSG-HPAQPTIAGPRDLVWQNKCTVDVEKTNAGA 446  
QY 246 RIIIVPATKPKPKM 260  
DB 447 RLQWESGRDVKM 461

Search completed: December 11, 2003, 13:55:46  
Job time: 9.20622 secs



## RESULT 8

abrin-c precursor - Indian licorice

N:Contains: RNA N-glycosidase (EC 3.2.2.22)

C:Species: *Morus precatensis* (Indian licorice)

C:Accession: S16022 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999

R:Wood, K.A.; Lord, J.M.; Wawrzyniak, E.U.; Platak, M.

Eur. J. Biochem. 198, 723-732, 1991

A:Title: Preproabrin: genomic cloning, characterization and the expression of the A-chain

A:Reference number: S16022; MIMD:91266957; PMID:2050149

A:Accession: S16022

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: EMBL:X55667; NID:G16084; PIRN:CA39202.1; PIR:G16085

C:Comment: Abirin consists of an A chain, which inhibits protein synthesis by inactivating

The A and B chains are linked by a single disulfide bond, which is essential for toxicity

C:Superfamily: ricin; RNA N-glycosidase homology

C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid

F:35-285/Product: abrin-c chain A #status predicted &lt;ACH&gt;

F:41-280/Domain: RNA N-glycosidase homology &lt;RNG&gt;

F:295-352/Product: abrin-c chain B #status predicted &lt;BCH&gt;

F:11-353/Region: 40-residue repeats

F:106-147/Region: carboxylic acid (Glu, Asn) #status predicted

F:139-201/Active site: Glu, Asn #status predicted

F:234-287/395-435/Binding site: carboxylate (Asn) (covariant) #status predicted

F:281-303/320-339/363-380/451-464/490-507/Disulfide bonds: #status predicted

F:322-346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 54.0%; Score 765; DB 2; Length 562;

Best Local Similarity 54.4%; Pred. No. 1.8e-56;

Matches 142; Conservative 46; Mismatches 71; Indels 2; Gaps 2;

5 GSAS-EPYVAVGKMGVYRDQDPHGNQQLMPSKSNQNDQMTKSDKTRISNGS 63

303 CSRYEPTVRIIGSDGKCVDDYDGHNGRILIMKCKDLRLENDQLTKSDKTRISNGK 362

64 CLTYGTAGVYVIMPCDINAVERTIWIINDGTINPISNVLAAASGIKGTLTVQT 123

363 CLTGTGAPENYVIMVICTSVALENTWEIMDNTIIPKSAVLVAESSWGCTIVQT 422

124 LDYTGAGTANQAPRRTVTCGRTCSNGSWRTCSQNGKQKMLVQDSI 183

423 NEYLMGQKRTGNTSPFTSISGVSDLCQAGSNMVLACDNKKEQ-QMLVYDSSI 481

184 RPKQNDQCLTSGRDSVSTVINIVSGSAGSOSQWTFNEGALILKNSLWVDAQAPK 243

482 RSVNTNNCLTSKDHKQSPVLMASGMSQSMFLKNDISYVLDNDWVQKSDPS 541

244 LKRLITVATGNGQKMLPVF 264

542 LKRLITVATGNGQKMLPVF 562

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

A:Cross-references: DB:W93346

R:Hung, C.; Lee, M.; Lee, T.; Lin, J.

submitted to the EMBL Data Library, March 1993

A:Reference number: S34408

A:Accession: S34408

A:Molecule type: mRNA

A:Residues: 1-169; C: 171-320; T: 322-528 #HD2

C:Comment: Abirin consists of an A chain, which inhibits protein synthesis by inactivating

The A and B chains are linked by a single disulfide bond, which is essential for toxicity

C:Superfamily: ricin; RNA N-glycosidase homology

C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin

F:1-251/Product: abrin-d chain A #status predicted &lt;ACH&gt;

F:7-246/Domain: RNA N-glycosidase homology &lt;RNG&gt;

F:281-328/Product: abrin-d chain B #status predicted &lt;BCH&gt;

F:1283-328/326-366/403-449/414-449/419-452/Region: 40-residue repeats

F:106-147/Region: carboxylic acid (Glu, Asn) #status predicted

F:134-167/Active site: Glu, Asn #status predicted

F:200-253/361-401/402/Binding site: carboxylate (Asn) (covariant) #status predicted

F:247-269/320-346/417-430/456-473/Disulfide bonds: #status predicted

F:289-312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:500-521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 54.0%; Score 764; DB 2; Length 528;

Best Local Similarity 54.4%; Pred. No. 1.8e-56;

Matches 142; Conservative 47; Mismatches 70; Indels 2; Gaps 2;

5 GSAS-EPYVAVGKMGVYRDQDPHGNQQLMPSKSNQNDQMTKSDKTRISNGS 63

269 CSRYEPTVRIIGSDGKCVDDYDGHNGRILIMKCKDLRLENDQLTKSDKTRISNGK 328

64 CLTYGTAGVYVIMPCDINAVERTIWIINDGTINPISNVLAAASGIKGTLTVQT 123

329 CLTGTGAPENYVIMVICTSVALENTWEIMDNTIIPKSAVLVAESSWGCTIVQT 388

124 LDYTGAGTANQAPRRTVTCGRTCSNGSWRTCSQNGKQKMLVQDSI 183

389 NEYLMGQKRTGNTSPFTSISGVSDLCQAGSNMVLACDNKKEQ-QMLVYDSSI 447

184 RPKQNDQCLTSGRDSVSTVINIVSGSAGSOSQWTFNEGALILKNSLWVDAQAPK 243

448 RSVNTNNCLTSKDHKQSPVLMASGMSQSMFLKNDISYVLDNDWVQKSDPS 507

244 LKRLITVATGNGQKMLPVF 264

508 LKRLITVATGNGQKMLPVF 528

Db

Qy

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Qy

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Qy

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506330  
Ricin E - castor bean (fragment)  
N:Contains: chain B: rRNA N-glycosidase (EC 3.2.2.22) (chain A)  
C:Species: Ricinus communis (castor bean)  
C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 20-Aug-1999  
A:Accession: S06330; J05381  
R:Plant Mol. Biol. 9, 287-295, 1987  
P:Plant Mol. Biol. 9, 287-295, 1987  
A:Title: Characterization of a cDNA encoding ricin E, a hybrid ricin-Ricinus communis ag  
A:Accession: S06330  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-263 <LAD>  
A:Cross-references: EMBL:M17631; NID:G169714; PIRN:AA63506.1; PTD:G169715  
B:J. Biol. Chem. 263, 191-200, 1987  
R:Plant. Biophys. Acta 911, 191-200, 1987  
A:Title: The complete amino acid sequence of the B-chain of ricin E isolated from small  
A:Reference number: J05381; MIMD:87101186; PMID:3801493  
A:Accession: J05381  
A:Molecule type: protein  
A:Residues: 1-69, 'P8', '72-209', 'A', '211-241', '243-250', 'V', '252-263 <ABA>  
A:Experimental source: seed  
A:Superfamily: ricin; rRNA N-glycosidase homology  
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase  
E:1-263/Product: ricin E chain B status experimental <BCH> residue repeats  
F:20-39, 61-80, 151-164, 190-207/Binding site: predicted  
F:95, 115/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 61.5%; Score 871; DB 2; Length 263;  
Best Local Similarity 61.3%; Pred. No. 7,66-66;  
Matches 160; Conservative 38; Mismatches 61; Indels 2; Gaps 2;

QY 5 GSASEPTATVGRNKRVDVDDPHDQICLPKSGNDPQVLTIKDQITRSNGC 64  
DB 4 CMDDPVTYKLSGKGLDVGKGRFRKSNIDLPKCSNDPQVLTIKDQITRSNGC 63  
QY 65 LITVYGTAGVYVMPDONTAVBEKTIWQINDGIIINPSNVLAASSGKATLVQY 124  
DB 64 LITVYGTAGVYVMPDONTAVBEKTIWQINDGIIINPSNVLAASSGKATLVQY 123  
QY 125 DYLGGSMAMNDTPREVITVGRNDLQMSNGSGVWETDSSQKQKQKALYGGSI 184  
DB 124 IYVSGQMLPNTVPEVITVGRNDLQMSNGSGVWETDSSQKQKQKALYGGSI 182  
QY 185 PKNQDQCLTSGSDVSTVYINVSQSGSGSRVPTNKGALINIKQSLMYVVAQANR-K 243  
DB 183 PKNQDQCLTSGSDVSTVYINVSQSGSGSRVPTNKGALINIKQSLMYVVAQANR-K 242  
QY 244 LERITVPTKGNQKQMTLTP 264  
DB 243 LKQITVHPKSNLQMTLTP 263

RESULT 5  
T2LSA  
Abirin-a precursor - Indian licorice (fragment)  
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Abrus precatorius (Indian licorice)  
C>Date: 31-Dec-1993 #sequence\_revision 01-Aug-1997 #text\_change 16-Jul-1999  
R:Plant Mol. Biol. 9, 287-295, 1987  
P:Plant Mol. Biol. 9, 287-295, 1987  
A:Title: Primary structure of three distinct isoforms determined by cDNA sequencing  
A:Accession: S32429; MIMD:93132798; PMID:8421313  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-263 <LAD>  
A:Cross-references: CB:089344; NID:G169714; PIRN:AA63506.1; PTD:G169715  
A:Note: the coding region for the sequence shown is preceded by an ATG codon  
A:Note: residues 1-8 were derived from the synthesized primer

R:Plant Mol. Biol. 9, 287-295, 1987  
P:Plant Mol. Biol. 9, 287-295, 1987  
A:Title: The complete amino acid sequence of the A-chain of abirin-a, a toxic protein  
A:Reference number: J02022  
A:Accession: J02022  
A:Molecule type: protein  
A:Residues: 1-201, 203-251 <FNU>  
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we  
R:Kjelson, G.; Mathiesen, E.; Sjaastad, A.  
A:Title: Direct molecular cloning and expression of two distinct abirin A-chains.  
A:Reference number: A39761; MIMD:91201323; PMID:2016300  
A:Accession: A39761  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-2, 2-251 <EVE>  
A:Cross-references: DB:024872  
R:Kjelson, G.; Mathiesen, E.; Sjaastad, A.  
A:Title: The complete amino acid sequence of the B-chains of abirin-a and abirin-b, tox  
A:Reference number: J01398; MIMD:93169023; PMID:7763422  
A:Accession: J01398  
A:Status: seeds  
A:Molecule type: protein  
A:Residues: 261-341, 'T', '349-351', 'A', '353-357', 'V', '359-528 <KIN>  
A:Experimental source: seed  
A:Superfamily: ricin; rRNA N-glycosidase homology  
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglycamic acid  
E:1-263/Product: ricin E chain B status experimental <BCH> residue repeats  
F:20-39, 61-80, 151-164, 190-207/Binding site: predicted  
F:95, 115/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 55.0%; Score 779; DB 1; Length 528;  
Best Local Similarity 55.2%; Pred. No. 1e-57;

RESULT 5  
T2LSA  
Abirin-a precursor - Indian licorice (fragment)  
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Abrus precatorius (Indian licorice)  
C>Date: 31-Dec-1993 #sequence\_revision 01-Aug-1997 #text\_change 16-Jul-1999  
R:Plant Mol. Biol. 9, 287-295, 1987  
P:Plant Mol. Biol. 9, 287-295, 1987  
A:Title: Primary structure of three distinct isoforms determined by cDNA sequencing  
A:Accession: S32429; MIMD:93132798; PMID:8421313  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-263 <LAD>  
A:Cross-references: CB:089344; NID:G169714; PIRN:AA63506.1; PTD:G169715  
A:Note: the coding region for the sequence shown is preceded by an ATG codon  
A:Note: residues 1-8 were derived from the synthesized primer







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[illegible]

Search completed: December 11, 2003, 14:11:35  
Job time : 9.14026 secs

Thu Dec 11 16:09:45 2003

us-09-601-667c-10.ra1

Page 7

QY 56 GTRISNG-SCLTGYGYWVIFPCNTAVREATTWOIMNGTINPNSLVAA--SS 112  
DB 411 GELAVYVKCLDPAAGTNSNSVQVYISCGWGDHOK--WRINSDSVGVSGCLDAVNG 468  
QY 113 GIKGTYLVQTLDTYLGQGM 132  
DB 469 TANGTILQVTCNSGNRW 488

RESULT 14

US-09-770-621-8  
Sequence 8, Application US/09770621

Patent No. 6506593

GENERAL INFORMATION:  
APPLICANT: M RYU, Arja

APPLICANT: Peltamäki, Jari

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Maria

APPLICANT: Suominen, Marko

APPLICANT: Lantinen, Taina

NUMBER OF SEQUENCES: 39

TITLE OF INVENTION: Production and secretion of proteins of

CORRESPONDENCE ADDRESS:

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,621

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/590,563

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/332,412

FILING DATE: 31-OCT-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/282,001

FILING DATE: 29-JUL-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Raimo Lantto, Esq.

REGISTRATION NUMBER: 1050.0340003

REFERENCE/DOCKET NUMBER: 1050.0340003

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 491 amino acids

STRANDEDNESS: No

STRUCTURE: linear

MOLECULE TYPE: peptide

POSITION IN GENOME:

CHROMOSOME/SEGMENT: M64551

US-09-770-621-8

Query Match

Best Local Similarity 8.64; Score 122.5; DB 4; Length 491;

Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

QY 7 ASP-----TVATVGRNGHVDVDDPHQDQGLQMPKSNNDNQGLTIKED 55  
DB 354 SSSPXXXXXXXXXADGGQIKNG--SGKCLDPAFASDGLQGLMDCHSGT--NQWMAATDA 410  
QY 56 GTRISNG-SCLTGYGYWVIFPCNTAVREATTWOIMNGTINPNSLVAA--SS 112  
DB 411 GELAVYVKCLDPAAGTNSNSVQVYISCGWGDHOK--WRINSDSVGVSGCLDAVNG 468  
QY 113 GIKGTYLVQTLDTYLGQGM 132  
DB 469 TANGTILQVTCNSGNRW 488

RESULT 15

US-08-468-812-4  
Sequence 4, Application US/08468812

Patent No. 6506593

GENERAL INFORMATION:  
APPLICANT: Vahmanper, Jari

APPLICANT: M RYU, Arja

APPLICANT: Peltamäki, Jari

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Maria

APPLICANT: Suominen, Marko

APPLICANT: Lantinen, Taina

NUMBER OF SEQUENCES: 25

TITLE OF INVENTION: of the

CORRESPONDENCE ADDRESS:

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,812

FILING DATE: 06-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/332,412

FILING DATE: 31-OCT-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/282,001

FILING DATE: 29-JUL-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Raimo Lantto, Esq.

REGISTRATION NUMBER: 1050.0340002

REFERENCE/DOCKET NUMBER: 1050.0340002

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 491 amino acids

STRANDEDNESS: No

STRUCTURE: linear

MOLECULE TYPE: protein

POSITION IN GENOME:

CHROMOSOME/SEGMENT: M64551

US-08-468-812-4

Query Match

Best Local Similarity 8.64; Score 122.5; DB 2; Length 492;

Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;

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Page 6

Db 437 CWMANOK--WELRADOTIVGSGCLDAVGGTANGTFLQ 476

RESULT 12  
US-08-468-812-8  
Sequence 8, Application US/08468812  
Patent No. 5950563  
GENERAL INFORMATION:  
APPLICANT: Vahmampet, Jari  
APPLICANT: M nyl, Arja  
APPLICANT: Pagersen m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Paloheimo, Marja  
APPLICANT: Suominen, Pirkko  
APPLICANT: Lahtinen, Tarja  
APPLICANT: Kristo, Paula  
TITLE OF INVENTION: Actinomadura xyloanae Sequences and Methods  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLSTEIN & FOX  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: US/08/468,812  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 05-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Larry B.  
REGISTRATION/DOCKET NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050,0340002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: M64551  
US-08-468-812-8

Query Match 8.6%; Score 122.5; DB 2; Length 491;

Best Local Similarity 28.6%; Pred. No. 0.00035;

Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

Db 354 SSSPXXXXXXXXXADGGQIKGVG-SGRCLDVPDASTGTSOTQJLMDCHSGT--NQWAAITDA 410  
QY 56 GTIRANG-SCLTYGTAGYVWIPDCNVAENETIMQIMNGTITMPSNIVAA--SS 112  
DB 411 GELRYADKCLDAAGTSGNSKVOIYSCWGDNOK--WELNSDGVYGVSGCLDAVNG 468

QY 113 GIKETITVOTLDTYLOGGM 132  
DB 469 TANGTILCLYTCNSNGRM 488

RESULT 13  
US-08-590-563-8  
Sequence 8, Application US/08590563  
Patent No. 6300114  
GENERAL INFORMATION:  
APPLICANT: Vahmampet, Jari  
APPLICANT: M nyl, Arja  
APPLICANT: Pagersen m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Paloheimo, Marja  
APPLICANT: Suominen, Pirkko  
APPLICANT: Lahtinen, Tarja  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 08/08/590,563  
APPLICATION NUMBER: 536  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/468,812  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 05-JUN-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION/DOCKET NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050,0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: M64551  
US-08-590-563-8

Query Match 8.6%; Score 122.5; DB 4; Length 491;

Best Local Similarity 28.6%; Pred. No. 0.00035;

Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

Db 354 SSSPXXXXXXXXXADGGQIKGVG-SGRCLDVPDASTGTSOTQJLMDCHSGT--NQWAAITDA 410  
QY 56 GTIRANG-SCLTYGTAGYVWIPDCNVAENETIMQIMNGTITMPSNIVAA--SS 112  
DB 411 GELRYADKCLDAAGTSGNSKVOIYSCWGDNOK--WELNSDGVYGVSGCLDAVNG 468

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Page 5

Db 437 CWGANOK-WELPADGTVGVSGLCLAVGSGTNRKQ 476

RESULT 10  
US-08-590-563-5  
Sequence 5, Application US/0850563  
PATENT INFORMATION:  
GENSEL INFORMATION:  
APPLICANT: M nyl, Arja  
APPLICANT: Vehmampet, Jari  
APPLICANT: Paegerst m, Richard  
APPLICANT: Lantto, Ralja  
APPLICANT: Palohelmo, Maria  
APPLICANT: Suominen, Pirkko  
APPLICANT: Lantinen, Tarja  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSER: STEPHEN KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,563  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/468,812  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugelsky, Lawrence B.  
REGISTRATION NUMBER: 35,085  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 480 amino acids  
TYPE: amino acid  
STRANDNESS: no. 6506593 Relevant  
MOLECULE TYPE: linear  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50

Query Match 8.6%; Score 122.5; DB 4; Length 480;  
Best Local Similarity 32.4%; Pred. No. 0.00034;  
Matches 33; Conservative 16; Mismatches 46; Indels 5; Gaps 3;

Qy 22 VYRDDPHGNGTGLWPKSKNDPQVLTIRKGTIRSNQS-CLTYGYTGYVIMFD 80  
Db 379 IDVPMKNTADGTVQVGLDCHSGS--NQWTYSSGEFRIFKWKLDAGSSSGAVVYIS 436  
Qy 81 CNTAVKATWQIWNQGTIIPRSNLVLAASGKRTLTQ 122

Db 437 CWGANOK-WELPADGTVGVSGLCLAVGSGTNRKQ 476

RESULT 11  
US-09-770-621-5  
Sequence 5, Application US/09770621  
PATENT INFORMATION:  
GENSEL INFORMATION:  
APPLICANT: M nyl, Arja  
APPLICANT: Vehmampet, Jari  
APPLICANT: Paegerst m, Richard  
APPLICANT: Lantto, Ralja  
APPLICANT: Palohelmo, Maria  
APPLICANT: Suominen, Pirkko  
APPLICANT: Lantinen, Tarja  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSER: STEPHEN KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,621  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/590,563  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugelsky, Lawrence B.  
REGISTRATION NUMBER: 35,085  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 480 amino acids  
TYPE: amino acid  
STRANDNESS: no. 6506593 Relevant  
MOLECULE TYPE: linear  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50

Query Match 8.6%; Score 122.5; DB 4; Length 480;  
Best Local Similarity 32.4%; Pred. No. 0.00034;  
Matches 33; Conservative 16; Mismatches 46; Indels 5; Gaps 3;

Qy 22 VYRDDPHGNGTGLWPKSKNDPQVLTIRKGTIRSNQS-CLTYGYTGYVIMFD 80  
Db 379 IDVPMKNTADGTVQVGLDCHSGS--NQWTYSSGEFRIFKWKLDAGSSSGAVVYIS 436  
Qy 81 CNTAVKATWQIWNQGTIIPRSNLVLAASGKRTLTQ 122

Thu Dec 11 16:09:45 2003

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Page 4

FILE REFERENCE: 4693.204-US  
CURRENT APPLICATION NUMBER: US/09/159.106  
EARLIER FILING DATE: 1998-09-23  
EARLIER APPLICATION NUMBER: 0427/96  
EARLIER FILING DATE: 1996-12-04  
EARLIER APPLICATION NUMBER: 0885/96  
EARLIER FILING DATE: 1996-08-23  
EARLIER APPLICATION NUMBER: 0427/DK97/00160  
EARLIER FILING DATE: 1997-04-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 132  
TYPE: PRT  
ORGANISM: Oerskovia xanthineolytica  
US-09-159-106-15

Query Match  
Best Local Similarity 36.6%; Score 136; DB 3; Length 132;  
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;

18 NGRVDPDDPHGNOIQIMPESKNDPVOLMTIRGOTIRNSGCTTT--GTAACT 75  
14 NMCVDVPAADPTDGNPVQIVTCSGN--AAQVTRSGDVTALCKICLDVDSSTTRAA 71  
76 VMIPTDCTAVRENTIQTIV--DNGT--IINPSNLVLAASSGI--KGTTLVQTIDYTL 128  
72 VQVWTCN-----GTGAQKMAVDKSKALRNPSGLCLDITGAGFLNDGQRLQVTCNGTT 126  
129 GCGW 132  
127 AQQW 130

RESULT 8  
US-09-159-106-11  
Sequence 11, Application US/09159106  
Patent No. 6284509  
GENERAL INFORMATION:  
APPLICANT: Petzer, Pau  
INVENTOR: Petzer, Pau  
APPLICANT: Halko, Stephen  
APPLICANT: Hedegard, Lisbeth  
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase  
FILE REFERENCE: 4693.204-US  
CURRENT APPLICATION NUMBER: US/09/159.106  
CURRENT FILING DATE: 1998-09-23  
EARLIER APPLICATION NUMBER: 0427/96  
EARLIER FILING DATE: 1996-12-04  
EARLIER APPLICATION NUMBER: 0885/96  
EARLIER FILING DATE: 1996-08-23  
EARLIER APPLICATION NUMBER: 0427/DK97/00160  
EARLIER FILING DATE: 1997-04-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 11  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Oerskovia xanthineolytica  
US-09-159-106-11

Query Match  
Best Local Similarity 36.6%; Score 136; DB 3; Length 435;  
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;

18 NGRVDPDDPHGNOIQIMPESKNDPVOLMTIRGOTIRNSGCTTT--GTAACT 75  
317 NMCVDVPAADPTDGNPVQIVTCSGN--AAQVTRSGDVTALCKICLDVDSSTTRAA 374  
76 VMIPTDCTAVRENTIQTIV--DNGT--IINPSNLVLAASSGI--KGTTLVQTIDYTL 128  
72 VQVWTCN-----GTGAQKMAVDKSKALRNPSGLCLDITGAGFLNDGQRLQVTCNGTT 429

129 GCGW 132  
430 AQQW 433

US-08-468-812-5  
Sequence 5, Application US/08468812  
Patent No. 5938836  
GENERAL INFORMATION:  
APPLICANT: Vermanier, Jari  
INVENTOR: Vermanier, Jari  
APPLICANT: Muly, Aija  
APPLICANT: Rastio, M. Richard  
APPLICANT: Rastio, Raimo  
APPLICANT: Palohelmo, Marja  
APPLICANT: Suominen, Eiriko  
APPLICANT: Lahtinen, Tarja  
APPLICANT: Kristo, Paula  
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods  
FILE REFERENCE: 4693.204-US  
CURRENT APPLICATION NUMBER: US/08/332.412  
CURRENT FILING DATE: 2003-01-28  
EARLIER APPLICATION NUMBER: 06-UD-1994  
EARLIER FILING DATE: 1996-08-23  
NUMBER OF SEQ ID NOS: 25  
CORRESPONDENCE ADDRESS:  
SHERIDAN, KESSLER, GOLDSTEIN & FOX  
ATTORNEYS  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.10  
CURRENT APPLICATION NUMBER: US/08/332.412  
CURRENT FILING DATE: 2003-01-28  
EARLIER APPLICATION NUMBER: 06-UD-1994  
EARLIER FILING DATE: 1996-08-23  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332.412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282.001  
FILING DATE: 29-JUL-1994  
TITLE OF INVENTION: Xylanase  
INVENTOR: Vermanier, Jari  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugelsky, Larry B.  
REGISTRATION NUMBER: 15 086  
REFERENCE/DOCKET NUMBER: 1050.0340002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 480 amino acids  
TYPE: amino acid  
SOURCE: not relevant  
TOPOLOGY: linear  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50  
US-08-468-812-5

Query Match  
Best Local Similarity 32.4%; Score 122.5; DB 2; Length 480;  
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;

22 VVDRDDPHGNOIQIMPESKNDPVOLMTIRGOTIRNSGCTTTGTAAGVMIPTD 80  
379 IDVPSKNDVQVQVLDVDSGS--NQQMTYSSGEFLFNKICLDAGSSNRAVVOIS 436  
81 CNVAVRENTIQTIV--DNGT--IINPSNLVLAASSGI--KGTTLVQTIDYTL 122



RESULT 2  
US-08-776-059-33  
Sequence 33, Application US/087760598  
Patent No. 6271368  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: ECK, Jürgen  
APPLICANT: AXEL, Axel  
APPLICANT: ZINKE, Rüdiger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 674503-2003  
CURRENT APPLICATION NUMBER: US/08/776, 0598  
CURRENT FILING DATE: 1999-06-19  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
EARLIER FILING DATE: 1996-06-25  
EARLIER APPLICATION NUMBER: 95109949.8  
EARLIER FILING DATE: 1995-06-26  
NUMBER OF SEQ ID NOS: 56  
SOURCE: Patentin Ver. 2.0  
SEQ ID NO 33  
LENGTH: 264  
TYPE: PRT  
ORGANISM: Viscum album  
US-08-776-059-33

Query Match 93.0%; Score 1320.5; DB 3; Length 264;  
Best Local Similarity 94.7%; Pred. No. 4, 1e-128;  
Matches 249; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 1 DNYTCSASEPTVRIYVGNMGRVDDDFHDSNQIOLMPSKSNNDPNOIATTKRGTIRS 60  
DB 2 DNYTCSASEPTVRIYVGNMGRVDDDFHDSNQIOLMPSKSNNDPNOIATTKRGTIRS 61  
QY 61 NSCLTTGYTAGYVYVIFDQNTAVREATTQIMDKGIIINRSNVLTAASGICGTTLT 120  
DB 62 NSCLTTGYTAGYVYVIFDQNTAVREATTQIMDKGIIINRSNVLTAASGICGTTLT 121  
QY 121 VQILDYTLGGMLAGNTAPREVTIYGFRLCMESNGSVWETCDSQKQKALYGD 180  
DB 122 VQILDYTLGGMLAGNTAPREVTIYGFRLCMESNGSVWETCDSQKQKALYGD 180  
QY 181 GSIRPKMODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGALINLKKGPADVQA 240  
DB 181 GSIRPKMODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGALINLKKGPADVQA 240  
QY 241 NPKLRRIIYPAATGKNQMLPV 263  
DB 241 NPKLRRIIYPAATGKNQMLPV 263

RESULT 3  
US-08-776-059-35  
Sequence 35, Application US/087760598  
Patent No. 6271368  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: ECK, Jürgen  
APPLICANT: AXEL, Axel  
APPLICANT: ZINKE, Rüdiger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
FILE REFERENCE: 674503-2003  
CURRENT APPLICATION NUMBER: US/08/776, 0598  
CURRENT FILING DATE: 1999-06-19  
EARLIER APPLICATION NUMBER: PCT/EP96/02273  
EARLIER FILING DATE: 1996-06-25  
EARLIER APPLICATION NUMBER: 95109949.8  
EARLIER FILING DATE: 1995-06-26  
NUMBER OF SEQ ID NOS: 56  
SOURCE: Patentin Ver. 2.0  
SEQ ID NO 35  
LENGTH: 564  
TYPE: PRT  
ORGANISM: Viscum album

US-08-776-059-35  
Query Match 93.0%; Score 1320.5; DB 3; Length 564;  
Best Local Similarity 94.7%; Pred. No. 1, 3e-127;  
Matches 249; Conservative 2; Mismatches 11; Indels 1; Gaps 1;  
QY 1 DNYTCSASEPTVRIYVGNMGRVDDDFHDSNQIOLMPSKSNNDPNOIATTKRGTIRS 60  
DB 302 DNYTCSASEPTVRIYVGNMGRVDDDFHDSNQIOLMPSKSNNDPNOIATTKRGTIRS 361  
QY 61 NSCLTTGYTAGYVYVIFDQNTAVREATTQIMDKGIIINRSNVLTAASGICGTTLT 120  
DB 362 NSCLTTGYTAGYVYVIFDQNTAVREATTQIMDKGIIINRSNVLTAASGICGTTLT 421  
QY 121 VQILDYTLGGMLAGNTAPREVTIYGFRLCMESNGSVWETCDSQKQKALYGD 180  
DB 422 VQILDYTLGGMLAGNTAPREVTIYGFRLCMESNGSVWETCDSQKQKALYGD 480  
QY 481 GSIRPKMODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGALINLKKGPADVQA 240  
DB 481 GSIRPKMODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGALINLKKGPADVQA 540  
QY 241 NPKLRRIIYPAATGKNQMLPV 263  
DB 541 NPKLRRIIYPAATGKNQMLPV 563

RESULT 4  
US-08-378-761A-77  
Sequence 77, Application US/08378761A  
Patent No. 5635384  
GENERAL INFORMATION:  
APPLICANT: MALSH, TERENCE A  
APPLICANT: BELL, TIMOTHY D  
APPLICANT: WILSON, ALBERT R  
TITLE OF INVENTION: BIOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: BIOSOME FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
PUBLICATION NO: 5635384  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378, 761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
ADDRESS: 9330 ZIONSVILLE ROAD, INDIANAPOLIS, IN 46228  
TELEPHONE: (317) 337-4846  
TELECOMMUNICATION INFORMATION:  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-378-761A-77  
Query Match 54.3%; Score 770.5; DB 1; Length 540;  
Best Local Similarity 55.4%; Pred. No. 2, 1e-74;  
Matches 144; Conservative 41; Mismatches 74; Indels 1; Gaps 1;





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CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
STRANDNESS: NA. US20010024815A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: M64551  
US-09-770-621-8

Query Match 8.6%; Score 122.5; DB 9; Length 491;  
Best Local Similarity 28.6%; Pred. No. 0.0007;  
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;  
QY 7 ASPP-----TWIVRNRKRVDRDDPHQVQLMPSKSNDDPQVLTIRSD 55  
DB 354 SSSPPXXXXXADGGGKNG-SGRCLDPDASISDGLMDCHSGT--NQQMALDA 410  
QY 56 GTRRANG-SCLTGYTAGVYVWIPDQNTAVREXATIMQNTIIPRSNVLAA--SS 112  
DB 411 GELRYGDKCLDAGTNGSKVQVQSCWGDNRK--WELNSDSVYVSGCLDAVNG 468  
QY 113 GIKGTLTWQNTIDVTLGGQW 132  
DB 469 TANGTILQATGCSNGSNQW 468

RESULT 15  
US-09-770-621-4  
Sequence 4, Application US/09770621  
Patent No. US20010024815A1  
GENERAL INFORMATION:  
APPLICANT: M rcy1, Arja  
APPLICANT: Velmampier, Jari  
APPLICANT: Fagerström, Richard  
APPLICANT: Lantto, Ralf  
APPLICANT: Soderlund, Maria  
APPLICANT: Soderlund, Maria  
APPLICANT: Lantto, Ralf  
TITLE OF INVENTION: Production and secretion of proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
FILING DATE: 31-OCT-1994  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,621  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/590,563  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-770-621-4

Query Match 8.6%; Score 122.5; DB 9; Length 492;  
Best Local Similarity 32.4%; Pred. No. 0.0007;  
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;  
QY 22 VVPRDDPHQVQLMPSKSNDDPQVLTIRSDS-SCLTGYTAGVYVWIPD 80  
DB 379 IYVNRNATQVQLDCHSG--NQQNTYSSEFIFRKCCLAGSSNCAVYVLS 436  
QY 81 CRTVREATIMQWMDNTIIPRSNVLAASSGIGKGTLLVQ 122  
DB 437 CWGAGNRK--WELRADDTIVGVSGCLDAVNGGTGNGTRIQ 476

Search completed: December 11, 2003, 14:48:50  
Job time: 17.0129 secs

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Db 576 SASTADAKRIQYDCN-----GTAAQWBN-----ASTQDYVNTADKCLDY 620  
Qy 127 TLGGQMLAGNDAPREVTYVGFADLCNENSGSGVWVETCSQKQKQKAL 117  
Db 621 T-----GNSA-----NBAQWNSC-TAAQO-KXKL 646

RESULT 12  
US-09-770-621-5  
Sequence 18 Application US/2013/077  
Publication No. US20030092109A1  
GENERAL INFORMATION:  
APPLICANT: Goldstein, Irwin J.  
APPLICANT: Winter, Harry C.  
APPLICANT: Kueger, Robert P.  
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin  
FILE REFERENCE: UM-07124  
CURRENT APPLICATION NUMBER: US/10/137,077  
PRIORITY FILING DATE: 2002-05-02  
PRIORITY FILING NUMBER: 60/354,596  
PRIOR FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 60/354,322  
PRIOR FILING DATE: 2002-02-04  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 18  
LENGTH: 41  
TYPE: PRT  
ORGANISM: Ricinus communis  
US-10-137-077-18

Query Match 8.84; Score 125; DB 15; Length 41;  
Best Local Similarity 53.74; Pred. No. 1.3e-05;  
Matches 22; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
Qy 224 GATLKKKGPADYVQANPKRRIITYPATCPQVQWMLPVF 264  
Db 1 GTLNLKSGALVDVPSADSDSKQIIVLPHSGPQIMLPVF 41

RESULT 13  
US-09-770-621-5  
Sequence 5, Application US/69770621  
Patent No. US20010024815A1  
GENERAL INFORMATION:  
APPLICANT: M nyl, Arja  
APPLICANT: Vehmamper, Jari  
APPLICANT: Paeester m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Lantto, Raija  
APPLICANT: Suominen, Pirko  
APPLICANT: Lantinen, Taina  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 08/09/770,621  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/590,563  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 480 amino acids  
TYPE: amino acid  
STRANDNESS: NC  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50  
US-09-770-621-5

Query Match 8.84; Score 122.5; DB 9; Length 480;  
Best Local Similarity 32.44; Pred. No. 0.00068;  
Matches 33; Conservative 16; Mismatches 49; Indels 5; Gaps 3;  
Qy 22 VVDDPDHFGNGCQLMPKSNNDPDLCTIRKDTIRNSG-CITTYGYTGYVMPD 80  
Db 379 IDVNNMADGTVQVLDYDCHGS-NOQWYSSGSEFRIPKNCIDAGSSNCAVQIYS 436

RESULT 14  
US-09-770-621-8  
Sequence 8, Application US/69770621  
Patent No. US20010024815A1  
GENERAL INFORMATION:  
APPLICANT: M nyl, Arja  
APPLICANT: Vehmamper, Jari  
APPLICANT: Paeester m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Lantto, Raija  
APPLICANT: Suominen, Pirko  
APPLICANT: Lantinen, Taina  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 08/09/770,621  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/590,563  
FILING DATE:

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; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8170
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match
; Score 134; DB 15; Length 536;
Best Local Similarity 30.1%; Pred. No. 5,2e-05;
Matches 40; Conservative 18; Mismatches 59; Indels 16; Gaps 6;

QY 14 IVGNNGMR-VVADDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--SCUTTY-- 68
DB 409 LVGASNNICDAVDNQTAPGTETIWDG--GGANQAVITIADELALYGTGCIANQR 465
QY 69 GTTAGVYVNIIPDQNTAVREKTIWQIDNQTINPNSULV-----NAGSITKLTWQ 122
DB 466 GTTGTGKTVQVLTGNGANQR--NSLNPNTVYGTGSLCLDVTGSDQSSNVTGALFLM 523
QY 123 TUDYTGCGKLAG 135
DB 524 TONGANQWELG 536

RESULT 9
US-09-973-457-5
; Sequence 5, Application US/09973457
; Patent No. US20020164746A1
; GENERAL INFORMATION:
; APPLICANT: Schell-Ilbmann, Rosena
; TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 10448-099001
; CURRENT APPLICATION NUMBER: US/09/973,457
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/238,849
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match
; Score 127; DB 10; Length 135;
Best Local Similarity 25.7%; Pred. No. 4.1e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNNGMR-VV--RDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 67
DB 7 IGVNNGMRVUV--RDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 64
QY 68 YGTAGVYVNIIPDQNTAVR--EATIWQIDNQTINPNSVLAASGIGKLTWQTLTD 125
DB 65 NG-----TVLYSCDGTGKNDQKQWVNDGTRNPK-NKKGVDG----- 106
QY 126 YTLGGWLAGNDTAPREVITIGFDLCME-SNQSIVWETIDSSQKQKXV 115
DB 107 -----LCIDYKQKXVQMLTNGSDAPKQXV 132

RESULT 10
US-10-074-527-6
; Sequence 6, Application US/10074527
; Publication No. US20020142426A1
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Meyers, Rachel E.
```

```

; APPLICANT: Galvin, Katherine A.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: 33948, Human Glycosyltransferase and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: WP/2001-018P(BP(LM))
; CURRENT APPLICATION NUMBER: US/10/074,527
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/269202
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: consensus
US-10-074-527-6

Query Match
; Score 127; DB 14; Length 135;
Best Local Similarity 25.7%; Pred. No. 4.1e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNNGMRVUV--RDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 67
DB 7 IGVNNGMRVUV--RDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 64
QY 68 YGTAGVYVNIIPDQNTAVR--EATIWQIDNQTINPNSVLAASGIGKLTWQTLTD 125
DB 65 NG-----TVLYSCDGTGKNDQKQWVNDGTRNPK-NKKGVDG----- 106
QY 126 YTLGGWLAGNDTAPREVITIGFDLCME-SNQSIVWETIDSSQKQKXV 115
DB 107 -----LCIDYKQKXVQMLTNGSDAPKQXV 132

RESULT 11
US-10-156-761-10246
; Sequence 10246, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OKURA, SATOSHI
; APPLICANT: OKURA, HARUO
; APPLICANT: ISHIDA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIRA, YUDAYOSHI
; APPLICANT: SAKAKI, TOSHIYUKI
; APPLICANT: KAWANO, TOSHIYUKI
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 243-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10246
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10246

Query Match
; Score 126; DB 15; Length 647;
Best Local Similarity 26.3%; Pred. No. 0.00044; Indels 46; Gaps 8;
Matches 45; Conservative 20; Mismatches 60;

QY 9 EPTVAVIYGNNGMRVYRDDDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 66
DB 520 DGTGSPVGLAKCLDVASSSSANSTAVQVLT--DNGSTAGKATYKALSSVQAKCLDVT 577
QY 67 TGTGTAGVYVNIIPDQNTAVREKTIWQIDNQTINPNSVLAASGIGKLTWQTLTD 126
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Publication No. US20020142426A1
GENERAL INFORMATION:
APPLICANT: Olandt, Peter J.
APPLICANT: Meyers, Rachel E.
APPLICANT: Galvin, Katherine A.
APPLICANT: Millennium Pharmaceuticals Inc.
TITLE OF INVENTION: Uses of a human glycosyltransferase and
a human glycosyltransferase
CURRENT FILING DATE: 2002-02-12
PRIOR FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/269202
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 145
TYPE: PRN
SEQUENCE: Artificial Sequence
GENERAL INFORMATION: consensus
US-10-074-527-5

Query Match 12.0% Score 171; DB 14; Length 145;
Best Local Similarity 32.8%; Pred. No. 1,3e-09;
Matches 45; Conservative 20; Mismatches 58; Indels 14; Gaps 4;
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```
QY 11 TTRIVGNGMRYVTRDDPHDQNOIQMPSKSNPNQMTI--KDDGTIR--NSGC 64
DB 7 TIVVNSRCLDYNSSSDPNQVQJNCHSPKQKNSITTDSDGSLSSVYNDK 66
QY 65 LETTGAGYVWIFPCCTAVREATTWQINDGTTIP-----FENLYV--AASSGIG 116
DB 67 LVVANSRGSSEVLYVCCDSATSDQKWEINDGLSKWILVTVNGVLDVKSADTONG 126
QY 117 TTVTVQTLDTYTLGQGM 133
DB 127 TRLIVTCGCGRNQOML 143
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RESULT 6
US-10-156-761-14970
Sequence 14970, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OKURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBATA, YOSHIO
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-09-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14970
LENGTH: 420
TYPE: PRN
SEQUENCE: Streptomyces avermitilis
US-10-156-761-14970
```

```
Query Match 10.8% Score 155; DB 15; Length 420;
Best Local Similarity 32.8%; Pred. No. 2.5e-06;
Matches 44; Conservative 19; Mismatches 68; Indels 10; Gaps 5;
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```
QY 1 DD--VTCASAEFTVIVKNGKRVYDDPHDQNOIQMPSKSNPNQMTI--KDDGTIR 58
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DB 284 DQVYVTRGSSGAPITGLAKGVVASSSANGAPVQLV--DQNTTAKRWTVASDQTL 341
QY 59 RNSGCL--TTGYVAGYVWIFPCCTAVREATTWQINDGTTIP--LVLAASGI 114
DB 342 EALGKCLDVTENGTDGSGTVQMDGCSANOK--WVTAAGDIVNPQAKCLDYGNSA 399
QY 115 KPTVLVQTLDTYTLGQGM 135
DB 400 KSTRVQVNSCGSANGKXKG 420
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RESULT 7
US-10-156-761-9724
Sequence 9724, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OKURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBATA, YOSHIO
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-09-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9724
LENGTH: 658
TYPE: PRN
SEQUENCE: Streptomyces avermitilis
US-10-156-761-9724

Query Match 9.8% Score 138.5; DB 15; Length 658;
Best Local Similarity 32.1%; Pred. No. 2.4e-05;
Matches 44; Conservative 17; Mismatches 57; Indels 19; Gaps 7;
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QY 11 TTR-IVGNGMRYV-----DVDDPHDQNOIQMPSKSNPNQMTI--KDDGTIR 59
DB 523 TVAPLPTGVALVYGKSGRCADIVNRTTGTQALW--DQKGRGSEVTSKKEVLY 580
QY 60 SNGSCLTY--GYVAGYVWIFPCCTAVREATTWQINDGTTIP--LVLAASGI 115
DB 581 GYKCLKLVNLTGNTVTVVYVMDGCAQNR--NAINSDGTVNNSGCLDLYNKA 638
QY 116 GTTLVQTLDTYTLGQGM 132
DB 639 GTSVLWSCGCGRNQOM 655
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RESULT 8
US-10-156-761-8170
Sequence 8170, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OKURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBATA, YOSHIO
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
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us-09-601-667c-10.rapb

Page 2

QY 121 VQTLDTLGGWMLAGNDTAREVTVYGFRLD/CMESNGSGSVWETCDSSQKQKMAVYD 180  
DB 121 VQTLDTLGGWMLAGNDTAREVTVYGFRLD/CMESNGSGSVWETCDSSQKQKMAVYD 179  
QY 181 GSIRPKONODCTLSGRDSVSTVIVIVSGSGASGQRMWFTNKGALINLKKGPAMVQA 240  
DB 180 GSIRPKONODCTLSGRDSVSTVIVIVSGSGASGQRMWFTNKGALINLKKGPAMVQA 239  
QY 241 NPKLRRIIYPATCKNQMLPV 263  
DB 240 NPKLRRIIYPATCKNQMLPV 262

RESULT 2  
US-09-347-064-4  
Sequence 4, Application US/09347064A  
Patent No. US20020045208A1  
GENERAL INFORMATION:  
APPLICANT: Eek, Jurgen  
APPLICANT: Schmidt, Arno  
APPLICANT: Zinke, Holger  
TITLE OF INVENTION: Recombinant Fusion Proteins Based on  
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum  
FILE REFERENCE: 09282-5  
CURRENT APPLICATION NUMBER: US/09/347,064A  
EARLIER APPLICATION NUMBER: EP/EP98/00009  
EARLIER FILING DATE: 1998-01-02  
EARLIER APPLICATION NUMBER: EP 97 10 0012.0  
EARLIER FILING DATE: 1997-01-02  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 4  
LENGTH: 267  
TYPE: PRT  
ORGANISM: Viscum album  
US-09-347-064-4

Query Match  
Best Local Similarity 94.7%; Pred. No. 1.5e-127;  
Matches 249; Conservative 2; Mismatches 11; Indels 1; Gaps 1;  
QY 1 DVTCSASEPTVIRVGRNKNKVDVDDDFHDGNGIOLMPKSKNDPNQMLTKKDTIRSG 60  
DB 1 DVTCSASEPTVIRVGRNKNKVDVDDDFHDGNGIOLMPKSKNDPNQMLTKKDTIRSG 60  
QY 61 NSGCLATVGTAGVYVIFDONTAVREATINQINDGTTINPESMLVLAASGIGKTTLT 120  
DB 61 NSGCLATVGTAGVYVIFDONTAVREATINQINDGTTINPESMLVLAASGIGKTTLT 120  
QY 121 VQTLDTLGGWMLAGNDTAREVTVYGFRLD/CMESNGSGSVWETCDSSQKQKMAVYD 180  
DB 121 VQTLDTLGGWMLAGNDTAREVTVYGFRLD/CMESNGSGSVWETCDSSQKQKMAVYD 179  
QY 181 GSIRPKONODCTLSGRDSVSTVIVIVSGSGASGQRMWFTNKGALINLKKGPAMVQA 240  
DB 180 GSIRPKONODCTLSGRDSVSTVIVIVSGSGASGQRMWFTNKGALINLKKGPAMVQA 239  
QY 241 NPKLRRIIYPATCKNQMLPV 263  
DB 240 NPKLRRIIYPATCKNQMLPV 262

RESULT 3  
US-10-083-336A-1  
Sequence 1, Application US/1008336A  
Publication No. US2003018165A1  
GENERAL INFORMATION:  
APPLICANT: Olson, Mark A  
APPLICANT: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Kamenecner, Robert W

FILE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
FILE REFERENCE: P6745200, R11D 01-58  
CURRENT APPLICATION NUMBER: US/10/083,336A  
EARLIER APPLICATION NUMBER: US/02-05-21  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 1  
LENGTH: 576  
TYPE: PRT  
ORGANISM: Ricinus communis  
US-10-083-336A-1

Query Match  
Best Local Similarity 63.3%; Score 899.5; DB 12; Length 576;  
Matches 165; Conservative 32; Mismatches 62; Indels 1; Gaps 1;  
QY 5 CSASEPTVIRVGRNKNKVDVDDDFHDGNGIOLMPKSKNDPNQMLTKKDTIRSGSC 64  
DB 318 CSASEPTVIRVGRNKNKVDVDDDFHDGNGIOLMPKSKNDPNQMLTKKDTIRSGSC 377  
QY 65 LTVGTAGVYVIFDONTAVREATINQINDGTTINPESMLVLAASGIGKTTLT 124  
DB 378 LTVGTAGVYVIFDONTAVREATINQINDGTTINPESMLVLAASGIGKTTLT 437  
QY 125 DVTCSASEPTVIRVGRNKNKVDVDDDFHDGNGIOLMPKSKNDPNQMLTKKDTIRSG 60  
DB 438 DVTCSASEPTVIRVGRNKNKVDVDDDFHDGNGIOLMPKSKNDPNQMLTKKDTIRSG 60  
QY 185 PRONODCTLSGRDSVSTVIVIVSGSGASGQRMWFTNKGALINLKKGPAMVQA 244  
DB 497 PRONODCTLSGRDSVSTVIVIVSGSGASGQRMWFTNKGALINLKKGPAMVQA 239  
QY 245 RRIIYPATCKNQMLPV 264  
DB 557 RRIIYPATCKNQMLPV 262

RESULT 4  
US-10-137-077-17  
Sequence 17, Application US/10137077  
Publication No. US20030092109A1  
GENERAL INFORMATION:  
APPLICANT: Goldstein, Irwin J.  
APPLICANT: Kruger, Robert P.  
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin  
FILE REFERENCE: US-01-12-88, US/01/0137,077  
CURRENT APPLICATION NUMBER: 60/288,596  
EARLIER FILING DATE: 2002-05-02  
PRIOR APPLICATION NUMBER: 60/288,596  
PRIOR FILING DATE: 2002-02-04  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 17  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Ricinus communis  
US-10-137-077-17

Query Match  
Best Local Similarity 77.3%; Pred. No. 7.4e-12;  
Matches 34; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 12 VAIIGRNRVYRDDDFHDGNGIOLMPKSKNDPNQMLTKKDTIRSG 55  
DB 1 VAIIGRNRVYRDDDFHDGNGIOLMPKSKNDPNQMLTKKDTIRSG 44  
RESULT 5  
US-10-074-527-5  
Sequence 5, Application US/10074527

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Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 Search time 17.0129 seconds  
(without alignments) 2886.029 Million cell updates/sec

Title: US-09-601-667C-10

Perfect score: 1420  
Sequence: 1 DVTGCSAEPTVRIWKNM.....RRIIVPATGKPNQWLPVF 264

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 684280 seqs, 185981659 residues

Total number of hits satisfying chosen parameters: 684280

Maximum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database: Published Applications AA.\*

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5: /cgn2\_6/prodata/1/pubpa/US07\_PUB.pep.\*  
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17: /cgn2\_6/prodata/1/pubpa/US10\_PUBCOMB.pep.\*  
18: /cgn2\_6/prodata/1/pubpa/US10\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1320.5	93.0	263	9	US-09-347-064-10
2	1320.5	93.0	267	9	US-09-347-064-10
3	889.5	63.3	576	12	US-10-063-336A-1
4	186	13.1	44	15	US-10-137-077-17
5	171	12.0	145	14	US-10-074-527-5
6	135	10.9	420	15	US-10-156-761-14970
7	138.5	9.4	658	15	US-10-156-761-9724
8	134	9.4	536	15	US-10-156-761-8170
9	127	8.9	135	14	US-09-973-457-5
10	126	8.9	135	14	US-10-156-761-10246
11	125	8.8	625	15	US-10-137-077-18
12	125	8.6	480	9	US-09-770-621-5
13	122.5	8.6	491	9	US-09-770-621-8
14	122.5	8.6	492	9	US-09-770-621-4
15	122.5	8.6	492	9	US-09-770-621-4

16	122.5	8.6	492	9	US-09-770-621-7	Sequence 7, Appl 1
17	122.5	8.6	492	12	US-10-286-993-4	Sequence 4, Appl 1
18	112	7.9	625	15	US-10-156-761-15008	Sequence 15008, A
19	108	7.6	41	15	US-10-137-077-20	Sequence 20, Appl 1
20	104	7.3	45	15	US-10-137-077-19	Sequence 19, Appl 1
21	102	7.0	612	14	US-10-101-851-25	Sequence 25, Appl 1
22	99.5	6.7	464	15	US-10-156-761-9647	Sequence 9647, Ap
23	93	6.2	1223	9	US-09-841-132-355	Sequence 3547, Ap
24	93	6.2	1223	9	US-09-841-132-355	Sequence 3547, Ap
25	93	6.2	1223	9	US-09-841-132-355	Sequence 3547, Ap
26	92	6.5	2771	10	US-09-808-602-82	Sequence 82, Appl 1
27	92	6.5	2771	10	US-09-808-602-82	Sequence 82, Appl 1
28	90.5	6.4	340	15	US-10-128-714-8037	Sequence 70, Appl 1
29	89	6.3	770	9	US-09-815-656-31	Sequence 8037, Ap
30	89	6.3	1706	12	US-10-229-066-10	Sequence 31, Appl 1
31	87	6.1	2732	12	US-10-238-075-119	Sequence 119, Ap
32	86.5	6.1	1032	11	US-09-133-643-16	Sequence 16, Appl 1
33	86.5	6.1	1032	11	US-10-150-884-120	Sequence 120, Appl 1
34	85.5	6.0	608	10	US-09-824-358-8	Sequence 8, Appl 1
35	85.5	6.0	1079	12	US-10-193-764-45	Sequence 45, Appl 1
36	85.5	6.0	1079	12	US-10-193-764-45	Sequence 45, Appl 1
37	85.5	6.0	1079	12	US-10-193-764-45	Sequence 45, Appl 1
38	84.5	6.0	239	10	US-09-839-996-6	Sequence 15, Appl 1
39	84	5.9	1848	11	US-09-839-996-6	Sequence 6, Appl 1
40	84	5.9	1848	11	US-10-080-505-6	Sequence 6, Appl 1
41	83	5.8	207	9	US-09-780-717-26	Sequence 26, Appl 1
42	83	5.8	2253	10	US-09-797-862-33	Sequence 33, Appl 1
43	83	5.8	2668	12	US-10-246-310-4	Sequence 4, Appl 1
44	82.5	5.8	871	10	US-09-858-525X-2	Sequence 2, Appl 1
45	82.5	5.8	871	10	US-09-858-525X-2	Sequence 2, Appl 1

#### ALIGNMENTS

RESULT 1	US-09-347-064-10
Sequence 10, Application US/09347064A	
Residue Number: 1-263	
APPLICANT: Eck, Jurgen	
APPLICANT: Schmidt, Arno	
TITLE OF INVENTION: Recombinant Fusion Proteins Based on	
TITLE OF INVENTION: Ribosome-inactivating proteins of the m1:lecAe Viscum	
FILE REFERENCE: 09282-3	
CURRENT APPLICATION NUMBER: US/09/347, 064A	
EARLIER APPLICATION NUMBER: PCT/EP98/00009	
EARLIER FILING DATE: 1998-01-02	
EARLIER APPLICATION NUMBER: EP 97 10 0012.0	
EARLIER FILING DATE: 1997-01-02	
NUMBER OF SEQ ID NOS: 38	
SOPNAME: Patentin Ver. 2.1	
SEQ ID NO 10	
LENGTH: 263	
TYPE: NT	
US-09-347-064-10	Viscum album
Query Match	93.0%; Score 1320.5; DB 9; Length 263;
Best Local Similarity	94.7%; Pred. No. 1.5e-127;
Matches 249; Conservative	2; Mismatches 11; Indels 1; Gaps 1;
QY	1 DVTGCSAEPTVRIWKNMVDVDDPDNDNQIQWSSNNPDQWTKKGGTTS 60
DB	1 DVTGCSAEPTVRIWKNMVDVDDPDNDNQIQWSSNNPDQWTKKGGTTS 60
QY	6 NSGCTVYGTAGYVIMIDNDVAREATVINDGTTIPSSNVYLAASGKRTT 120
DB	6 NSGCTVYGTAGYVIMIDNDVAREATVINDGTTIPSSNVYLAASGKRTT 120
QY	61 NSGCTVYGTAGYVIMIDNDVAREATVINDGTTIPSSNVYLAASGKRTT 120
DB	61 NSGCTVYGTAGYVIMIDNDVAREATVINDGTTIPSSNVYLAASGKRTT 120



CC ribosome-non-cyclo-oxy forms of (I) activate T-cell and  
CC lymphokine-producing macrophages, so stimulate immunity, (I) and its  
CC fragments are also immunogenic, and the immunogenicity of the  
CC cancer) and if they lack cyclo-oxy to increase the strength of the  
CC immune response, particularly to a co-administered antigen  
CC (tumour-associated, bacterial, or viral). The method allows production  
CC and on a large scale at any time of the year, recombinant products  
CC free from toxins present in natural mactean extracts. This sequence  
CC represents a fragment of a mactean lactin I protein variant.

AA	Sequence	532 AA;
SQ		

Query Match	93.4%;	Score 1326.5;	DB 20;	Length 532
Best Local Similarity	95.1%;	Pred. No. 7.5e-123;		
Matches 250;	Conservative	2;	Mismatches 10;	Indels 1;

[illegible]

## RESULT 15

AAW64662  
ID AAW64662 standard; Protein; 263 AA

XX  
32WE4662-[illegible]

DT 23-OCT-1998 (first entry)  
XX

DE Mistletoe rMLB variant protein.  
XX

Lectin B-cha

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XX autoimmune disease; allergy; tumour

Viscum album.

Key	Value
Key	Value

Protein	FT	FT
---------	----	----

XX  
XX  
PN

WC09820540-72

XX  
XX

09-JUL-1998.  
PD  
XX

PF 02-JAN-1998; 98WQ-EP000009.  
XX

02-JAN-1997; 97EP-

XX  
PA (BRAI -) BRAIN BIO

XX Nucleic acid encoding Fusion protein containing mistletoe lectin A  
PT chan - useful for treatment of proliferative and autoimmune  
XX diseases, allergies and tumours  
XX Disclosure: Fig 11b'; 155p; German.

CC This sequence represents a variant m

sequence can be used in the construction of a fusion protein which comprises an effector module that is cytotoxic intracellularly, and processing a proteinase recognition sequence, and a targeting module containing a membrane binding domain. The fusion protein is specifically cytotoxic to the surface of a cell so as to mediate internalisation of the fusion protein. Such a fusion protein can be used for treating disorders involving proliferation and/or elevated activation of cells, especially autoimmune diseases, allergy and tumours. The proteins can be administered e.g. by injection or topically but especially by intravenous injection, at 1 ng to 500  $\mu\text{m g/kg/day}$ , or for ex vivo use at 1 pg to 500 ng/ml. Fusion proteins can develop toxic activity in a wide range of target cells. The processing module prevents extracellular dissociation, and fusion proteins based on mistletoe lectin A-chain are far more active than those based on mistletoe lectin B-chain. The proteins are non-specifically cytotoxic. The protein may be expressed in a non-glycosylated form that does not bind to sugar receptors in the liver, and which has long half-life in the blood. Where the mistletoe lectin B-chain is used, it actively assists in translocation of the ML A-chain from the endoplasmic reticulum to the cytoplasm.

AA	Sequence	263	AA:
SQ			

Query Match 93.0%; Score 1320.5; DB 19; Length 263

Match	Local Similarity	Pred. No.	Game
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356	94.7%	1.1e-122	1
357	94.7%	1.1e-122	1
358	94.7%	1.1e-122	1
359	94.7%	1.1e-122	1
360	94.7%	1.1e-122	1
361	94.7%	1.1e-122	1
362	94.7%	1.1e-122	1
363	94.7%	1.1e-122	1
364	94.7%	1.1e-122	1
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386	94.7%	1.1e-122	1
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392	94.7%	1.1e-122	1
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394	94.7%	1.1e-122	1
395	94.7%	1.1e-122	1
396	94.7%	1.1e-122	1
397	94.7%	1.1e-122	1
398	94.7%	1.1e-122	1
399	94.7%	1.1e-122	1
400	94.7%	1.1e-122	1

[illegible]

Search completed: December 11, 2003, 14:07:45  
Job time : 26.0864 secs

Job time : 26.0864 secs



XX Sequence 264 AA;  
 SQ  
 Query Match 93.4%; Score 1326.5; DB 20; Length 264;  
 Best Local Similarity 95.1%; Pred. No. 286-123;  
 Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 DVTCSASBETVRIYGNKRVKVDVDDPHDGNQIQLPKSKNNDPQOLMTIKDGTIR 60  
 DB 1 DVTCSASBETVRIYGNKRVKVDVDDPHDGNQIQLPKSKNNDPQOLMTIKDGTIR 60

QY 61 NSCLTTGYTAGYVMIPECNVAREATTIWIQNGTINPRSNVLAASSGKGTTLT 120  
 DB 61 NSCLTTGYTAGYVMIPECNVAREATTIWIQNGTINPRSNVLAASSGKGTTLT 120

QY 121 VOTLDYTLGQMLAGNDTPAREVTIYGRDLCHESNGSVWETCTSSQKQNALYGD 180  
 DB 121 VOTLDYTLGQMLAGNDTPAREVTIYGRDLCHESNGSVWETCTSSQKQNALYGD 180

QY 121 VOTLDYTLGQMLAGNDTPAREVTIYGRDLCHESNGSVWETCTSSQKQNALYGD 179  
 DB 121 VOTLDYTLGQMLAGNDTPAREVTIYGRDLCHESNGSVWETCTSSQKQNALYGD 179

QY 181 GSIRPKQNOPDCLTGRDSVSTVINIVSCSAGSQRWFTNKGALINLKNGLANDVAQA 240  
 DB 181 GSIRPKQNOPDCLTGRDSVSTVINIVSCSAGSQRWFTNKGALINLKNGLANDVAQA 239

QY 241 NPKLRRIIYPATGKPNQMLPV 263  
 DB 240 NPKLRRIIYPATGKPNQMLPV 262

## RESULT 13

AA25979  
 ID AA25979 standard; Protein: 531 AA.

XX AC AA25979;

XX DT 18-OCT-1999 (first entry)

XX Mistletoe lectin I protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin I.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Walters P;

XX MPI; 1999-445335/38.

XX N-PSDB; AA209103.

XX Preparation of mistletoe lectins in heterologous systems.

XX particularly for use as anticancer agents and immunostimulants

XX Claim 7; Fig 1B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumour and immunostimulatory activity. The A-chain (MIA)

XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and

CC (tumour-associated bacterial or viral). The method allows production of  
 CC mistletoe lectin and its A-chain in many different isoforms  
 CC and in many different media. The A-chain is a protein chain of many  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a mistletoe lectin I protein fragment.

XX Sequence 531 AA;  
 SQ  
 Query Match 93.4%; Score 1326.5; DB 20; Length 531;  
 Best Local Similarity 95.1%; Pred. No. 736-123;  
 Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 DVTCSASBETVRIYGNKRVKVDVDDPHDGNQIQLPKSKNNDPQOLMTIKDGTIR 60  
 DB 1 DVTCSASBETVRIYGNKRVKVDVDDPHDGNQIQLPKSKNNDPQOLMTIKDGTIR 60

QY 61 NSCLTTGYTAGYVMIPECNVAREATTIWIQNGTINPRSNVLAASSGKGTTLT 120  
 DB 61 NSCLTTGYTAGYVMIPECNVAREATTIWIQNGTINPRSNVLAASSGKGTTLT 120

QY 121 VOTLDYTLGQMLAGNDTPAREVTIYGRDLCHESNGSVWETCTSSQKQNALYGD 180  
 DB 121 VOTLDYTLGQMLAGNDTPAREVTIYGRDLCHESNGSVWETCTSSQKQNALYGD 180

QY 121 VOTLDYTLGQMLAGNDTPAREVTIYGRDLCHESNGSVWETCTSSQKQNALYGD 179  
 DB 121 VOTLDYTLGQMLAGNDTPAREVTIYGRDLCHESNGSVWETCTSSQKQNALYGD 179

QY 181 GSIRPKQNOPDCLTGRDSVSTVINIVSCSAGSQRWFTNKGALINLKNGLANDVAQA 240  
 DB 181 GSIRPKQNOPDCLTGRDSVSTVINIVSCSAGSQRWFTNKGALINLKNGLANDVAQA 240

QY 241 NPKLRRIIYPATGKPNQMLPV 263  
 DB 240 NPKLRRIIYPATGKPNQMLPV 262

## RESULT 14

AA25982  
 ID AA25982 standard; Protein: 532 AA.

XX AC AA25982;

XX DT 18-OCT-1999 (first entry)

XX Mistletoe lectin I (variant) protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin I.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Walters P;

XX MPI; 1999-445335/38.

XX N-PSDB; AA209106.

XX Preparation of mistletoe lectins in heterologous systems.

XX particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 4B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumour and immunostimulatory activity. The A-chain (MIA)

Qy 61 NSGCLTTGATGAGYVWIPDCNRAVEKTIWQIMWNNIIPSPNLYAAASGIGTLE 120  
Db 61 NSGCLTTGATGAGYVWIPDCNRAVEKTIWQIMWNNIIPSPNLYAAASGIGTLE 120  
Qy 121 VQTDLYTQSGMLANDRAPEVITIGFRLCMESNGSVWETFCDSGQKQKALYCD 180  
Db 121 VQTDLYTQSGMLANDRAPEVITIGFRLCMESNGSVWETFCDSGQKQKALYCD 180  
Qy 121 GSTRPNKQDCLTSGRDSVETVINYVSCGASGSGQWFTNEMALNLSGLANDRA 240  
Db 121 GSTRPNKQDCLTSGRDSVETVINYVSCGASGSGQWFTNEMALNLSGLANDRA 240  
Qy 241 NPRLRIITIPATKRNQMWLPVF 264  
Db 241 NPRLRIITIPATKRNQMWLPVF 264

RESULT 11  
AAV25985  
ID AAV25985 standard; Protein; 263 AA.  
vv

DT	18-OCT-1999	(first entry)
XX		
DE	Mistletoe lectin B protein	
XX		

KV Mistletoe; lectin, antitumour, immunostimulant, A-chain; MIA; immunity;  
 KN ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KV cancer; cytotoxicity; antigen; isoform; lectin B.

OS	Viscum album.
XX	
PN	DE19804210-A1.
XX	
PD	12-AUG-1999.
XX	

PF	03-FEB-1998;	98DE-1004210.
XX		
PR	03-FEB-1998;	98DE-1004210.
XX		
PA	(BIOS-) BIOSYN	ARZNEIMITTEL.

PI	Morris P, Stufel T, Voelter W, Walters P,
XX	
DR	WPI, 1999-445335/38.
DR	N-PSDB; AA209109.
XX	

PT particularly for use as anticancer agents and immunostimulants  
XX  
PS Claim 9; Fig 7B; 78pp; German.  
XX  
CC This invention describes a novel mistletoe lectin (I) and its

of the nucleoside lectin binds to and inactivates, the 28S subunit of ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-producing macrophages, so stimulate immunity. (I) and its fragments are used to treat uncontrolled cell growth (particularly cancers) and if they lack cytotoxicity, to increase the strength of the

(tumour-associated, bacterial or viral). The method allows production of mistletoe lectins, and its individual chains, in many different isoforms CC and on a large scale, at any time of the year. Recombinant products are free from toxins present in natural mistletoe extracts. This sequence represents a fragment of a mistletoe lectin B protein.

Query Match 93.4%; Score 1326.5; DB 20; Length 263;  
Best Local Similarity 95.1%; Pred. No. 2.7e-123;

	Matches	250;	Conservative	2;	Mismatches	10;	Indels	1;	Gaps	1
Qy	1	DVDTSSASPEPTVIRV	QNRGV	VDVDDDFD	CAQIOLWPKSND	PNQWLMTK	DDTTS	60		
Db	1	DVDTSSASPEPTVIRV	QNRGV	VDVDDDFD	CAQIOLWPKSND	PNQWLMTK	DDTTS	60		
Qy	61	NSCLTYVYTAGVYV	MFPCNTAV	REATVQI	WIDNGIIN	SPSLVLA	SSGKOTLT	120		
Db	61	NSCLTYVYTAGVYV	MFPCNTAV	REATVQI	WIDNGIIN	SPSLVLA	SSGKOTLT	120		
Qy	121	VQCDLPTLQGLAGND	TRREPTV	YGFDF	CENSGS	SVYETV	TSQSGK	QWALYED	180	
Db	121	VQCDLPTLQGLAGND	TRREPTV	YGFDF	CENSGS	SVYETV	TSQSGK	QWALYED	180	
Qy	181	GSIRPKNQDDQL	SGRSV	SYINIV	SGSAS	SGSRV	VTENGL	INIKSGP	MMVQA	240
Db	181	GSIRPKNQDDQL	SGRSV	SYINIV	SGSAS	SGSRV	VTENGL	INIKSGP	MMVQA	240
Qy	241	NPETLRIRIY	PAKGR	PNML	PLV	263				
Db	241	NPETLRIRIY	PAKGR	PNML	PLV	263				
Qy	240	NPETLRIRIY	PAKGR	PNML	PLV	262				
Db	240	NPETLRIRIY	PAKGR	PNML	PLV	262				

AY25991 12  
 AY25991  
 ID AY25991 standard; Protein; 264 AA  
 XX

XX	18-OCT-1999 (first entry)
DT	
XX	
DE	Mistletoe lectin B variant

MM Mistletoe, lectin; antitumour; immunostimulant; A-chain; MHA; immunity;  
 MM ribzyme 26S subunit; non-cytotoxic; T-cell activation; immune response  
 MM lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
 CX cancer; cytotoxicity; antigen; isoforn; lectin B.

XX	DE19804210-A1
PN	
XX	
PD	12-AUG-1999.
XX	

XX	03-FEB-1998;	98DE-1004210.
XX	03-FEB-1998;	98DE-1004210.
PR	03-FEB-1998;	98DE-1004210.
XX		
PA	(BIOS-) BIOSYN ARZNEIMITTEL	
XX		

FI Molins F, Sletten L, Voelter W, Melkers E;  
 XX  
 DR WPI; 1999-44535/38.  
 DR N-PSDB; AA209115.  
 XX  
 PI Preparation of mistletoe lectins in heterologous systems.

XX particularly for use as anticancer agents and immunostimulants  
XX  
XX  
PS Disclosure; Fig 13B; 78pp; German.  
CC This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumor and immunostimulatory activity. The A-chain (M<sub>r</sub>)  
XX

of the histidine lectin binds to, and inactivates, the 28S subunit of ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-producing macrophages, so stimulate immunity. (I) and its fragments are used to treat uncontrolled cell growth (particularly cancers) and if they lack cytotoxicity, to increase the strength of the immune response, particularly to co-administered antigen

CC mistletoe lectin, and its individual chains, in many different isoforms  
CC  
CC and on a large scale, at any time of the year. Recombinant products are  
CC free from toxins present in natural mistletoe extracts. This sequence  
CC represents a fragment of a variant mistletoe lectin B protein.

DB 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSRWFTEGAILNKSLANDVAK 240  
QY 241 NPKLRRIIYPATCKENQWLPVF 264  
DB 241 NPKLRRIIYPATCKENQWLPVF 264

## RESULT 9

AAZ55987 ID AAZ55987 standard; Protein; 264 AA.

AAZ55987; XX

DT 18-OCT-1999 (first entry)

XX Mistletoe lectin B2 protein fragment.

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;

XX ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;

XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin B2.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Welters P;

XX WPI, 1999-44535/38.

XX N-PDB; AA209111.

XX Preparation of mistletoe lectins in heterologous systems,

XX particularly for use as anticancer agents and immunostimulants

XX Claim 9; Fig 9B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumor and immunostimulatory activity. The A-chain (MIA)

XX of the mistletoe lectin binds to (II) activate T-cell and

XX lymphokine-producing macrophages, so stimulate immunity. (I) and its

XX fragments are used to treat uncontrolled cell growth (particularly

XX cancers) and if they lack cytotoxicity, to increase the strength of the

XX immune response, particularly to a co-administered antigen

XX (tumour-associated, bacterial or viral). The method allows production of

XX mistletoe lectin, and its individual chains, in many different isoforms

XX and on a large scale, at any time of the year. Recombinant products are

XX free from toxins present in natural mistletoe extracts. This sequence

XX represents a fragment of a mistletoe lectin B2 protein.

XX Sequence 264 AA.

XX Query Match 96.5%; Score 1371; DB 20; Length 264;

XX Best Local Similarity 97.3%; Pred. No. 1e-127;

XX Matches 257; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

XX 1 DDTVCASBPRTVIRVSGNMGVVDVDDFDNDQIQIQLMFSKSNNDPNDLWTIKDGTIRS 60

XX 1 DDTVCASBPRTVIRVSGNMGVVDVDDFDNDQIQIQLMFSKSNNDPNDLWTIKDGTIRS 60

XX 61 NSCLTGYTAGVYVWFDCNFAVEATFQVNDGNTIIPRSNLYLAASSGKKTLLT 120

XX 61 NSCLTGYTAGVYVWFDCNFAVEATFQVNDGNTIIPRSNLYLAASSGKKTLLT 120

QY 121 VDTLDYTLQGMWLAGNDPRAREVITYGFRDLCNENSGSYVWETCDSSQKQKALYGD 180  
DB 121 VDTLDYTLQGMWLAGNDPRAREVITYGFRDLCNENSGSYVWETCDSSQKQKALYGD 180  
QY 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSRWFTEGAILNKSLANDVAK 240  
DB 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSRWFTEGAILNKSLANDVAK 240

## RESULT 10

AAZ55993 ID AAZ55993 standard; Protein; 265 AA.

AAZ55993; XX

DT 18-OCT-1999 (first entry)

XX Mistletoe lectin B2 variant protein fragment.

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;

XX ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;

XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin B2.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Welters P;

XX WPI, 1999-44535/38.

XX N-PDB; AA209117.

XX Preparation of mistletoe lectins in heterologous systems,

XX particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 15B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumor and immunostimulatory activity. The A-chain (MIA)

XX of the mistletoe lectin binds to (II) activate T-cell and (I) and its

XX fragments are used to treat uncontrolled cell growth (particularly

XX cancers) and if they lack cytotoxicity, to increase the strength of the

XX immune response, particularly to a co-administered antigen

XX (tumour-associated, bacterial or viral). The method allows production of

XX mistletoe lectin, and its individual chains, in many different isoforms

XX and on a large scale, at any time of the year. Recombinant products are

XX free from toxins present in natural mistletoe extracts. This sequence

XX represents a fragment of a variant mistletoe lectin B2 protein.

XX Sequence 265 AA.

XX Query Match 96.5%; Score 1371; DB 20; Length 265;

XX Best Local Similarity 97.3%; Pred. No. 1e-127;

XX Matches 257; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

XX 1 DDTVCASBPRTVIRVSGNMGVVDVDDFDNDQIQIQLMFSKSNNDPNDLWTIKDGTIRS 60

XX 1 DDTVCASBPRTVIRVSGNMGVVDVDDFDNDQIQIQLMFSKSNNDPNDLWTIKDGTIRS 60

XX 61 NSCLTGYTAGVYVWFDCNFAVEATFQVNDGNTIIPRSNLYLAASSGKKTLLT 120

XX 61 NSCLTGYTAGVYVWFDCNFAVEATFQVNDGNTIIPRSNLYLAASSGKKTLLT 120

ID AAY25990 standard; Protein: 264 AA.  
 XX AAY25990;  
 AC  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Mistletoe lectin B5 protein fragment.  
 XX  
 KW Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;  
 KM ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KN lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B5.  
 XX  
 OS Viscum album.  
 XX  
 PN DEJ904210-A1.  
 XX  
 KD 12-AUG-1999.  
 XX  
 PF 03-FEB-1998; 98DE-1004210.  
 XX  
 PR 03-FEB-1998; 98DE-1004210.  
 XX  
 PA (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 PI Morris P, Stiefel T, Voelter W, Welters P;  
 XX  
 DR WPI: 1999-445335/38.  
 XX  
 N-PSDB; AA209114.  
 XX  
 PT Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX  
 PS Claim 9; Fig 12B; 78pp; German.  
 XX  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumor and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly of  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a mistletoe lectin B5 protein.  
 XX  
 SQ Sequence 264 AA;  
 XX  
 Query Match 97.9%; Score 1390; DB 20; Length 264;  
 Best Local Similarity 98.1%; Pred. No. 1,46-129;  
 Matches 259; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DDTYCSASEPTVRIYGRNGKRVVDVDDPHDQNOIQLPKSKSNPDQMLWTIKKDGITIS 60  
 DB 1 DDTYCSASEPTVRIYGRNGKRVVDVDDPHDQNOIQLPKSKSNPDQMLWTIKKDGITIS 60  
 QY 61 NSGCLTYGTAGTYVYMFPCDQNAVRARATIMQINDGTTINPNSVLVLAASGIGKTTLT 120  
 DB 61 NSGCLTYGTAGTYVYMFPCDQNAVRARATIMQINDGTTINPNSVLVLAASGIGKTTLT 120  
 QY 121 VQTLDTLQGMWLAGNUTAPREVTYVGRDLQWESNGSVVETCDSSQKQGMALYED 180  
 DB 121 VQTLDTLQGMWLAGNUTAPREVTYVGRDLQWESNGSVVETCDSSQKQGMALYED 180  
 QY 121 VQTLDTLQGMWLAGNUTAPREVTYVGRDLQWESNGSVVETCDSSQKQGMALYED 180  
 DB 121 VQTLDTLQGMWLAGNUTAPREVTYVGRDLQWESNGSVVETCDSSQKQGMALYED 180  
 QY 181 GSIRKXNOCQCLTSGRDSVSTYINIVYSCASGSRVWFTNEGAILNKKGPRAMOVQA 240  
 DB 181 GSIRKXNOCQCLTSGRDSVSTYINIVYSCASGSRVWFTNEGAILNKKGPRAMOVQA 240  
 QY 241 NPLERLIIYPAIKXNOMLVPVF 264  
 DB 241 NPLERLIIYPAIKXNOMLVPVF 264

ID AAY25996 standard; Protein: 265 AA.  
 XX AAY25996;  
 AC  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Mistletoe lectin B5 variant protein fragment.  
 XX  
 KW Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;  
 KM ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KN lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B5.  
 XX  
 OS Viscum album.  
 XX  
 PN DEJ904210-A1.  
 XX  
 KD 12-AUG-1999.  
 XX  
 PF 03-FEB-1998; 98DE-1004210.  
 XX  
 PR 03-FEB-1998; 98DE-1004210.  
 XX  
 PA (BIO-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 PI Morris P, Stiefel T, Voelter W, Welters P;  
 XX  
 DR WPI: 1999-445335/38.  
 XX  
 N-PSDB; AA209120.  
 XX  
 PT Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX  
 PS Disclosure; Fig 18B; 78pp; German.  
 XX  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumor and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly of  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a variant mistletoe lectin B5 protein.  
 XX  
 SQ Sequence 265 AA;  
 XX  
 Query Match 97.9%; Score 1390; DB 20; Length 265;  
 Best Local Similarity 98.1%; Pred. No. 1,46-129;  
 Matches 259; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DDTYCSASEPTVRIYGRNGKRVVDVDDPHDQNOIQLPKSKSNPDQMLWTIKKDGITIS 60  
 DB 1 DDTYCSASEPTVRIYGRNGKRVVDVDDPHDQNOIQLPKSKSNPDQMLWTIKKDGITIS 60  
 QY 61 NSGCLTYGTAGTYVYMFPCDQNAVRARATIMQINDGTTINPNSVLVLAASGIGKTTLT 120  
 DB 61 NSGCLTYGTAGTYVYMFPCDQNAVRARATIMQINDGTTINPNSVLVLAASGIGKTTLT 120  
 QY 121 VQTLDTLQGMWLAGNUTAPREVTYVGRDLQWESNGSVVETCDSSQKQGMALYED 180  
 DB 121 VQTLDTLQGMWLAGNUTAPREVTYVGRDLQWESNGSVVETCDSSQKQGMALYED 180  
 QY 121 VQTLDTLQGMWLAGNUTAPREVTYVGRDLQWESNGSVVETCDSSQKQGMALYED 180  
 DB 121 VQTLDTLQGMWLAGNUTAPREVTYVGRDLQWESNGSVVETCDSSQKQGMALYED 180  
 QY 181 GSIRKXNOCQCLTSGRDSVSTYINIVYSCASGSRVWFTNEGAILNKKGPRAMOVQA 240  
 DB 181 GSIRKXNOCQCLTSGRDSVSTYINIVYSCASGSRVWFTNEGAILNKKGPRAMOVQA 240

KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin B3.  
XX  
XX Viscum album.  
XX  
XX DE19804210-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX (BIO5-) BIOSYN ARZNEIMITTEL GMBH.  
XX  
XX Morris P, Stiefel T, Voelter W, Welters P;  
XX WPI, 1999-44535/38.  
XX DR N-PSDB; AA209112.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Claim 9; Fig 10B; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (MA)  
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
XX ribosomes. Non-cytotoxic forms of (I) stimulate immunity (I) and its  
XX lymphokine-producing macrophages (II) stimulate immunity (I) and its  
XX fragments (II) stimulate uncontrolled cell growth (particularly of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a mistletoe lectin B3 protein.  
XX  
XX Sequence 264 AA;  
XX  
XX Query Match 98.9%; Score 1404; DB 20; Length 265;  
XX Best Local Similarity 99.2%; Pred. No. 5,5e-131;  
XX Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
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DB 1 DDTVCSASEPTVIRVGRNGRVVDVDDDFDGNQIQIOWPSKSNPNQMTIKKDGRTS 60  
QY 61 NSGCTIYGYTGYVWIFPCNTAVREATTQIOWNDGTTINPSSNVLAASSGKTTLT 120  
DB 61 NSGCTIYGYTGYVWIFPCNTAVREATTQIOWNDGTTINPSSNVLAASSGKTTLT 120  
QY 121 VQTLDTLTCQGLAANDTAPRETTVYGFRLCMESNGSVWVETDSSQNGKMAIYGD 180  
DB 121 VQTLDTLTCQGLAANDTAPRETTVYGFRLCMESNGSVWVETDSSQNGKMAIYGD 180  
QY 181 GSIRPKXONQDCLTSGRDSVSTVINIVSCGASGSGRWVFNBSGAILNLTGKLPADVQA 240  
DB 181 GSIRPKXONQDCLTSGRDSVSTVINIVSCGASGSGRWVFNBSGAILNLTGKLPADVQA 240  
QY 241 NPKLRITITPATGKNQWMLPVF 264  
DB 241 NPKLRITITPATGKNQWMLPVF 264  
XX  
XX RESULT 6  
XX AAY25994  
XX ID AAY25994 standard; Protein; 265 AA.  
XX AC AAY25994;  
XX XX  
XX 18-OCT-1999 (first entry)

XX  
XX Mistletoe lectin B3 variant protein fragment.  
XX  
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
XX cancer; cytotoxicity; antigen; isoform; lectin B3.  
XX  
XX Viscum album.  
XX  
XX DE19804210-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX 03-FEB-1998; 98DE-1004210.  
XX  
XX (BIO5-) BIOSYN ARZNEIMITTEL GMBH.  
XX  
XX Morris P, Stiefel T, Voelter W, Welters P;  
XX WPI, 1999-44535/38.  
XX DR N-PSDB; AA209118.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure; Fig 16B; 78pp; German.  
XX  
XX This invention describes a novel mistletoe lectin (I) and its fragments  
XX which have antitumour and immunostimulatory activity. The A-chain (MA)  
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
XX ribosomes. Non-cytotoxic forms of (I) stimulate immunity (I) and its  
XX lymphokine-producing macrophages (II) stimulate immunity (I) and its  
XX fragments (II) stimulate uncontrolled cell growth (particularly of the  
XX immune response, particularly to a co-administered antigen  
XX (tumour-associated, bacterial or viral). The method allows production of  
XX mistletoe lectin, and its individual chains, in many different isoforms  
XX and on a large scale, at any time of the year. Recombinant products are  
XX free from toxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a variant mistletoe lectin B3 protein.  
XX  
XX Sequence 265 AA;  
XX  
XX Query Match 98.9%; Score 1404; DB 20; Length 265;  
XX Best Local Similarity 99.2%; Pred. No. 5,5e-131;  
XX Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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QY 1 DDTVCSASEPTVIRVGRNGRVVDVDDDFDGNQIQIOWPSKSNPNQMTIKKDGRTS 60  
DB 1 DDTVCSASEPTVIRVGRNGRVVDVDDDFDGNQIQIOWPSKSNPNQMTIKKDGRTS 60  
QY 61 NSGCTIYGYTGYVWIFPCNTAVREATTQIOWNDGTTINPSSNVLAASSGKTTLT 120  
DB 61 NSGCTIYGYTGYVWIFPCNTAVREATTQIOWNDGTTINPSSNVLAASSGKTTLT 120  
QY 121 VQTLDTLTCQGLAANDTAPRETTVYGFRLCMESNGSVWVETDSSQNGKMAIYGD 180  
DB 121 VQTLDTLTCQGLAANDTAPRETTVYGFRLCMESNGSVWVETDSSQNGKMAIYGD 180  
QY 181 GSIRPKXONQDCLTSGRDSVSTVINIVSCGASGSGRWVFNBSGAILNLTGKLPADVQA 240  
DB 181 GSIRPKXONQDCLTSGRDSVSTVINIVSCGASGSGRWVFNBSGAILNLTGKLPADVQA 240  
QY 241 NPKLRITITPATGKNQWMLPVF 264  
DB 241 NPKLRITITPATGKNQWMLPVF 264  
XX  
XX RESULT 7  
XX AAY25990

XX 03-FEB-1998; 98DS-1004210.  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 XX WPI: 1999-44535/38.  
 XX N-PSDB; A4209110.  
 XX Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX Claim 9; Fig 9B; 78pp; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumor and immunostimulatory activity. The A-chain (MA)  
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and its  
 XX lymphokine-producing macrophages so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX and on a large scale, at any time of the year. Recombinant products are  
 XX free from toxins present in natural mistletoe extracts. This sequence  
 XX represents a fragment of a mistletoe lectin B1 protein.  
 XX Sequence 264 AA;  
 XX  
 XX Query Match 98.9%; Score 1405; DB 20; Length 264;  
 XX Best Local Similarity 99.2%; Pred. No. 4.4e-131;  
 XX Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX QY 1 DVTGCSASEPTVRIYGNMGMVDVDDDFDGNQ:OLMPSKSNNDPQNLTKRDTGTRS 60  
 XX DB 1 DVTGCSASEPTVRIYGNMGMVDVDDDFDGNQ:OLMPSKSNNDPQNLTKRDTGTRS 60  
 XX QY 61 NSCLTYGYTAGYVWIFDCNFAVEATITWQMDNGTINPNSNVLAAASGIGKTTLT 120  
 XX DB 61 NSCLTYGYTAGYVWIFDCNFAVEATITWQMDNGTINPNSNVLAAASGIGKTTLT 120  
 XX QY 121 VQTLDTLGGGMLAGNDTAPREVTIYGRFLCMSNGSGSWWETCSSQKQKALYGD 180  
 XX DB 121 VQTLDTLGGGMLAGNDTAPREVTIYGRFLCMSNGSGSWWETCSSQKQKALYGD 180  
 XX QY 181 GSIRPKQKODCLTSGDSVSTVINVSCGSGSGRWFFNEGAILNLKGLAMVDAQ 240  
 XX DB 181 GSIRPKQKODCLTSGDSVSTVINVSCGSGSGRWFFNEGAILNLKGLAMVDAQ 240  
 XX QY 241 NPKLRRIITIPATKPNQWMLPVF 264  
 XX DB 241 NPKLRRIITIPATKPNQWMLPVF 264  
 XX  
 XX RESULT 4  
 XX AAY25992  
 XX ID AAY25992 standard; Protein; 265 AA.  
 XX AC AAY25992;  
 XX XX 18-OCT-1999 (first entry)  
 XX DE Mistletoe lectin B1 variant protein fragment.  
 XX KM Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
 XX KW lymphokine-producing macrophages; T-cell activation; immune response;  
 XX cancer; cytotoxicity; antigen; isoform; lectin B1.  
 XX Viscum album.

XX DEL9804210-A1.  
 XX 12-AUG-1999.  
 XX 03-FEB-1998; 98DS-1004210.  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 XX WPI: 1999-44535/38.  
 XX N-PSDB; A4209116.  
 XX Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX Disclosure; Fig 14B; 78pp; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumor and immunostimulatory activity. The A-chain (MA)  
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and its  
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX and on a large scale, at any time of the year. Recombinant products are  
 XX free from toxins present in natural mistletoe extracts. This sequence  
 XX represents a fragment of a variant mistletoe lectin B1 protein.  
 XX Sequence 265 AA;  
 XX  
 XX Query Match 98.9%; Score 1405; DB 20; Length 265;  
 XX Best Local Similarity 99.2%; Pred. No. 4.4e-131;  
 XX Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX QY 1 DVTGCSASEPTVRIYGNMGMVDVDDDFDGNQ:OLMPSKSNNDPQNLTKRDTGTRS 60  
 XX DB 1 DVTGCSASEPTVRIYGNMGMVDVDDDFDGNQ:OLMPSKSNNDPQNLTKRDTGTRS 60  
 XX QY 61 NSCLTYGYTAGYVWIFDCNFAVEATITWQMDNGTINPNSNVLAAASGIGKTTLT 120  
 XX DB 61 NSCLTYGYTAGYVWIFDCNFAVEATITWQMDNGTINPNSNVLAAASGIGKTTLT 120  
 XX QY 121 VQTLDTLGGGMLAGNDTAPREVTIYGRFLCMSNGSGSWWETCSSQKQKALYGD 180  
 XX DB 121 VQTLDTLGGGMLAGNDTAPREVTIYGRFLCMSNGSGSWWETCSSQKQKALYGD 180  
 XX QY 181 GSIRPKQKODCLTSGDSVSTVINVSCGSGSGRWFFNEGAILNLKGLAMVDAQ 240  
 XX DB 181 GSIRPKQKODCLTSGDSVSTVINVSCGSGSGRWFFNEGAILNLKGLAMVDAQ 240  
 XX QY 241 NPKLRRIITIPATKPNQWMLPVF 264  
 XX DB 241 NPKLRRIITIPATKPNQWMLPVF 264  
 XX  
 XX RESULT 5  
 XX AAY25988  
 XX ID AAY25988 standard; Protein; 264 AA.  
 XX AC AAY25988;  
 XX XX 18-OCT-1999 (first entry)  
 XX DE Mistletoe lectin B3 protein fragment.  
 XX KM Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
 XX KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

PT Preparation of mistletoe lectins in heterologous systems,  
 particularly for use as anticancer agents and immunostimulants

XX Claim 9, Fig 11B, 78pp, German.

XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly of  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen (particularly  
 CC tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in recombinant forms  
 CC and on a large scale, at any time of the year. Anticancer products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a mistletoe lectin B4 protein.

XX Sequence 264 AA;

Query Match 100.0%; Score 1420; DB 20; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-132;  
 Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTYCSASEPTVRIYGNKNGRYVDDDDFDHGNQQLMPKSNNDPQMLTKKGGTTS 60  
 DB 1 DVTYCSASEPTVRIYGNKNGRYVDDDDFDHGNQQLMPKSNNDPQMLTKKGGTTS 60

QY 61 NSGCLTYGTAGYVIMFDGCTAVREATTIQTNDGTTINPSNLVLAASGKGTTLT 120  
 DB 61 NSGCLTYGTAGYVIMFDGCTAVREATTIQTNDGTTINPSNLVLAASGKGTTLT 120

QY 61 NSGCLTYGTAGYVIMFDGCTAVREATTIQTNDGTTINPSNLVLAASGKGTTLT 120  
 DB 61 NSGCLTYGTAGYVIMFDGCTAVREATTIQTNDGTTINPSNLVLAASGKGTTLT 120

QY 121 VQILDYTLQGMWLAGNDIAFREVTIYGFDFLCMESNGSVWETCDSSQKQKALYGD 180  
 DB 121 VQILDYTLQGMWLAGNDIAFREVTIYGFDFLCMESNGSVWETCDSSQKQKALYGD 180

QY 121 VQILDYTLQGMWLAGNDIAFREVTIYGFDFLCMESNGSVWETCDSSQKQKALYGD 180  
 DB 121 VQILDYTLQGMWLAGNDIAFREVTIYGFDFLCMESNGSVWETCDSSQKQKALYGD 180

QY 181 GSIRKQNDQCLTSGRDSYSTVINIVSCASGSGKMTTMEGAILNTKGPAMVQA 240  
 DB 181 GSIRKQNDQCLTSGRDSYSTVINIVSCASGSGKMTTMEGAILNTKGPAMVQA 240

QY 241 NPKLRRIITYPATKQKQMLPVF 264  
 DB 241 NPKLRRIITYPATKQKQMLPVF 264

RESULT 2  
 AAY25995  
 ID AAY25995 standard; Protein: 265 AA.  
 AC AAY25995;  
 XX 18-OCT-1999 (first entry)  
 XX Mistletoe lectin B4 variant protein fragment.  
 DB Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B4.  
 XX Viscum album.  
 XX DE19804210-A1.  
 XX 12-AUG-1999.  
 PD 03-FEB-1998; 98DE-1004210.  
 PF 03-FEB-1998; 98DE-1004210.  
 PR 03-FEB-1998; 98DE-1004210.  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

PI Morris P, Stiefel T, Voelker W, Walters P;  
 XX MPl, 1999-44515/38.  
 DB N-PDB; AA209119.

PT Preparation of mistletoe lectins in heterologous systems,  
 particularly for use as anticancer agents and immunostimulants

XX Disclosure, Fig 17B, 78pp, German.

XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly of  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen (particularly  
 CC tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Anticancer products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a variant mistletoe lectin B4 protein.

XX Sequence 265 AA;

Query Match 100.0%; Score 1420; DB 20; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-132;  
 Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTYCSASEPTVRIYGNKNGRYVDDDDFDHGNQQLMPKSNNDPQMLTKKGGTTS 60  
 DB 1 DVTYCSASEPTVRIYGNKNGRYVDDDDFDHGNQQLMPKSNNDPQMLTKKGGTTS 60

QY 61 NSGCLTYGTAGYVIMFDGCTAVREATTIQTNDGTTINPSNLVLAASGKGTTLT 120  
 DB 61 NSGCLTYGTAGYVIMFDGCTAVREATTIQTNDGTTINPSNLVLAASGKGTTLT 120

QY 61 NSGCLTYGTAGYVIMFDGCTAVREATTIQTNDGTTINPSNLVLAASGKGTTLT 120  
 DB 61 NSGCLTYGTAGYVIMFDGCTAVREATTIQTNDGTTINPSNLVLAASGKGTTLT 120

QY 121 VQILDYTLQGMWLAGNDIAFREVTIYGFDFLCMESNGSVWETCDSSQKQKALYGD 180  
 DB 121 VQILDYTLQGMWLAGNDIAFREVTIYGFDFLCMESNGSVWETCDSSQKQKALYGD 180

QY 121 VQILDYTLQGMWLAGNDIAFREVTIYGFDFLCMESNGSVWETCDSSQKQKALYGD 180  
 DB 121 VQILDYTLQGMWLAGNDIAFREVTIYGFDFLCMESNGSVWETCDSSQKQKALYGD 180

QY 181 GSIRKQNDQCLTSGRDSYSTVINIVSCASGSGKMTTMEGAILNTKGPAMVQA 240  
 DB 181 GSIRKQNDQCLTSGRDSYSTVINIVSCASGSGKMTTMEGAILNTKGPAMVQA 240

QY 241 NPKLRRIITYPATKQKQMLPVF 264  
 DB 241 NPKLRRIITYPATKQKQMLPVF 264

RESULT 3  
 AAY25986  
 ID AAY25986 standard; Protein: 264 AA.  
 AC AAY25986;  
 XX 18-OCT-1999 (first entry)  
 XX Mistletoe lectin B1 protein fragment.  
 DB Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin B1.  
 XX Viscum album.  
 XX DE19804210-A1.  
 XX 12-AUG-1999.  
 PD 03-FEB-1998; 98DE-1004210.  
 PF 03-FEB-1998; 98DE-1004210.

Thu Dec 11 16:09:44 2003

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Page 1

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 26.0864 Seconds  
(without alignments)  
1606.345 Million cell updates/sec

Title: US-09-601-667c-10

Sequence: 1420  
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Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneexp-emb1/AA2003.DAT.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1420	100.0	264	20	AAV25989
2	1420	100.0	265	20	AAV25995
3	1405	98.9	264	20	AAV25986
4	1405	98.9	265	20	AAV25992
5	1404	98.9	264	20	AAV25988
6	1404	98.9	265	20	AAV25994
7	1390	97.9	264	20	AAV25990
8	1390	97.9	265	20	AAV25996
9	1371	96.5	264	20	AAV25987

11	1371	96.5	265	20	AAV25993	Mistletoe lectin B
12	1326.5	93.4	264	20	AAV25985	Mistletoe lectin B
13	1326.5	93.4	264	20	AAV25991	Mistletoe lectin B
14	1326.5	93.4	531	20	AAV25979	Mistletoe lectin I
15	1326.5	93.0	263	19	AAV25982	Mistletoe lectin I
16	1320.5	93.0	263	19	AAV25982	Mistletoe lectin I
17	1320.5	93.0	264	18	AAV25982	Mistletoe lectin I
18	1320.5	93.0	264	18	AAV25982	Mistletoe lectin I
19	1320.5	93.0	564	18	AAV25982	Mistletoe lectin I
20	1320.5	93.0	564	18	AAV25982	Mistletoe lectin I
21	1289	90.8	264	20	AAV25978	Mistletoe lectin B
22	1289	90.8	264	20	AAV25978	Mistletoe lectin B
23	1289	90.8	264	20	AAV25975	Mistletoe lectin B
24	1289	90.8	533	20	AAV25975	Mistletoe lectin B
25	1289	90.8	533	20	AAV25973	Mistletoe lectin P
26	1289	90.8	533	20	AAV25976	Mistletoe lectin P
27	1246.5	87.8	267	19	AAV25976	Mistletoe lectin P
28	1142.5	78.3	263	22	AAV25976	Mistletoe lectin P
29	1078.5	76.0	263	22	AAV25976	Mistletoe lectin P
30	1078.5	76.0	263	22	AAV25976	Mistletoe lectin P
31	901.5	63.5	565	22	AAV25976	Mistletoe lectin P
32	901.5	63.5	565	22	AAV25976	Mistletoe lectin P
33	899.5	63.3	565	22	AAV25976	Mistletoe lectin P
34	899.5	63.3	565	22	AAV25976	Mistletoe lectin P
35	899.5	63.3	574	8	AAV25976	Mistletoe lectin P
36	899.5	63.3	574	10	AAV25976	Mistletoe lectin P
37	899.5	63.3	576	18	AAV25976	Mistletoe lectin P
38	899.5	63.3	576	21	AAV25976	Mistletoe lectin P
39	899.5	63.3	576	21	AAV25976	Mistletoe lectin P
40	899.5	63.3	576	22	AAV25976	Mistletoe lectin P
41	899.5	63.3	576	22	AAV25976	Mistletoe lectin P
42	899.5	63.3	576	22	AAV25976	Mistletoe lectin P
43	899.5	63.3	576	22	AAV25976	Mistletoe lectin P
44	899.5	63.3	576	22	AAV25976	Mistletoe lectin P
45	899.5	63.3	576	22	AAV25976	Mistletoe lectin P

## ALIGNMENTS

AAV25989	RESULT 1
AAV25989	AAV25989 standard; Protein; 264 AA.
AAV25989	18-OCT-1999 (first entry)
AAV25989	Mistletoe lectin B4 protein fragment.
AAV25989	Mistletoe lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
AAV25989	lymphokine-288 subunit; non-cytotoxic; T-cell activation; immune response;
AAV25989	lymphokine-producing macrophage; uncontrolled cell growth; treatment;
AAV25989	cancer; cytotoxicity; antigen; isoform; lectin B4.
AAV25989	Viscum album.
AAV25989	DEL9804210-A1.
AAV25989	12-AUG-1999.
AAV25989	03-FEB-1998; 98DE-1004210.
AAV25989	03-FEB-1998; 98DE-1004210.
AAV25989	(BIO-) BIOGEN ARZNEIMITTEL GMBH.
AAV25989	Morris P, Stiefel T, Voelter W, Welters P;
AAV25989	WPI; 1999-445335/38.
AAV25989	N-PSDB; AA209113.



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Ov 240 ANPELRRIIYPATGKPNQWMLPVF 264  
Db 549 SDPSLOQIILWSTGNPNQWMLTF 573

Search completed: December 11, 2003, 14:01:03  
Job time : 20.3487 secs

Query Match 52.4%; Score 744.5; DB 10; Length 382;  
Best Local Similarity 54.3%; Pred. No. 9,9e-55;  
Matches 133; Conservative 40; Mismatches 76; Indels 1; Gaps 1;  
DB 128 EPTVRIYGRNENRVDYDDPHDQNOQLMSKSNNDPNOQLTKEDGTHNSGCTLTW 68  
QY 9 EPTVRIYGRNENRVDYDDPHDQNOQLMSKSNNDPNOQLTKEDGTHNSGCTLTW 68  
QY 69 GTTAGVYVWIPDCNTAVREATTIWOINDGTIINFRSNLYLAASGIGTLYVQLDYTL 128  
DB 188 GIDPKNVWITDCTSAVEATWEIWDNGTIINPKSALYLSASSAMGKLTVOQRNDYRX 247  
QY 129 GQGLAGNTAPREVTIYGRDLQMSNGSIVWETCSSQKQKQKALYGDGSIIRPKON 188  
DB 248 RQNRKNDIISFTSINGSDCHMSNMALDCKRKKEQ-QMALIPDGSIRPVON 306  
QY 189 OQCLTSGRDSVSTVINVSQSGASGQWFTNEGATLAKGPMNDPAQPLKRLII 248  
DB 307 TNNCLTSKDHKQSGTIVLMGCSNMAQSWFTNKGDSYVSLVDPMWVYKSDPSLKOII 366  
QY 249 IYPATGKQNMALFVE 264  
DB 367 LWPYTKQKQIWLTLF 382  
RESULT 14  
QWME9 PRELIMINARY; PRT; 547 AA.  
AC QWME9;  
DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Preproagglutinin (EC 3.2.2.22) (RNA N-glycosidase).  
GN Agg.  
OS Abrys precatorius (Indian licorice) (Crab's eye).  
OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;  
OC Fabales; Fabaceae; Papilionoideae; Adreaceae; Abrys.  
CX NCBI\_TaxID=35876;  
RN [1]\_taxid=35876;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20102702; PubMed=10636890;  
RA Liu C.L., Teal C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,  
Lin C.Y.;  
RT "Primary Structure and Function Analysis of the Abrys precatorius  
Agglutinin A Chain by Site-directed Mutagenesis: Pro199 of Amphiphilic  
Alpha-Helix H Impacts Protein Synthesis Inhibitory Activity.";  
RT J. Biol. Chem. 275:1897-1901(2000).  
CC -1- CATALYTIC ACTIVITY: ENDOW/GENBANK/DDBJ DATABASES OF THE N-GLYCOSIDIC BOND AT ONE  
CC -1- SPECIFIC ADENOSINE OF THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: AF190173; AAF2809.1; .  
DR HSSP: P1140; 1ABR.  
DR InterPro: IPR006772; Ricin\_B\_lectin.  
DR eFam: PF00652; Ricin\_B\_lectin; 6.  
DR eFam: PF00161; RIF; 1.  
DR PRINTS: PR00396; SHIGARICIN.  
DR SMART: SM00458; RICIN\_2.  
DR PROSITE: PS00225; RICIN\_B\_LECTIN; 2.  
DR PROSITE: PS00225; SHIGA\_RICIN; 1.  
KM Hydrolyase; Toxin.  
SQ SEQUENCE 547 AA; 61248 MW; 355A32C03354A1BD CRC64;

Query Match 52.4%; Score 744; DB 10; Length 547;  
Best Local Similarity 54.0%; Pred. No. 1.7e-54;  
Matches 141; Conservative 39; Mismatches 79; Indels 2; Gaps 2;  
DB 288 CSHTPEYRIKGRDGLCVNSDVAHNSNIDITLAKCKDGLTVOQLMTLKSDYTRSKQ 347

QY 64 CLITGYTAGVYVWIPDCNTAVREATTIWOINDGTIINFRSNLYLAASGIGKATTLVOT 123  
DB 348 CLITGYTAGVYVWIPDCNTAVREATTIWOINDGTIINFRSNLYLAASGIGKATTLVOT 123  
QY 124 LDYTLQGMALNSDAPREVTIYGRDLQMSNGSIVWETCSSQKQKQKALYGDGSIIRPKON 183  
DB 408 NQYKMQQMTNSDPSFTSINGSDCHMSNMALDCKRKKEQ-QMALIPDGSIRPVON 306  
QY 184 RQNRKNDIISFTSINGSDCHMSNMALDCKRKKEQ-QMALIPDGSIRPVON 306  
DB 467 RQNRKNDIISFTSINGSDCHMSNMALDCKRKKEQ-QMALIPDGSIRPVON 306  
QY 244 LRRITIIYPATGKQNMALFVE 264  
DB 527 LKQIIMPYTKQKQIWLTLF 382  
RESULT 15  
QWME9 PRELIMINARY; PRT; 573 AA.  
AC QWME9;  
DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Ribosome-inactivating protein IPak (EC 3.2.2.22) (RNA N-glycosidase) (Fragment).  
GN LECTINAR.  
OS Itis hollandica (Dutch iris).  
OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;  
CX NCBI\_TaxID=35876;  
RN [1]\_taxid=35876;  
RP SEQUENCE FROM N.A.  
RX Van Damme E.J.M., Peumans W.J.;  
RT "Itis (Itis hollandica var. Professor Blaauw) plants express both type  
RT 1 and type 2 ribosome-inactivating proteins in bulb tissue.";  
RT Submitted (Apr-2000) to the EMBL/GenBank/DDBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOW/GENBANK/DDBJ DATABASES OF THE N-GLYCOSIDIC BOND AT ONE  
CC -1- SPECIFIC ADENOSINE OF THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL: AF265900; AF26591.1; .  
DR HSSP: P1140; 1ABR.  
DR InterPro: IPR001574; RIF; 1.  
DR eFam: PF00652; Ricin\_B\_lectin; 6.  
DR eFam: PF00161; RIF; 1.  
DR PRINTS: PR00396; SHIGARICIN.  
DR SMART: SM00458; RICIN\_2.  
DR PROSITE: PS00221; RICIN\_B\_LECTIN; 2.  
DR PROSITE: PS00225; SHIGA\_RICIN; 1.  
KM Hydrolyase; Toxin.  
SQ SEQUENCE 573 AA; 63759 MW; 141A39A8C04F5C CRC64;  
Query Match 47.6%; Score 676.5; DB 10; Length 573;  
Best Local Similarity 50.2%; Pred. No. 9e-49;  
Matches 133; Conservative 39; Mismatches 90; Indels 3; Gaps 3;  
DB 1 DWTGASAEPTVRIYGRNENRVDYDDPHDQNOQLMSKSNNDPNOQLTKEDGTHNSGCTLTW 68  
QY 311 EDDTCSEPTVRIYGRNENRVDYDDPHDQNOQLMSKSNNDPNOQLTKEDGTHNSGCTLTW 68  
DB 371 NQYKMQQMTNSDPSFTSINGSDCHMSNMALDCKRKKEQ-QMALIPDGSIRPVON 306  
QY 124 LDYTLQGMALNSDAPREVTIYGRDLQMSNGSIVWETCSSQKQKQKALYGDGSIIRPKON 183  
DB 408 NQYKMQQMTNSDPSFTSINGSDCHMSNMALDCKRKKEQ-QMALIPDGSIRPVON 306  
QY 184 RQNRKNDIISFTSINGSDCHMSNMALDCKRKKEQ-QMALIPDGSIRPVON 306  
DB 467 RQNRKNDIISFTSINGSDCHMSNMALDCKRKKEQ-QMALIPDGSIRPVON 306  
QY 244 LRRITIIYPATGKQNMALFVE 264  
DB 527 LKQIIMPYTKQKQIWLTLF 382

RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)  
 RT genes encoding cinnamomin proteins and study of their expression  
 RT patterns" (JUN-2001) to the EMBL/GenBank/DBJ databases  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases  
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: AY039801; AK82458.1; -  
 DR Interpro: IPR000772; RICHIN\_B\_lectin.  
 DR Interpro: IPR001574; RIP.  
 DR Pfam: PF00652; RICHIN\_B\_lectin; 5.  
 DR PRINTS: PR00386; SHIGA\_RICHIN.  
 DR SMART: SM00458; RICHIN\_2.  
 DR PROSITE: PS0231; RICHIN\_B\_lectin; 2.  
 DR SIGNAL: Signal; RICHIN.  
 FT CHAIN 33 581  
 FT SIGNAL 32  
 FT CHAIN 33 581  
 SQ SEQUENCE 581 AA; 64215 MW; 6882F88FBAAD196 CRC64;  
 CINNAMOMIN I.  
 Query Match 57.6%; Score 817.5; DB 10; Length 581;  
 Best Local Similarity 59.2%; Pred. No. 1.2e-60;  
 Matches 157; Conservative 32; Mismatches 73; Indels 3; Gaps 2;  
 QY 1 DDTTCSASPTTAVGKRGKRVDDPHQNGQIQIIPKSNDDPQGLTIRKGTIS 60  
 DB 317 NDTICADPEPTVRLSGKGLCDVDDKXKNQNTLWFCQNSDVQGLTRDGLAIS 376  
 QY 61 NSCLITGVYAGVYVMIFCQNTAVREATIQTQINDGRTINPESNVLAASSGKLTIT 120  
 DB 377 NGKCLITNGVSGDYVMIYDCRTPTVASIYQFWANGTIIINPQSLVALASGSPFTLT 436  
 QY 121 VQTLDTLQCGMLAGNDTAPREVTIYFEDLQNSGSGVWVETDSSQKQKALYGD 180  
 DB 437 VQANTVSRQGLMGNTEPTVTSIVGFNDLQWAGMAMVBCSSQAGQ-KMALTPD 495  
 QY 181 GSTRPKQND--CCTSGRDSVSTVNIYSGSGASQGRVTEGAILINKKPKNDRA 238  
 DB 436 GSTRHODPEPAQCEFLDNRHQSGLIISSCSPOSSEGRWPFMDGVYINLAKGLWVQK 555  
 QY 239 QANPLRRIITVPATKRNQWMLPV 263  
 DB 556 GSRPELHQIILWPAKRNPMHMLPV 580  
 RESULT 12  
 Q06076 PRELIMINARY; PRT; 528 AA.  
 ID Q06076  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Abirin-d (BC 3.2.2.22) (rRNA N-glycosylase) (Fragment).  
 OS Abrus precatorius (Indian licorice) (Crab's eye).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
 NX NCBI\_TaxID=3816;  
 RX 111  
 SEQUENCE FROM N.B.  
 RA Huang C.H., Lee M.-C., Lee T.-Y.;  
 RA "Primary structure of three distinct isobutins determined by cDNA  
 RA sequencing: conservation and significance";  
 RL J. Mol. Biol. 229:263-267(1993).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: M89346; AA83626.1; -  
 DR HSR; F1140; IAAK.  
 DR Interpro: IPR000772; RICHIN\_B\_lectin.  
 DR Interpro: IPR001574; RIP.  
 SQ SEQUENCE 382 AA; 42743 MW; B08AB341913AD2EE CRC64;

DR Pfam: PF00652; RICHIN\_B\_lectin; 6.  
 DR PRINTS: PR00386; SHIGA\_RICHIN.  
 DR SMART: SM00458; RICHIN\_2.  
 DR PROSITE: PS0231; RICHIN\_B\_lectin; 2.  
 DR PROSITE: PS00275; SHIGA\_RICHIN; 1.  
 KW Hydrolyase; Toxin.  
 FT NON-TER 1  
 FT NON-TER 528  
 SQ SEQUENCE 528 AA; 58870 MW; 62BD42F88FEE60F8 CRC64;  
 Query Match 53.4%; Score 789; DB 10; Length 528;  
 Best Local Similarity 54.8%; Pred. No. 1.1e-55;  
 Matches 143; Conservative 43; Mismatches 73; Indels 2; Gaps 2;  
 QY 5 CSAS-EPYVAVGKRGKRVDDPHQNGQIQIIPKSNDDPQGLTIRKGTIS 63  
 DB 269 GSRVEPTVRLSGKGLCDVDDKXKNQNTLWFCQNSDVQGLTRDGLAIS 328  
 QY 64 CLITGVYAGVYVMIFCQNTAVREATIQTQINDGRTINPESNVLAASSGKLTITVQT 123  
 DB 329 CLITGVYAGVYVMIYDCRTPTVASIYQFWANGTIIINPQSLVALASGSPFTLT 388  
 QY 124 DDTTCSASPTTAVGKRGKRVDDPHQNGQIQIIPKSNDDPQGLTIRKGTIS 183  
 DB 389 NDTICADPEPTVRLSGKGLCDVDDKXKNQNTLWFCQNSDVQGLTRDGLAIS 507  
 QY 184 RPKNDQDCLTSGRDSVSTVNIYSGSGASQGRVTEGAILINKKPKNDRA 243  
 DB 448 RSVQNTNNCLTSGRDSVSTVNIYSGSGASQGRVTEGAILINKKPKNDRA 507  
 QY 244 LERITIIYVPATKRNQWMLPV 264  
 DB 508 LKQIILWPAKRNPMHMLPV 528  
 RESULT 13  
 ID Q88A43  
 AC Q88A43  
 DT 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Abirin isoform G (BC 3.2.2.22) (rRNA N-glycosylase) (Fragment).  
 OS Abrus precatorius (Indian licorice) (Crab's eye).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
 NX NCBI\_TaxID=3816;  
 RX 111  
 SEQUENCE FROM N.A.  
 RA Cook J.P., Roberts L.M., Lord M.;  
 RA "New isoform of abirin - Abirin G";  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: AY039801; AK82458.1; -  
 DR Interpro: IPR000772; RICHIN\_B\_lectin.  
 DR Interpro: IPR001574; RIP.  
 DR Pfam: PF00652; RICHIN\_B\_lectin; 6.  
 DR PRINTS: PR00386; SHIGA\_RICHIN; 2.  
 DR PROSITE: PS0231; RICHIN\_B\_lectin; 2.  
 DR PROSITE: PS00275; SHIGA\_RICHIN; 1.  
 KW Hydrolyase; Toxin.  
 FT NON-TER 1  
 FT NON-TER 528  
 SQ SEQUENCE 382 AA; 42743 MW; B08AB341913AD2EE CRC64;

Db 496 GSIRPHODRCLSTIDNHSQSLIIISCSFSSBQGRVFWMDGLTLNKLNGLVMDVK 555  
 QY 240 ANPKLRRIIYPATGKPNQMWLPV 263  
 Db 556 SNPSLHQLIIPATGKPNQMWLP 579

## RESULT 9

Q94BM3 PRELIMINARY; PRT; 580 AA.  
 ID Q94BM3  
 DT 01-MAR-2001 (TRENBERL 19, Created)  
 DT 01-DEC-2001 (TRENBERL 19, Last sequence update)  
 DT 01-MAR-2003 (TRENBERL 22, Last annotation update)  
 DE Type 2 ribosome-inactivating protein cinnamomin III precursor  
 DE (EC 3.2.2.22) (RNA N-glycosidase)  
 OS Cinnamomum camphora (Camphor tree)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 NCBI\_TaxID=13429;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Yang Q., Gong Z.Z., Liu W.Y.;  
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)  
 RT genes encoding cinnamomin proteins and study of their expression  
 RT status."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SITE.  
 CC DR EMBL; AY039803; AK82460.1; -  
 CC DR Interpro; IPR000772; RiciB\_B\_lectin.  
 CC DR Pfam; PF00652; RiciB\_B\_lectin; 6.  
 CC DR PRINTS; PR00161; RIP; 1.  
 CC DR SMART; PR00396; SHIGARICIN.  
 CC DR PROSITE; PS0231; RICIIN\_2.  
 CC DR PROSITE; PS0231; RICIIN\_2.  
 CC DR Hydroxylase; Toxin.  
 CC KW SIGNAL 33  
 CC FT CHAIN 1  
 CC FT SIGNAL 32  
 CC FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN  
 CC FT CINNAMOMIN III.  
 CC SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7F558 CRC64;

Query Match 60.3%; Score 856; DB 10; Length 580;  
 Best Local Similarity 62.1%; Pseq. No. 6,5e-64;  
 Matches 164; Conservative 33; Mismatches 65; Indels 2; Gaps 2;

QY 1 DDTYCSASEPTVYVGNKGVNVDPPDFDNDQIOLMPSKSNNDPQGLTIRGRTIS 60  
 Db 317 NDDTCADDEPTVYVGNKGVNVDPPDFDNDQIOLMPSKSNNDPQGLTIRGRTIS 376  
 QY 61 NSGCLTYGTAGYVWVIFPCVTAWEATVITQVINGIINPESNLVLAASGIGCTLT 120  
 Db 377 NCKLTNGVSGDYVWVIFPCVTAWEATVITQVINGIINPESNLVLAASGIGCTLT 436  
 QY 121 VGLDLYTLAGQWLAGNDPAFREVIITGPFDDIOMESNGSVWVETCSQKQKVALYGD 180  
 Db 437 VQADLYTLAGQWLAGNDPAFREVIITGPFDDIOMESNGSVWVETCSQKQKVALYGD 495  
 QY 181 GSIRPKONODCLTS-GRDSVYTVINIVGSGASGQWTFINEGLINLKKGPAMDVQA 239  
 Db 496 GSIRPHODRCLSTIDNHSQSLIIISCSFSSBQGRVFWMDGLTLNKLNGLVMDVK 555  
 QY 240 ANPKLRRIIYPATGKPNQMWLPV 263  
 Db 556 SNPSLHQLIIPATGKPNQMWLP 579

RESULT 10  
 Q94BM3 PRELIMINARY; PRT; 549 AA.  
 ID Q94BM3

AC Q94BM3  
 DT 01-MAR-2001 (TRENBERL 16, Created)  
 DT 01-MAR-2001 (TRENBERL 16, Last sequence update)  
 DT 01-OCT-2002 (TRENBERL 22, Last annotation update)  
 DE Type II ribosome-inactivating protein cinnamomin IEC 3.2.2.22) (RNA  
 DE N-glycosidase) (Fragment)  
 OS Cinnamomum camphora (Camphor tree)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 NCBI\_TaxID=13429;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Xie L., Liu W.-Y., Wang E.-D.;  
 RT "Molecular cloning of cinnamomin A-, B-chain and the expression,  
 RT purification, characterization and mutagenesis of the A-chain."  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SITE.  
 CC CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC EMBL; AF23548; AF68978.2; -  
 CC DR Interpro; IPR000772; RiciB\_B\_lectin.  
 CC DR Pfam; PF00652; RiciB\_B\_lectin; 5.  
 CC DR PRINTS; PR00161; RIP; 1.  
 CC DR SMART; SM00458; RICIIN\_2.  
 CC DR PROSITE; PS0231; RICIIN\_2.  
 CC DR Hydroxylase; Toxin.  
 CC KW NON-TER  
 CC FT CHAIN 1  
 CC FT SIGNAL 1  
 CC SQ SEQUENCE 549 AA; 60648 MW; 02607E607C44B0 CRC64;

Query Match 57.6%; Score 817.5; DB 10; Length 549;  
 Best Local Similarity 59.2%; Pseq. No. 1.1e-60;  
 Matches 167; Conservative 32; Mismatches 75; Indels 3; Gaps 2;

QY 1 DDTYCSASEPTVYVGNKGVNVDPPDFDNDQIOLMPSKSNNDPQGLTIRGRTIS 60  
 Db 285 NDDTCADDEPTVYVGNKGVNVDPPDFDNDQIOLMPSKSNNDPQGLTIRGRTIS 344  
 QY 61 NSGCLTYGTAGYVWVIFPCVTAWEATVITQVINGIINPESNLVLAASGIGCTLT 120  
 Db 345 NCKLTNGVSGDYVWVIFPCVTAWEATVITQVINGIINPESNLVLAASGIGCTLT 404  
 QY 121 VGLDLYTLAGQWLAGNDPAFREVIITGPFDDIOMESNGSVWVETCSQKQKVALYGD 180  
 Db 405 VQADLYTLAGQWLAGNDPAFREVIITGPFDDIOMESNGSVWVETCSQKQKVALYGD 463  
 QY 181 GSIRPKONODCLTS-GRDSVYTVINIVGSGASGQWTFINEGLINLKKGPAMDVQA 239  
 Db 466 GSIRPHODRCLSTIDNHSQSLIIISCSFSSBQGRVFWMDGLTLNKLNGLVMDVK 523  
 QY 239 ANPKLRRIIYPATGKPNQMWLPV 263  
 Db 524 SNPSLHQLIIPATGKPNQMWLP 548

RESULT 11  
 Q94BM3 PRELIMINARY; PRT; 581 AA.  
 ID Q94BM3  
 DT 01-DEC-2001 (TRENBERL 19, Created)  
 DT 01-DEC-2001 (TRENBERL 19, Last sequence update)  
 DT 01-MAR-2003 (TRENBERL 23, Last annotation update)  
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor  
 DE (EC 3.2.2.22) (RNA N-glycosidase)  
 OS Cinnamomum camphora (Camphor tree)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC NCBI\_TaxID=13429;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Yang Q., Gong Z.Z., Liu W.Y.;

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us-09-601-667c-10.rsp

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[illegible]

Query Match	63.5%;	Score 901.5;	DB 10;	Length 541;
Best Local Similarity	63.5%;	Pred. No. 8.6e-68;		
Matches 165;	Conservative 33;	Mismatches 61;	Indels 1;	Gaps 1

[illegible]

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RESULT 7
O41143
ID O41143      PRELIMINARY;      PRT;      263 AA.
AC O41143
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ricin E beta chain (Fragment).
GN R1CIN E BETA CHAIN.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosoids I; Malviales; Euphorbiales; Euphorbiaceae; Ricinus.
OC NCBI_TaxId=3988;
OX

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RP SEQUENCE FROM N.A.  
 RA Ladin B.F., Wmzey S.E., Halling A.C., Halling K.C., Tilketeane N.F.,  
 XA Long G.L., Houston J.L., Weaver R.F.,  
 DR "The effect of the *Pinus strobus* seedling root system on the growth of  
 DR *Pinus strobus* seedlings in the presence of the castor *Rhus glabra* commu-  
 RT nities",  
 PL Plant Mol. Biol. 9:287-295 (1987).  
 DL EMBL: J16761; AAB63506.1. -.  
 DR HSSP: P02879; 2A41.  
 DR InterPro: IR0000772; Rctin\_B lectin.  
 DR InterPro: IR001400; Somatostatin.  
 DR SMART: SM0045; RCTIN\_6.  
 DR PROSITE: PS00231; RCTIN\_B\_LECTIN.  
 DR PROSITE: PS00338; SOMATOSTATIN\_2; 1.  
 FT NON TER 1  
 SC SEQUENCE 263 AA; 29136 MW; ABB80FDDDD1D1E144 CRC64;

Query Match 60.8%; Score 864; DB 10; length 263;  
Best Local Similarity 60.9%; Pred. No. 5, 1e-65;  
Matches 159; Conservative 37; Mismatches 63; Indels 2; Gaps 2

QY 5 CSASEPTVRIVGRNGMRVDVRDDDFHDGNOIQWPSKSNNDPNQJWTKRDGTRNSGSC 6

Db 4 GADPPEVLEVARNGACVDSDFRHNHGAIDLCKECSKSTDAQMLTKLSDYDLSNMGK  
Qy 65 LITVGTAGTYWMLPDCNTANKEATITQWMDGTTINPESNVLAASSGIKSTLWYCL 124  
D5 64 LITVGTAGTYWMLPDCNTANKEATITQWMDGTTINPESNVLAASSGIKSTLWYCL 123  
Db 65 LITVGTAGTYWMLPDCNTANKEATITQWMDGTTINPESNVLAASSGIKSTLWYCL 124  
Qy 125 DLTGCGGACAGDPAARETITVDFPDLCAMSGSGYVWFEDSGNONGKMLYQDSIR 184  
D5 124 IYVSGGMLPENNQGFYITIVGLYGMCIQANSSKWELED-ITSEAPQOMALYVDSIR 183  
Qy 124 IYVSGGMLPENNQGFYITIVGLYGMCIQANSSKWELED-ITSEAPQOMALYVDSIR 184  
D5 165 PRONDDCLTSRDSYSTVNIIVYSGASGSSQWVFWETNEGATLNLKKPDMVDAQAP-K-243  
Qy 183 PQONDDCLITDAINIKGYLVYLLSGVSSQGWFWEDNDGTTLNLYGLVLDVRSDDPS 242  
Db 244 LRRLITVPATKPNQMLPVE 264  
Qy 243 LKQIIVHFPAGNLNQTWLEP 263

QY		244 LRRIITPATGKPNQMILPVF	264
	:: ::   :: :		
DB		243 LKOIIVHPHGMLNQIMLPVF	263

```

RESULT 8
O34BW4
ID O34BW4 PRELIMINARY; ERT; 580 AA.
AC O34BW4;
DT 01-DEC-2001 (7-EMBLrel. 19 Created)
DT 01-MAR-2003 (1-EMBLrel. 23 last annotation update)
DT 01-MAR-2003 (7-EMBLrel. 23 last annotation update)
DB Type 2- ribosome-inactivating protein cinnaomom II precursor
DB (EC 3.2.2.22) (tRNA N-glycosidase) .
DE Cinnamomum camphora (Camphor tree).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
OC Spermatophyta; Magnoliophyta; Laurales;
OC NCBITaxID=13129;
NCBI [1]

```

RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)  
RT genes encoding cinnamomyl proteins and study of their expression  
RT patterns"  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RL -1- CATALYTIC ACTIVITY: ENOHDYOLYSIS OF THE N-GLYCOSIDIC BOND AT OHEN  
CC SPECIFIC ADENOSINE ON THE 24S RRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC EMBL, AF039802; AKR82459.1; "  
DR InterPro; IPR000772; R1chB\_1lectin.  
DR InterPro; IPR001574; R1P.  
DR Pfam; PF00652; R1chB\_1lectin. 6.  
DR Pfam; PF00161; R1P. 1.  
DR PRINTS; PR00386; SH1GALICIN.  
DR SMART; SM00458; R1chB\_2\_Activity 3.

[illegible]

121 VQILDYTI GOGWLAGNDTAPREVTIYCFRDLMESNGSVWVETCDSSQJKNQKXWALYGD 18

181 CSTRBKONODOCI.TS-CBDSVSTVNTIVSCSGASGSOBWHTNKGALLNI.KRGDAMNVZO 23

[illegible]

RA	PAK C.-H., Lee D.-Y., Kang T.-B., Lee K.-H., Yoon T.-Y., Kim J.-B.,	
RA	Do M.-S., Song S.K.,	
RT	"cDNA cloning and sequence analysis of the lectin genes of the Korean	
RT	"mistlecote (Viscum album coloratum)."	
RA	W01. Cells 12:215-220(2001).	
AP	SEQUENCE FROM N.A.	
RA	Park C.-H., Lee D.-Y., Kang T.-B., Lee K.-H., Yoon T.-Y., Kim J.-B.,	
RA	Do M.-S., Song S.K.,	
RL	Submitted (May-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL, AF506917; AAM6635.1; "	
DR	InterPro: IPR000772; Rctin_B_lectin.	
DR	PIRSM, P00652; Rctin_B_lectin; 5.	
DR	PROSITE, PS00453; Rctin_B_lectin; 5.	
DR	PROSITE, PS00453; Rctin_B_lectin; 2.	
FT	NON TER 1	
FT	NON TER 265	
FT	NON TER 266	
SQ	SEQUENCE 266 AA; 29537 MW; 4A51473C37B94C73 CRC64;	
Query Match	63.9%; Score 992; DB 10; Length 266;	
Best Local Similarity	69.2%; Match No. 6; e-1e-76;	
Matches 184;	Consecutive 31; Pseudocores 47; Indels 4; Gaps 2;	
Ds	1 DDTCTGSAAPVAVYVGRNGKRDYRDPDHPHQNGIQIDMPKSKNPGQCTATKGGCTGRS 50	
Ds	1 DDTCTGSAAPVAVYVGRNGKRDYRDPDHPHQNGIQIDMPKSKNPGQCTATKGGCTGRS 60	
Ds	1 DDTCTGSAAPVAVYVGRNGKRDYRDPDHPHQNGIQIDMPKSKNPGQCTATKGGCTGRS 117	
Ds	61 NSGCLTYGVGVGVVYVYVPCGNVAVRATVQINDGTVINPESVLT--AAAGSIXGT 117	
Ds	61 NSGCLTYGVGVGVVYVYVPCGNVAVRATVQINDGTVINPESVLT--AAAGSIXGT 120	
Ds	61 NSGCLTYGVGVGVVYVYVPCGNVAVRATVQINDGTVINPESVLT--AAAGSIXGT 179	
Ds	121 LTFDVLDSVAGQAGVADNDKARVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 179	
Ds	118 TLTVOVLDTVYV 177	
Ds	118 YGVSGIPKPNODCLTSGEDSVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 227	
Ds	186 YGVSGIPKPNODCLTSGEDSVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 239	
Ds	238 AANPKLRRITVYV 263	
Ds	240 AASNSPLRRITVYV 265	
RESULT 6		
ID	Q41174	PRELIMINARY; PRT; 541 AA.
AC	Q41174;	
DT	01-NOV-1996 (TREMBLrel. 01, Created)	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 03, Last annotation update)	
DS	Protein A chain (BC 3.2.2.22) (TRNA N-glycosylase)	
OS	Ricinus communis (Castor bean).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliopsida; eudicotyledons; Core eudicots; Rosidae;	
OC	eurosid 1; Malpighiales; Euphorbiaceae; Ricinus.	
OX	NCBI_taxid=3989;	
EN	[1]	
EN	SEQUENCE FROM N.A.	
KX	MEHLINS-93383.7; PubMed:1633211;	
KX	MEHLINS-93383.7; PubMed:1633211;	
RT	"Molecular cloning of ricin." by Z.M.,	
RL	Tagged Disgn. Theor. 7:81-97(1992).	
CC	-1- CATALYTIC ACTIVITY. ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE	
CC	SPECIFIC ADENOSINE ON THE 28S RNA.	
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
DR	EMBL, 540365; AAB2582.1; "	
DR	HSBP, P02879; 186.	
DR	InterPro: IPR000772; Rctin_B_lectin.	
DR	InterPro: IPR001574; RfP.	
DR	InterPro: IPR001400; Semotocropin.	
DR	PIRSM, P00652; Rctin_B_lectin; 6.	

Matches 245; Conservative 4; Mismatches 13; Indels 1; Gaps 1;  
QY 1 DDTVCASEPTAIVGKNGKGVVVDHDDPHDNOIQIWPESKNDPNQIWKEDGTIRS 60  
DB 269 DDTVCASEPTAIVGKNGKGVVVDHDDPHDNOIQIWPESKNDPNQIWKEDGTIRS 328  
QY 61 NSGCLTYGTAGYVMIEDCNVAREKATITWIMDNGITINPSNVLAASSGKGTIT 120  
DB 329 NSGCLTYGTAGYVMIEDCNVAREKATITWIMDNGITINPSNVLAASSGKGTIT 388  
QY 121 VQTLDTYLGQGLAGNDTAPREVTIYGRDLCSNNGSVWVETCVSGKQNG-KMALYCD 180  
DB 389 VQTLDTYLGQGLAGNDTAPREVTIYGRDLCSNNGSVWVETCVSGKQNG-KMALYCD 447  
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNEGAILNKGPAMDVAQA 240  
DB 448 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNEGAILNKGLAMDVAQS 507  
QY 241 NPKLRRIITYPATGKNQMWLPV 263  
DB 508 NPKLRRIITYPATGKNQMWLPV 570  
RESULT 2  
ID Q8LK02 PRELIMINARY; FRT; 263 AA.  
AC Q8LK02;  
DT 01-OCT-2002 (Tremblrel. 22, Created).  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Lectin Chain B isoform 2 (fragment).  
OS Viscum album subsp. coloratum.  
OC Burkariaceae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicot;  
OC Spectralia; Viscaceae; Viscum.  
NCBI\_TaxID:159976;  
RN [1]\_TaxID:159976;  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21566752; PubMed-11710524;  
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,  
Do M.-S., Song S.K.;  
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean  
mistletoe (Viscum album coloratum).";  
RT M01. Cells 12:215-220(2001).  
RN [1]\_TaxID:159976;  
RA SEQUENCE FROM N.A.  
RX Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,  
Do M.-S., Song S.K.;  
RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF508918; AA04636.1; -;  
DR InterPro: IPR000772; Ricin\_B\_lectin.  
DR Pfam: PF00652; Ricin\_B\_lectin; 5.  
DR SMART: SM00458; RICIN\_2.  
DR PROSITE: PS50231; RICIN\_B\_LECTIN; 2.  
FT NON\_TER 1  
FT NON\_TER 263  
SQ SEQUENCE 263 AA; 29150 MW; 8685BCB7C4CDD1P CRC64;  
Query Match 78.3%; Score 1112.5; DB 10; Length 263;  
Best Local Similarity 78.7%; Pred. No. 5,46-86;  
Matches 207; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNEGAILNKGPAMDVAQA 240  
DB 180 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGRWFTNEGAILNKGLAMDVAQS 239  
QY 241 NPKLRRIITYPATGKNQMWLPV 263  
DB 240 NPKLRRIITYPATGKNQMWLPV 262  
RESULT 3  
ID Q8W243 PRELIMINARY; FRT; 565 AA.  
AC Q8W243;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE VCA precursor (EC 3.2.2.23) (RNA N-glycosidase).  
OS Viscum album subsp. coloratum.  
OC Burkariaceae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicot;  
OC Spectralia; Viscaceae; Viscum.  
NCBI\_TaxID:159976;  
RN [1]\_TaxID:159976;  
RP SEQUENCE FROM N.A.  
RX Park W.-B., Lyu S.-I.  
RT Cloning of Viscum album subsp. coloratum (Korean mistletoe)."  
RT Biochem. Biophys. Res. Commun. 0:0(2002).  
CC -I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC EMBL: AF508918; AA04636.1; -;  
DR InterPro: IPR000772; Ricin\_B\_lectin.  
DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
DR PRINTS: PR00396; SHIGARICIN.  
DR SMART: SM00459; RICIN\_2.  
DR PROSITE: PS50231; RICIN\_B\_LECTIN; 2.  
RX Hydrolyase; Signal; Toxin.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 273 VCA ALPHA CHAIN.  
FT CHAIN 309 565  
SQ SEQUENCE 565 AA; 62401 MW; 591E394D005F11 CRC64;  
Query Match 77.4%; Score 1099.5; DB 10; Length 565;  
Best Local Similarity 79.8%; Pred. No. 1,66-84;  
Matches 210; Conservative 15; Mismatches 33; Indels 5; Gaps 2;

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us-09-601-667c-10.rpt

Page 1

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 20.3487 seconds  
(without alignments)  
3347.915 Million cell updates/sec

Title: US-09-601-667C-10  
Perfect score: 1420  
Sequence: 1 DDVTCSSASEPTRIIVGRNKN.....RRITIPATCKDNQMLPVF 264

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_reptile:\*  
13: sp\_wetphare:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1303.5	91.8	531	10 QBRX6	QBRX6 viscum albu
2	1112.5	78.3	263	10 QBRX2	QBRX2 viscum albu
3	1099.5	77.4	565	10 QBRW43	QBRW43 viscum albu
4	1078.5	76.0	263	10 QBRX01	QBRX01 viscum albu
5	992	63.9	266	10 QBRX03	QBRX03 viscum albu
6	901.5	63.5	541	10 QBRX03	QBRX03 viscum albu
7	883	60.8	263	10 QBRX03	QBRX03 viscum albu
8	866	60.3	580	10 QBRX03	QBRX03 viscum albu
9	817.5	57.6	549	10 QBRX03	QBRX03 viscum albu
10	817.5	57.6	581	10 QBRX03	QBRX03 viscum albu
11	758	53.4	528	10 QBRX03	QBRX03 viscum albu
12	744.5	52.4	382	10 QBRX03	QBRX03 viscum albu
13	744	52.4	547	10 QBRX03	QBRX03 viscum albu
14	744	52.4	547	10 QBRX03	QBRX03 viscum albu
15	676.5	47.6	573	10 QBRX03	QBRX03 viscum albu
16	676.5	47.6	592	10 QBRX03	QBRX03 viscum albu

17	571	40.2	570	10 QBRX03	QBRX03 viscum albu
18	560.5	39.5	564	10 QBRX03	QBRX03 viscum albu
19	558.5	39.3	316	10 QBRX03	QBRX03 viscum albu
20	557.5	39.3	316	10 QBRX03	QBRX03 viscum albu
21	556.5	39.2	316	10 QBRX03	QBRX03 viscum albu
22	539.5	38.0	563	10 QBRX03	QBRX03 viscum albu
23	537	37.8	570	10 QBRX03	QBRX03 viscum albu
24	520.5	37.4	520	10 QBRX03	QBRX03 viscum albu
25	520.5	37.4	520	10 QBRX03	QBRX03 viscum albu
26	528.5	37.2	563	10 QBRX03	QBRX03 viscum albu
27	527	37.1	604	10 QBRX03	QBRX03 viscum albu
28	522	36.8	603	10 QBRX03	QBRX03 viscum albu
29	519.5	36.6	320	10 QBRX03	QBRX03 viscum albu
30	509	35.8	565	10 QBRX03	QBRX03 viscum albu
31	507	35.7	307	10 QBRX03	QBRX03 viscum albu
32	506	35.6	566	10 QBRX03	QBRX03 viscum albu
33	441	31.1	569	10 QBRX03	QBRX03 viscum albu
34	182.5	13.9	293	10 QBRX03	QBRX03 viscum albu
35	142	10.0	422	10 QBRX03	QBRX03 viscum albu
36	136	9.6	377	2 QBRX03	QBRX03 viscum albu
37	136	9.6	377	2 QBRX03	QBRX03 viscum albu
38	122.5	8.2	422	10 QBRX03	QBRX03 viscum albu
39	122.5	8.2	422	10 QBRX03	QBRX03 viscum albu
40	120.5	8.5	962	16 QBRX03	QBRX03 viscum albu
41	120.5	8.5	962	16 QBRX03	QBRX03 viscum albu
42	120	8.5	579	16 QBRX03	QBRX03 viscum albu
43	113.5	8.0	476	2 QBRX03	QBRX03 viscum albu
44	113.5	8.0	476	2 QBRX03	QBRX03 viscum albu
45	113.5	8.0	1545	16 QBRX03	QBRX03 viscum albu

ALIGNMENTS

RESULT 1

ID QBRX6 PRELIMINARY; PRT: 531 AA.

AC QBRX6; 01-JUN-2002 (TREMUR1, 21, Created)

DT 01-JUN-2002 (TREMUR1, 21, Last sequence update)

DT 01-MAR-2003 (TREMUR1, 23, Last annotation update)

DE Lectin chain A isoform 1 (EC 3.2.2.22) (RNA N-glycosidase)

DS (Fragment)

OS Viscum album (European mistletoe)

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta

OC Stereocaulon (Mistletoe), Stereocaulon, Eubryophyta, Tracheophyta



Thu Dec 11 16:09:46 2003

us-09-601-667c-10.rsp

FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 545 AA; 60148 MM; 2DCSN710CB95D9C CRC64;

Query Match 6.9%; Score 97.5; DB 1; Length 545;  
Best Local Similarity 20.2%; Pred. No. 0.66; Indels 45; Gaps 8;  
Matches 46; Conservative 40; Mismatches 97;

QY 22 VDVRRDDPFDQNOIQLPSPKSNDDPNQIWKQDGTIRNSCLTYGYTA----- 72  
DB 342 LDIITRSLAMGBRLITVINKNT-----TVTRDIPVQWLGLETTCYTAEDLMGKTQ 395  
QY 73 ----GYVWIFDCNTAVENTWQ---IMDNTILNRSNLYLAASGIXGTTLVQTL 124  
DB 396 KISHIKIKILASHATNVRRLSLPQCSVVPDGLVFNASGCLTAA--NSSVAFQSC 452  
QY 125 DYTLGGWLAGNDTAPREVTIVGFRDLCEWNSGSIWETCCDSQAKGKALYQGLR 184  
DB 453 NGETSCIQWVTPSGVIREFS--QTQCLADNLYKLQACDSDSDSDQKWTVPYTHLK 509  
QY 185 PRONODQCLTSGRDSVSTVINIVCSAGSGCRWFTNEGAILNLKKG 232  
DB 510 -NAKTDGCLTEGS-----VQKMSC-----LYERDQVFGLESG 541

Search completed: December 11, 2003, 14:09:07  
Job time : 5.6201 secs

RC STRAIN-Bristol N2;  
RA MEDLINE=9819620; PubMed=9525933;  
RT Hagen F.R., Netter K.;  
RV "GENE cloning and expression of a family of UDP-N-acetyl-D-  
galactosamine-4-epimerase polypeptides catalyzing galactose-4-epimerase activity"  
RL J Biol. Chem. 273:8266-8277(1998).  
R [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN-Bristol N2;  
RY MEDLINE=9415071; PubMed=7906396;  
RZ Watson R., Atkinson R., Connell M.C., Baynes C., Berts M., Coulson A.,  
RA Bonfield U., Burton D., Crowell S., Copey T., Cooper U., Craxton W.,  
R Craxton W., Dear S., Du Z., Durbin R., Farrell A., Fraser A.,  
RA Fulton L., Gardner A., Green P., Hawkins I., Hillier L., Oler M.,  
RA Johnston L., Jones M., Karimov U., Kilstein E., Kishner P., Kishner P.,  
RA Paterson J., Perce G., Rifkin L., Rogers A., Sanders D., Shawken R.,  
RA Sims M., Smalton N., Smith A., Smith M., Sommer R., Staden R.,  
RA Sutcliffe J., Thayer-Wieg T., Thomas K., Vaughn M., Vaughan K.,  
RA Waterson R., Watson A., Weinstein L., Wilkinson-Spratt U.,  
RA Wohlschlag P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RV Nature 368:32-38(1994).  
RN [3]  
RU Deirions  
RV Watson R.;  
RW Submitted (Oct-2001) to the EMBL/Genbank/DDBB databases.  
CC -!- FUNCTION: THIS PROTEIN CATALYZES THE INITIAL REACTION IN O-LINKED  
CC OLIGOSACCHARIDE BIOSYNTHESIS, THE TRANSFER OF AN N-ACETYL-D-  
CC GALACTOSAMINE RESIDUE TO A SERINE OR THREONINE RESIDUE ON THE  
CC PROTEIN RECEPTOR.  
CC -!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactose + polypeptide =  
CC UDP + N-acetyl-D-galactosaminyl-polypeptide.  
CC -!- PATHWAY: glycosylation.  
CC -!- SUBSTRATE: GLYCOSYLATION TYPE II membrane protein [POTENTIAL].  
CC -!- COFACTOR: CALYX CYTOPLASMIC MEMBRANE PMWIX 2.  
CC -!- SIMILARITY: Contains 1 ricin B-type lectin domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See <http://www.isb-slc.ch/announcements>  
CC or send an email to [license@isb-slb.ch](mailto:license@isb-slb.ch)).  
CC -----  
CC EMBL: AF019337; AF019669.1;  
CC DR AF0221; AF0224.5f;  
DR EPI: AF0243; AF0243.1;  
DB MIMPEP: ZK68.8; CE96649.  
DR InterPro: IPRO01173; Glyco trans 2.  
DR InterPro: IPRO00772; Ricin\_B\_lectin.  
DR Pfam: PF00535; Glycosyltransferase\_2; 1.  
DR Pfam: PF00652; Ricin B\_lectin; 2.  
DR SMART: SM00458; Ricin\_I.  
DR PROSITE: PS00231; RICIN\_B\_LLECTIN; 1.  
DR Transmembrane; Glycosyltransferase; Transmembrane; Signal-anchor;  
KV Transmembrane; Lectin  
FT DOVAIN 1 33  
FT TRANSMEM 14 34  
CYTOPLASMIC (CYTOPLASMIC)  
CYTO-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
DOVAIN 35 612  
LUMENAL (POTENTIAL).  
RICIN\_B\_TYPB\_LLECTIN.  
RICIN\_B\_TYPB\_LLECTIN.  
N-LINKED (GLNAC... ) {POTENTIAL}.  
N-LINKED (GLNAC... ) {POTENTIAL}.  
SEQUENCE 612 AA; 66911 MW; 1031CFEFS319F858 CCKC64;  
Query Match 7.23; Score 102; DB 1; Length 612;  
Best Local Similarity 26.4%; Read No. 0,311.  
Matches 32; Conservative 23; Mismatches 50; Indels 16; Gaps 6

[illegible]

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DR EMBL; M64551; AAC26524.1; -  
 DR InterPro; IPR005193; Glyco\_hydro.62.  
 DR InterPro; IPR00772; Ricin\_B\_lectin.  
 DR Pfam; PF03654; Glyco\_hydro.62; 1.  
 DR SMART; SMO0254; Ricin\_B\_lectin; 3.  
 DR PROSITE; PS00231; Ricin\_B\_lectin; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lactin.  
 FT SIGNAL 1 37  
 FT CHAIN 38 475  
 FT DOMAIN 39 166  
 SEQUENCE 475 AA; 50369 MW; C1C6H4E87B85AD CRC64;

Query Match: 7.9%; Score 112.5; DB 1; Length 475;  
 Local Similarity 24.1%; Pred. No. 0.029; 104; Indels 25; Gaps 10;  
 Matches 52; Conservative 35; Mismatches 104;

DR 6 SASBPYRIVGKNGKAVYDDDFHQNQIQMPSKSNNDPQWLTIRKDGTRNSG-SC 64  
 DR 37 AAGSGALRKAAGSNEG-LDVAGSSQDQALADLDYDCMCGT--HQOMISYTGRLTYGDK 93  
 QY 65 LITVGYTA--GYVMIFDQNTAVRANTWQIMQNTIIPRSENLV-AASSGI-KGTLT 120  
 DB 94 LDVPSHADVAGTRVQVWCSGKSNQ--WRVNSDFVGVESGLCLBAAGAPNRTAVQ 151  
 QY 121 VQTDLYTLQCHLAGNDTARPT-----YGERDLCNENSGSVYETCP-SSQNRCK 174  
 DB 132 LMTGSGGNGKMTGLTGTFIDTGLPSTYRNSSTYGLAQPKSGWALMDFTVTINR 211  
 QY 175 WALYDGS-----IREKQNOQCLTSRDSVS 201  
 DB 212 HLYGSTSGSGSVGWFSPPTWMDYASAGQVANN 247

RESULT 13  
 SPL RARA  
 ID SPL RARA STANDARD; PRT; 525 AA.  
 AC 005308;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serine protease I precursor (EC 3.4.21.-) (RPI).  
 OS Rarobacter faecitabidus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Rarobacteriaceae; Rarobacteraceae; Rarobacter.  
 CX NCBI\_TaxID=13243;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.  
 RC STRAIN-TLM-50;  
 RX MEDLINE=93094226; PubMed=1339445;  
 RA Shimoi H., Iimura Y., Obara T., Tadenuma M.;  
 RT "Molecular structure of Rarobacter faecitabidus protease I. A yeast-  
 lytic serine protease having mannose-binding activity.";  
 RL J. Biochem. 110:608-613(1991).  
 RL J. Biochem. 110:608-613(1991).  
 CC - FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD  
 SPECIFICITY AND HAS A HIGHLY SPECIFICITY FOR SUBSTRATE  
 MANNOSE.  
 CC MANNOSE-PROTEIN MAY BE THE NATIVE SUBSTRATE FOR RPI.  
 CC - SUBCELLULAR LOCATION: secreted.  
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY 52A.  
 CC - SIMILARITY: Contains 1 ricin B-type lectin domain.

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DR EMBL; D10753; A001585.1; -  
 DR PIR; A001585.1;  
 DR HSP; P00718; 102A.  
 DR MEMOPS; 501.276; -  
 DR InterPro; IPR004236; AL protease.  
 DR InterPro; IPR001316; Endopeptidase2.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001254; Ser. protease\_TY.  
 DR Pfam; PF02983; AL protease; 1.  
 DR Pfam; PF02983; AL protease; 1.  
 DR Pfam; PF02983; AL protease; 1.  
 DR SMART; SMO0254; Ricin\_B\_lectin; 3.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR PROSITE; PS00231; Ricin\_B\_lectin; 1.  
 DR Hydrolase; Serine protease; Mannose-binding; Signal; Zymogen;  
 FT SIGNAL 1 32  
 FT PROPEP 33 211  
 FT CHAIN 212 525  
 FT DOMAIN 401 525  
 FT DISULFID 223 239  
 FT DISULFID 310 320  
 FT DISULFID 346 376  
 FT DISULFID 412 431  
 FT DISULFID 453 472  
 FT DISULFID 496 514  
 FT ACT\_SITE 270 270  
 FT ACT\_SITE 352 352  
 SEQUENCE 525 AA; 55654 MW; DABCFD330BB61 CRC64;

Query Match: 7.9%; Score 111; DB 1; Length 525;  
 Local Similarity 31.1%; Pred. No. 0.044;  
 Matches 33; Conservative 17; Mismatches 44; Indels 12; Gaps 5;

DR 2 DVTSASBPYRIVGKNGKAVYDDDFHQNQIQMPSKSNNDPQWLTIRKDGTRNSG 61  
 QY 62 GSGLT-TYGYT-AGYVMIFDQNTAVRANTWQIMQNTIIPRSENLV-AASSGI-KGTLT 105  
 DB 451 GKCLDARMVHNTQTEVLDANCKGHI--AQKFTLNAGQDLVANN 494

RESULT 14  
 SPL RARA  
 ID SPL RARA STANDARD; PRT; 512 AA.  
 AC 034676; OSU003;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Polypeptide N-acetylglucosaminyltransferase 3 (EC 2.4.1.41)  
 DE (Protein-UDP-acetylglucosaminyltransferase) (UDP-galnac-polypeptide,  
 N-acetylglucosaminyltransferase) (Galnac-TI) (ppGalnac 3).  
 OS Caenorhabditis elegans.  
 OC Caenorhabditidae; Nematoda; Chordata; Rhabdicolidae; Rhabdicolidae;  
 OC Rhabdicolidae; Caenorhabditidae; Caenorhabditis.  
 CX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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DR EMBL: D2368; BAO4892.1; -  
DR HSSP: P02879; 2NAI.  
DR InterPro: IPR000772; Ricin\_B\_lectin.  
DR Pfam: P00652; Ricin\_B\_lectin\_3.  
DR PROSITE: PS0231; Ricin\_B\_lectin\_1.  
DR PROSITE: PS0231; Ricin\_B\_lectin\_1.  
KM Hydroxylase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.  
FT SIGNAL 1 36  
FT CHAIN 37 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.  
FT DOMAIN 422 548 RICIN B-TYPE LECTIN.  
SQ SEQUENCE 548 AA; 58164 MW; BD5654315750596 CRC64;

Query Match  
Best Local Similarity 31.3%; Score 114; DB 1; Length 548;  
Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7;

QY 16 GRNQRV-----DYRDDPHFGNQIQLPSSKSNNDPQVLTIRKDTIRSNQSGT--TT 67  
DB 422 GTGALIGSTGLDVPADPTVNOVL--ATCGMAAQQVTRKGTVPALSKCLDVAR 479  
QY 68 YGVTAQYVWTFDCK-TAVKATVWQNGT--ITPNSNVLAAASGCI--KATITLV 121  
DB 480 SGTADGTAVWITVCTGTGAGQKWT---YDAKTKALNPGSGKCLDAGAPLADQKVOL 535  
QY 122 QTLDTYLTGGQW 132  
DB 536 WTCNQTEDQRW 546

RESULT 11  
ID B1B1 OEEXA STANDARD; PRT; 548 AA.  
AC P22222;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Glucan endo-1,3-beta-glucosidase precursor (BC 3.2.1.39) ((1->3)-beta-glucan endohydroxylase) ((1->3)-beta-glucanase).  
OS Oerskovia xanthineolytica.  
OC Bacteria; Actinobacteriales; Actinobacteridae; Actinomycetales;  
OC Streptomyces; Streptomyces; Streptomyces.  
OX NCBI\_TaxID=1710;  
RN [1] J. Biol. Chem. 266:1058-1063 (1991).  
RP SEQUENCE FROM N.A. AND SEQUENCE OF 37-63.  
RX MEDLINE=91093212; PubMed=1985933;  
RA Shen S.-H., Chretien P., Bastien L., Siliaty S.N.;  
RT "Primary sequence of the glucanase gene from Oerskovia xanthineolytica. Expression and purification of the enzyme from Escherichia coli.";  
RT Escherichia coli.";  
RL J. Biol. Chem. 266:1058-1063 (1991).  
CC -1- FUNCTION: LISTS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.  
CC -1- IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages  
CC -1- SUBCELLULAR LOCATION: Periplasmic.  
CC -1- SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.  
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.  
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DR EMBL: M60826; AAA25520.1; -  
DR PIR: A30994; A30994.  
DR HSSP: P02879; 2NAI.  
DR InterPro: IPR000772; Ricin\_B\_lectin.

DR Pfam: P00652; Ricin\_B\_lectin\_3.  
DR SMART: SM00486; Ricin\_B\_lectin\_1.  
DR PROSITE: PS0231; Ricin\_B\_lectin\_1.  
KM Hydroxylase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.  
FT SIGNAL 1 36  
FT CHAIN 37 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.  
FT DOMAIN 422 548 RICIN B-TYPE LECTIN.  
FT DOMAIN 37 430 POSSIBLE BETA-GLUCANASE ACTIVITY, BUT IS  
FT FT ESSENTIAL FOR THE HYDROLYTIC ACTIVITY, BUT NOT  
FT FT FOR THE BETA-GLUCANASE FUNCTION.  
SQ SEQUENCE 548 AA; 58088 MW; 4125544A424C048D CRC64;

Query Match  
Best Local Similarity 31.3%; Score 114; DB 1; Length 548;  
Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7;

QY 16 GRNQRV-----DYRDDPHFGNQIQLPSSKSNNDPQVLTIRKDTIRSNQSGT--TT 67  
DB 422 GTGALIGSTGLDVPADPTVNOVL--ATCGMAAQQVTRKGTVPALSKCLDVAR 479  
QY 68 YGVTAQYVWTFDCK-TAVKATVWQNGT--ITPNSNVLAAASGCI--KATITLV 121  
DB 480 SGTADGTAVWITVCTGTGAGQKWT---YDAKTKALNPGSGKCLDAGAPLADQKVOL 535  
QY 122 QTLDTYLTGGQW 132  
DB 536 WTCNQTEDQRW 546

RESULT 12  
ID ABRF STRL1 STANDARD; PRT; 475 AA.  
AC P22222;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-SEP-2003 (Rel. 41, Last annotation update)  
DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).  
GN ABRF.  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteriales; Actinobacteridae; Actinomycetales;  
OC Streptomyces; Streptomyces; Streptomyces.  
OX NCBI\_TaxID=1916;  
RN [1] J. Biol. Chem. 266:11326-11336;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9148759; PubMed=9148759;  
RA Vincent P., Sharek P., Dupont C., Morosoli R., Kluepfel D.;  
RT "New alpha-L-arabinofuranosidase produced by Streptomyces lividans:  
RT cloning and DNA sequence of the abrf gene and characterization of the  
RT enzyme.";  
RL Biochem. J. 322:845-852 (1997).  
CC -1- FUNCTION: LISTS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.  
CC -1- IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages  
CC -1- SUBCELLULAR LOCATION: Periplasmic.  
CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.  
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.  
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CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL  
 CC SUBUNIT. THE SUBUNIT IS FORMED FROM A 28S RNA. THE  
 CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE  
 CC BINDING OF RIBOSIN B TO THE CELL MEMBRANE THAT PRECEDES  
 CC ENDOCYTOSIS.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.  
 CC -----  
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 CC -----  
 DR EMBL: 441299; AB039475.1; -  
 DR EMBL: 537322; AB020292; Ricin B lectin.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam: PF00161; RIP\_1\_lectin; 6.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR SMART: SM00458; SHIGA\_RICIN; 1.  
 DR PROSITE: PS00231; SHIGA\_RICIN; 2.  
 DR PROSITE: PS00231; RICIN\_B\_LECTIN; 2.  
 KM Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 KM Glycoprotein; Lectin; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 2 53  
 FT DOMAIN 305 431 NIGRIN B A CHAIN  
 FT DOMAIN 434 559 RICIN B-TYPE LECTIN 1.  
 FT REPEAT 316 356 RICIN B-TYPE LECTIN 2.  
 FT REPEAT 357 397 1-BETA.  
 FT REPEAT 400 432 1-BETA.  
 FT REPEAT 445 482 2-ALPHA.  
 FT REPEAT 486 524 2-BETA.  
 FT REPEAT 527 554 2-GAMMA.  
 FT ACT\_SITE 188 188 BY SIMILARITY.  
 FT DISULFID 234 302 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 302 356 BY SIMILARITY.  
 FT DISULFID 350 377 BY SIMILARITY.  
 FT DISULFID 448 463 BY SIMILARITY.  
 FT DISULFID 489 506 BY SIMILARITY.  
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT COMPLECT 39 39 K -> V (IN REF. 2).  
 SQ SEQUENCE 563 AA; 62300 MW; F250CE24621BF14 CRC64;  
 Query Match 37.2% Score 528.5; DB 1; Length 563;  
 Best Local Similarity 41.3%; Pred No 1,1e-37;  
 Matches 109; Conservative 44; Mismatches 104; Indels 7; Gaps 5;

QY 178 VGGGSRKQNDQGLNSGRDSVYINIVSSGASGSGRFTMEGLIKKPKPMRV 237  
 DB 475 YGDHIVNSTGDLCTVINGKNSKDLILKQLLP-SGRFNSGALVNRKRNMOV 533  
 QY 238 AANPPLRRIIYYPATKKNOML 261  
 DB 534 RASNVLEIIPATKNQGMV 557  
 RESULT 8  
 XRNA\_XRNA  
 AC P2614; P96464; STANDARD; FRT; 477 AA.  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 18-SEP-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) [Xylanase A]  
 DE (1,4-beta-D-xylan xylanohydrolase A).  
 GN XLNA.  
 OS Streptomyces lividans.  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 CC Streptomyces; Streptomycetaceae; Streptomyces.  
 CX XLNA\_XLNA110;  
 RX MEDLINE=92077439; PubMed=1743521;  
 RA Sharek F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.,  
 RT "Sequences of three genes specifying xylanases in Streptomyces  
 RT lividans.";  
 RL Gene 107:75-82(1991).  
 RN (2)  
 RP REVISIONS TO 20 AND 140-141.  
 RP STRAIN 1326;  
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBD databases.  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 42-340.  
 RX MEDLINE=94342232; PubMed=8063693;  
 RA Derwenda U., Swenson L., Green R., Wei Y.Y., Morosoli R., Sharek F.,  
 RT Kluepfel D., Derwenda Z.S.;  
 RT "Crystal structure, at 2.6-A resolution, of the Streptomyces lividans  
 RT xylanase A, a member of the F family of beta-1,4-D-glycanases";  
 RL J. Biol. Chem. 269:20811-20814(1994).  
 CC -1- FUNCTION: contributes to hydrolyse hemicellulose, the major  
 CC component of plant cell walls, to yield xylobiose and xylose  
 CC as carbon sources.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylofuranosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL  
 CC HYDROLASES).  
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.  
 CC -----  
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 CC -----  
 DR EMBL: M64551; AAC6525.1; -  
 DR PIR: J05059; J05059;  
 DR PDB: 1XAS; 31-MAY-95.  
 DR PDB: 1X04; 23-MAY-01.  
 DR PDB: 1XN1; 19-JUN-02.  
 DR PDB: 1XN1; 19-JUN-02.  
 DR PDB: 1XN1; 19-JUN-02.  
 DR InterPro: IPR001000; glyco\_hydro\_10.



DR		EMBL; M98345; AAA3625.1; -.
DR	PIR; S32430; S32430.	
DR	HSP; P1140; HSR.	
DR	InterPro; IPR000772; Ricin_B_lectin.	
DR	InterPro; IPR001574; RIP.	
DR	Fam; PF00652; Ricin_B_lectin; 6.	
DR	Fam; PF00161; Rip; 1.	
DR	PRINTS; PR00396; SHGARCIN.	
DR	SMART; SM0458; RICIN_2.	
DR	PROSITE; PS00231; RICIN_B_LECTIN; 2.	
DR	PROSITE; PS00275; SHIGA_RICIN; 1.	
KM	Plant defense, Hydrolyase, Protein synthesis inhibitor; Toxin; Repeat;	
KM	Glycoprotein; Lectin; Pyridoxane carboxylic acid.	
KT	CHAIN 1 250 ARIN-B A CHAIN.	
FT	PEPTIDE 251 260 LINKER PEPTIDE.	
FT	CHAIN 261 527 ARIN-B B CHAIN.	
FT	DOMAIN 272 399 RICIN B-TYPE LECTIN 1.	
FT	DOMAIN 402 526 RICIN B-TYPE LECTIN 2.	

## FT REPEAT

FT	413	448	2-ALPHA.
REPEAT			
FT	452	491	2-BETA

REPEAT	492	804	2 GAMMA,
FT	494	527	2-GAMMA,
REPEAT	496	529	2-GAMMA,
FT	498	531	2-GAMMA,
REPEAT	500	533	2-GAMMA,
FT	502	535	2-GAMMA,
REPEAT	504	537	2-GAMMA,
FT	506	539	2-GAMMA,
REPEAT	508	541	2-GAMMA,
FT	510	543	2-GAMMA,
REPEAT	512	545	2-GAMMA,
FT	514	547	2-GAMMA,
REPEAT	516	549	2-GAMMA,
FT	518	551	2-GAMMA,
REPEAT	520	553	2-GAMMA,
FT	522	555	2-GAMMA,
REPEAT	524	557	2-GAMMA,
FT	526	559	2-GAMMA,
REPEAT	528	561	2-GAMMA,
FT	530	563	2-GAMMA,
REPEAT	532	565	2-GAMMA,
FT	534	567	2-GAMMA,
REPEAT	536	569	2-GAMMA,
FT	538	571	2-GAMMA,
REPEAT	540	573	2-GAMMA,
FT	542	575	2-GAMMA,
REPEAT	544	577	2-GAMMA,
FT	546	579	2-GAMMA,
REPEAT	548	581	2-GAMMA,
FT	550	583	2-GAMMA,
REPEAT	552	585	2-GAMMA,
FT	554	587	2-GAMMA,
REPEAT	556	589	2-GAMMA,
FT	558	591	2-GAMMA,
REPEAT	560	593	2-GAMMA,
FT	562	595	2-GAMMA,
REPEAT	564	597	2-GAMMA,
FT	566	599	2-GAMMA,
REPEAT	568	601	2-GAMMA,
FT	570	603	2-GAMMA,
REPEAT	572	605	2-GAMMA,
FT	574	607	2-GAMMA,
REPEAT	576	609	2-GAMMA,
FT	578	611	2-GAMMA,
REPEAT	580	613	2-GAMMA,
FT	582	615	2-GAMMA,
REPEAT	584	617	2-GAMMA,
FT	586	619	2-GAMMA,
REPEAT	588	621	2-GAMMA,
FT	590	623	2-GAMMA,
REPEAT	592	625	2-GAMMA,
FT	594	627	2-GAMMA,
REPEAT	596	629	2-GAMMA,
FT	598	631	2-GAMMA,
REPEAT	600	633	2-GAMMA,
FT	602	635	2-GAMMA,
REPEAT	604	637	2-GAMMA,
FT	606	639	2-GAMMA,
REPEAT	608	641	2-GAMMA,
FT	610	643	2-GAMMA,
REPEAT	612	645	2-GAMMA,
FT	614	647	2-GAMMA,
REPEAT	616	649	2-GAMMA,
FT	618	651	2-GAMMA,
REPEAT	620	653	2-GAMMA,
FT	622	655	2-GAMMA,
REPEAT	624	657	2-GAMMA,
FT	626	659	2-GAMMA,
REPEAT	628	661	2-GAMMA,
FT	630	663	2-GAMMA,
REPEAT	632	665	2-GAMMA,
FT	634	667	2-GAMMA,
REPEAT	636	669	2-GAMMA,
FT	638	671	2-GAMMA,
REPEAT	640	673	2-GAMMA,
FT	642	675	2-GAMMA,
REPEAT	644	677	2-GAMMA,
FT	646	679	2-GAMMA,
REPEAT	648	681	2-GAMMA,
FT	650	683	2-GAMMA,
REPEAT	652	685	2-GAMMA,
FT	654	687	2-GAMMA,
REPEAT	656	689	2-GAMMA,
FT	658	691	2-GAMMA,
REPEAT	660	693	2-GAMMA,
FT	662	695	2-GAMMA,
REPEAT	664	697	2-GAMMA,
FT	666	699	2-GAMMA,
REPEAT	668	701	2-GAMMA,
FT	670	703	2-GAMMA,
REPEAT	672	705	2-GAMMA,
FT	674	707	2-GAMMA,
REPEAT	676	709	2-GAMMA,
FT	678	711	2-GAMMA,
REPEAT	680	713	2-GAMMA,
FT	682	715	2-GAMMA,
REPEAT	684	717	2-GAMMA,
FT	686	719	2-GAMMA,
REPEAT	688	721	2-GAMMA,
FT	690	723	2-GAMMA,
REPEAT	692	725	2-GAMMA,
FT	694	727	2-GAMMA,
REPEAT	696	729	2-GAMMA,
FT	698	731	2-GAMMA,
REPEAT	700	733	2-GAMMA,
FT	702	735	2-GAMMA,
REPEAT	704	737	2-GAMMA,
FT	706	739	2-GAMMA,
REPEAT	708	741	2-GAMMA,

FT	ACT_SIZE	163	163	BY SIMILARITY;
FT	DISU_FID	246	268	INTERCHAIN (BY SIMILARITY).

PT	DISULFID	285	304	BY SIMILARITY.
PT	DISULFID	328	345	BY SIMILARITY.

FT		BY SIMILARITY:
DISULFID	416	
FT	429	
DISULFID	429	

FT	MOD_RES	1	1	BI SIMILARITY:
F1	DISOLFID	455	4/2	PYRROLIDONE CARBOXYLIC ACID (BY

FT	110	SIMILARITY).
FT	110	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	110	CARBOHYD
FT	110	

CARBOHYD	360		N-LINKED	(GLCNAC.	)	(POTENTIAL).
FET	400		M- LINKED	(CYCLOO	)	(DOENENTIAL)
FT	360					

FT	CONFLICT	282	282	N -> D (IN REF. 2).
FT	CARBONID	400	400	N-LINKED (GLUCNAO. . . ) (POLYMERIAL) :

FT	CONFLICT	291	D -> N (IN REF. 2).
FT	CONFLICT	350	AE -> PO (IN REF. 2).
FT	CONFLICT	351	

FT	CONFLICT	378	378	S -> N (IN REF. 2).
FT	CONFLICT	436	436	T -> M (IN REF. 3).

FT	428	Y -> D (IN REF. 2).
CONFLICT	428	
CONFLICT	428	

FT	CONFLICT	431	431	N -> S (IN REF. 2).
FT	CONFLICT	484	484	R -> K (IN REF. 2).

FT CONFLICT 491 N -> S (IN REF. 2).  
EE CONFLICT 491  
CONFLICT 491

F1	CONFLICT	493	H -> I (IN REF. 2).
FT	CONFLICT	502	R -> G (IN REF. 2).

ET	CONFLICT	509	509	E -> Q (IN REF. 2).
ET	CONFLICT	513	513	H -> W (IN REF. 2).

FT 516 H -> T (IN REF. 2).  
CONFLICT 516  
CONFIDENTIAL

52/ AA; 59114 MW; 3253AE490CE9494A CRC64;

Query Match	53.9%	Score 765;	DB 1;	Length 527;
Best Local Similarity	55.2%	Pred. No. 6.4e-58;		

Matches 144; Conservative 41; Mismatches 74; Indels 2; Gaps 2;

5 CSAS-EPTVRIVGKMGMRVDVDRDDPFHDGNQIQLMPSKSNNDPNQLWTIKRGGTIRSNGS 63

Dib 268 CSSRYEPTVIRIGRNGMCVDVYDPGYHNGNRIIAWKCKDRIEENOIWLTKSDPTIRSNKG 327

[illegible]

04 CIIIIGIHOVIVWTFDCNIAVNEHTIMQIMENGIIINFONBVEPRSSGINSILIIIVQI 423

328 CTTGGYAPGNVMIYDCTSAVAEATYMEIWDNGTIIINPKALVLSAESSSSMGILLVQT 387

QY 124 LDYTLGGWLAGNDTAPREVTIYGFRDLCMESNGGSVWVETCDSSQKNQGWALYGDGSI 183

Db 388 NEIIMRQGMRTGNNTSPFVTSISGISDLCMQAGGSNVMILAYCDNNKKEQ-QWALITYDGS 446

QY 184 RPKONODOCLTSGRDSVSTVINIVSCSGASGSORWFTNEGAILNLKKGPA MDVAQANPK 243

447 BUNIMANCI ESCHIVOOCSTUW KACONOWA SOBUT PRINOCSTUW UDUMUWOWENDE EAC

20 21 / NOV 21 AM 01:15:00 WASH DC KMWJF KIN0601 INDEBDEMVID VAKRSDPS 300

QY 244 LRRITYPATGKPNQMWLPV? 264







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FT     DISULPID      377    394
FT     DISULPID      465    478
FT     DISULPID      504    521
FT     CARBOHYD      45
FT     CARBOHYD      271    271
FT     CARBOHYD      409    409
FT     CARBOHYD      449    449
FT     CONFLICT      76    76
FT     CONFLICT      551    551
FT     STRAND        43    47
FT     TURN          49    50

Query Match      63.3%   Score 899.5; DB 1; Length 576;
Best Local Similarity 63.5%; Pred. No. 2.3e-69;
Branches 165; Conservative 35; Missatches 62; Indels 1; Gaps 1

Dy       5 CASAPPTVYIGNCRVDYDDPDGPHQMOIWPSSNNDDPGLMTIRKGTIPRNSQC 64
         QMDEPIYVIGNRGLCYDRGRFRNGNAQLMPCKSDNDANQMILFRLPNITRNSKC 377
Dy       318 LTTGYTAAQVWMIPECKTFVEATNIWMQMGNTINERSNVWLAAASQIKGTLVTGL 124
         LTTYGVSEFYVMWIMYCMALDARFMQWNGHINRSSTLVLAASNGSTLT-VTGN 437
Db       378 LTYGVSEFYVMWIMYCMALDARFMQWNGHINRSSTLVLAASNGSTLT-VTGN 437
Dy       125 DTTCGGCMAAGNPAARETYTYGRDLCEMGSGSYWETCTSSQAQCKNALXCGSIFR 184
         IYVAGQMLPNTNQTPPTTIYGVLGCLQANGQVMLEDCSERVADQAMLYADGSIR 496
Dy       185 EKPMQDDCTGTSQDSYSVTVNTVSCSGASGQQRMVFTEBALINKKKSGANDVAQNMYKL 244
         PQQRMDICTISDINSREVVVKLISLCSGASGQQRMFKNDQTINI.VSGLVLDVARSPSL 596
Db       497 PQQRMDICTISDINSREVVVKLISLCSGASGQQRMFKNDQTINI.VSGLVLDVARSPSL 596
Dy       245 KRIIIITPATGSEPNOMALPVF 264
         KQIIIVYLHSDQWMLNLF 576
Db       557 KQIIIVYLHSDQWMLNLF 576

RESULT 3
ABRA_ABRP
ID ABRA_ABRP STANDARD; PRT; 528 AA.
AC P11101.P28589;
DT 01-JUN-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB DISEASES [Rel. 11] Abtin-a chain (ZRR A N-glycosidase)
DB NCBI TaxId=3915;
OC Abtin precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes;
OC Spermatophyta; Magnoliopsida; eudicotyledons; Core eudicots; Rosidae;
OC eurosid 1; Fabales; Fabaceae; Papilionoideae; Abrusae; Abrus;
CX NCBI_TaxId=3915;
LN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93132796; PubMed=8421213;
RC J Mol Biol. 1993; 229(2):263-267. In T-Y.;
RC "Primary structure of three distinct isoforms determined by cDNA
RC sequencing. Conservation and significance."
RC J. Mol. Biol. 229:263-267 (1993).
RN [2]
RP SEQUENCE OF 1-251.
RC TISSUE=seed.
RC Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
RC "The complete amino acid sequence of the A-chain of abtin-a, a toxic
RC protein from seeds of the cruciferous";
RC J. Biol. Chem. 267:1095-1099 (1992).
RN [3]
RP SEQUENCE OF 1-251 FROM N.A.
RC TISSUE=leaf.
RC MEDLINE=91201329; PubMed=2016300;
RC Evensen G., Mathiesen A., Sundan A.;
RC "Direct molecular cloning and expression of two distinct abtin

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FT VARIANT 231 231 N -> S OR T.  
FT VARIANT 231 233 MEL -> KGP.  
FT VARIANT 232 235 GLAM -> SLAV.  
SQ SEQUENCE 264 AA: 28981 MW: 700DC326CCF6F5A4 CCG64,  
Query Match 88.9%; Score 1405 DB 11 Length 264;  
Sequence Similarity 88.9%; Free N-terminus 11;  
Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 DDVTCASSEPTVRIYGRGKRVVDVDDDPDGNQIQIMPSSKNDPQQLTIKRGITRS 60  
DB 1 DDVTCASSEPTVRIYGRGKRVVDVDDDPDGNQIQIMPSSKNDPQQLTIKRGITRS 60  
OY 61 NSGCLTYGTAAGYVYMFPCNTAVREATTQIWDGTTIPRSNVLAASSGKQTTLT 120  
DB 61 NSGCLTYGTAAGYVYMFPCNTAVREATTQIWDGTTIPRSNVLAASSGKQTTLT 120  
OY 121 VQTLDTLQCGMLAGNTARRETTTGERDQCSNGSGVTEPCDSGQCGVALVGD 180  
DB 121 VQTLDTLQCGMLAGNTARRETTTGERDQCSNGSGVTEPCDSGQCGVALVGD 180  
OY 181 GSIRPKONODCLSGRDSVSTIVIVSCGASGSGQWTFNKGALINKKGPMDVQAQ 240  
DB 181 GSIRPKONODCLSGRDSVSTIVIVSCGASGSGQWTFNKGALINKKGPMDVQAQ 240  
OY 241 NPELRRTIIPATGKPNQWMLPVF 264  
DB 241 NPELRRTIIPATGKPNQWMLPVF 264  
RESULT 2  
ID RIC1.RICCO STANDARD; PRT: 576 AA.  
AC P02879; P02880;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ricin precursor [Contains: Ricin A chain (RNA N-glycosidase)  
DS (EC 3.2.2.22); Ricin B chain).  
OS Ricinus communis (Castor bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Eucommiales; Rosales;  
OC Fabiales; Leguminosae; Papilionales; Leguminales; Leguminales;  
OC NCBI\_TaxID=3988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86067214; PubMed=2999712;  
RA Halling K.C., Halling A.C., Murray B.E., Ladin B.F., Houston L.L.,  
RA Weaver R.P.;  
RT "Genomic cloning and characterization of a ricin gene from Ricinus  
RT communis";  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9163016; PubMed=1371405;  
RA Tregear J.W., Roberts L.M.;  
RT "The lectin gene family of Ricinus communis: cloning of a functional  
RT ricin gene and three lectin pseudogenes";  
RN [3]  
RP SEQUENCE OF 12-576 FROM N.A.  
RX MEDLINE=85179479; PubMed=858923;  
RA Lamb A., Roberts L.M., Lord J.W.;  
RT Nucleotide sequence of cloned cDNA coding for preproricin";  
RN [4]  
RP J. Biochem. 148:265-270(1985).  
RP SEQUENCE OF 36-302.  
RA Yoshitake S., Funatsu G., Funatsu M.;  
RT "Isolation and sequences of peptic peptides, and the complete  
RT sequence of the chain of ricin-D";  
RN Agric. Biol. Chem. 42:1267-1274(1978).  
RP [5]  
RP SEQUENCE OF 315-576.

RA Funatsu G., Kimura M., Funatsu M.;  
RT "Primary structure of Aa chain of ricin D";  
RN Agric. Biol. Chem. 43:2221-2224(1979).  
RA [6]  
RP OBOYDPAPE-LINAGR SITRS AND PARTIAL SEQUENCE.  
RX MEDLINE=90344223; PubMed=1368517;  
RA Kimura Y., Kusoku H., Tada M., Takagi S., Funatsu G.;  
RT "Structural analyses of sugar chains from ricin A-chain variant";  
RN Agric. Biol. Chem. 54:157-162(1990).  
RP [7]  
RP REVIEW.  
RX MEDLINE=21480122; PubMed=11595634;  
RA Olines S., Kozlov J.V.;  
RT "Ricin";  
RN [8]  
RP TOXICON 39:1723-1728(2001).  
RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
RA Montfort M., Villafraña J.E., Monzinger A.F., Ernst S.R., Katzin B.,  
RA Rutenber E., Xiong N.H., Hamlin R., Rutenber J.D.;  
RT "The three-dimensional structure of ricin at 2.8 A";  
RN J. Biol. Chem. 262:5398-5403(1987).  
RP [9]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
RX MEDLINE=91552004; PubMed=1881881;  
RA Katzin B.J., Collins E., Rutenber J.D.;  
RT "Structure of ricin A-chain at 2.5 A";  
RN J. Biol. Chem. 262:251-259(1991).  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.  
RX MEDLINE=91552005; PubMed=1881882;  
RA Rutenber E., Rutenber J.D.;  
RT "Structure of ricin B-chain at 2.5-A resolution";  
RN Proteins 10:260-269(1991).  
RP [11]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.  
RX MEDLINE=95082010; PubMed=7991307;  
RA Weston S.A., Tucker A.D., Thatcher D.R., Detschire D.J.,  
RA Rutenber J.D.;  
RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution";  
RN J. Biol. Chem. 264:410-422(1994).  
RP [12]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.  
RX MEDLINE=95374222; PubMed=8780513;  
RA Day P.J., Ernst S.R., Frankel A.E., Monzinger A.F., Pascal J.M.,  
RA Molina-Svintch M.C., Roberts J.D.;  
RT "Structure and activity of an active site substitution of ricin A  
RT chain";  
RN Biochemistry 35:11098-11103(1996).  
RP [13]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
RX MEDLINE=97240820; PubMed=9068280;  
RA Yan X., Hollis T., Svintch M., Day P., Monzinger A.F., Milne G.W.,  
RA Roberts J.D.;  
RT "Structure-based identification of a ricin inhibitor";  
RN J. Mol. Biol. 266:1043-1049(1997).  
RP [14]  
RP MYOGENESIS.  
RX MEDLINE=93165632; PubMed=1287657;  
RA Kin Y., Rutenber J.D.;  
RT "Analysis of several key active site residues of ricin A chain by  
RT mutagenesis and X-ray crystallography";  
RN J. Biol. Chem. 268:1279-1283(1993).  
RP [15]  
RP "Ricin is highly toxic to animal cells and to a less  
RP extent to plant cells. The A chain is responsible for inhibiting  
RP ribosomal subunits. It acts as a glycosylase that removes a  
RP specific adenine residue from an exposed loop of 28S ribosomal  
RP RNA. As this loop is involved in the binding of elongation  
RP factors, the modified ribosomes are unable to support protein  
RP synthesis. The A chain can inactivate a few thousand ribosomes  
RP per minute, thus inactivating them faster than the cell can make  
RP new ones. A single A-chain molecule can therefore kill an animal

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OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18, Search time 4.61677 Seconds  
(without alignments)  
2736.539 Million cell updates/sec

Title: US-09-601-667c-10

Sequence: 1 DDVTCASSEFTVAVGKNNK.....RRIIVPATKPKQMWLPVF 264

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

127863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt\_41.1\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1405	98.9	264	1	MLB_VISAL
2	899.5	63.3	576	1	P02870 ricinus albu
3	775	54.6	528	1	P02870 ricinus albu
4	770.5	54.3	527	1	P02870 ricinus albu
5	765	52.2	527	1	P02870 ricinus albu
6	763	52.2	527	1	P02870 ricinus albu
7	528.5	37.2	563	1	P02870 ricinus albu
8	125.5	8.8	477	1	P02870 ricinus albu
9	115.5	8.1	475	1	P02870 ricinus albu
10	114	8.0	548	1	P02870 ricinus albu
11	114	8.0	548	1	P02870 ricinus albu
12	112.5	7.9	475	1	P02870 ricinus albu
13	111	7.8	525	1	P02870 ricinus albu
14	102	6.2	612	1	P02870 ricinus albu
15	97.5	6.2	612	1	P02870 ricinus albu
16	94.5	6.7	363	1	P02870 ricinus albu
17	93	6.5	1723	1	P02870 ricinus albu
18	92	6.5	860	1	P02870 ricinus albu
19	92	6.5	4074	1	P02870 ricinus albu
20	88	6.2	989	1	P02870 ricinus albu
21	88	6.2	1526	1	P02870 ricinus albu
22	86.5	6.1	1157	1	P02870 ricinus albu
23	86	6.1	1290	1	P02870 ricinus albu
24	85	6.0	1443	1	P02870 ricinus albu
25	84.5	6.0	1443	1	P02870 ricinus albu
26	84.5	6.0	1443	1	P02870 ricinus albu
27	84.5	6.0	1443	1	P02870 ricinus albu
28	84.5	6.0	1443	1	P02870 ricinus albu
29	84	5.9	193	1	P02870 ricinus albu
30	84	5.9	280	1	P02870 ricinus albu
31	84	5.9	1693	1	P02870 ricinus albu
32	83.5	5.9	552	1	P02870 ricinus albu
33	83.5	5.9	583	1	P02870 ricinus albu

## ALIGNMENTS

Result No.	Score	Match	Length	DB ID	Description
1	1405	98.9	264	1	MLB_VISAL
2	899.5	63.3	576	1	P02870 ricinus albu
3	775	54.6	528	1	P02870 ricinus albu
4	770.5	54.3	527	1	P02870 ricinus albu
5	765	52.2	527	1	P02870 ricinus albu
6	763	52.2	527	1	P02870 ricinus albu
7	528.5	37.2	563	1	P02870 ricinus albu
8	125.5	8.8	477	1	P02870 ricinus albu
9	115.5	8.1	475	1	P02870 ricinus albu
10	114	8.0	548	1	P02870 ricinus albu
11	114	8.0	548	1	P02870 ricinus albu
12	112.5	7.9	475	1	P02870 ricinus albu
13	111	7.8	525	1	P02870 ricinus albu
14	102	6.2	612	1	P02870 ricinus albu
15	97.5	6.2	612	1	P02870 ricinus albu
16	94.5	6.7	363	1	P02870 ricinus albu
17	93	6.5	1723	1	P02870 ricinus albu
18	92	6.5	860	1	P02870 ricinus albu
19	92	6.5	4074	1	P02870 ricinus albu
20	88	6.2	989	1	P02870 ricinus albu
21	88	6.2	1526	1	P02870 ricinus albu
22	86.5	6.1	1157	1	P02870 ricinus albu
23	86	6.1	1290	1	P02870 ricinus albu
24	85	6.0	1443	1	P02870 ricinus albu
25	84.5	6.0	1443	1	P02870 ricinus albu
26	84.5	6.0	1443	1	P02870 ricinus albu
27	84.5	6.0	1443	1	P02870 ricinus albu
28	84.5	6.0	1443	1	P02870 ricinus albu
29	84	5.9	193	1	P02870 ricinus albu
30	84	5.9	280	1	P02870 ricinus albu
31	84	5.9	1693	1	P02870 ricinus albu
32	83.5	5.9	552	1	P02870 ricinus albu
33	83.5	5.9	583	1	P02870 ricinus albu

Thu Dec 11 16:09:46 2003

us-09-601-667c-10.rpt

Page 7

Db	309	GEKDLAAGTANSHKQVJRWGAGDNR--WRNDSVYVQVGSLELNAVNTANGTL	366
QY	119	LTVTGLDPTLGGC	132
		:::	
Db	367	IQDYTCNSGNSQNR	380

RESULT 14  
T35697

arabinofuranosylase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Nov-1999 #sequence, revision 05-Nov-1999 #text, change 03-Dec-1999  
C:Accession: J35697  
R:MapBy: L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
Submitted to the EMBL Data Library, January 1998  
A:Reference number: J221948  
A:Accession: J35697  
A>Status: preliminary; translated from GB/EMBL/DDBL  
A:Molecule type: DNA  
A:Residues: 1-475 >DNR>  
A:Cross-references: EMBL:AL021411; FIDN:CA6189-1; GSPD:GN00070; SCSDB:SCTH1.02  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: abfB; SCSDB:SCTH1.02

Query Match	8.13;	Score 115.5;	DB 2;	Length 475;
Best Local Similarity	24.13;	Pred. No. 0.052;		
Matches 52;	Conservative 35;	Mismatches 104;	Indels 25;	Gaps 10;

D6  
QY 6 SASEPTTRIVGRNGRMVDVRRDDDFHGNQLQIMPSPNNPNQLMTIKKDGTTISNG-SC 64

| | : || : || :

D8 37 AAGSGALRGAGSNCRC-IDVLGSSQQDCCALLQLIDCWGGT--NQMWITSTDTGRLLTVYGDKC 93

Ddb

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94 LDVPGHATAPGTRVQIMSGSGANQQ--WRVVSIGTVGVESGLCEAAGGTANGTAIVQ 151
```

Db 152 LMTGCGGQKWTG1GTPTDTCALPSTYRMSSTGVLAQPKSGWALADFTTVTHNGR 211

Db 212 HLYIGSTSSGSSYSGSMVFSEPTNNSDMAAGQNNAN 247

RESULT 15

glucan endo-1,4-beta-glucosidase (EC 3.2.1.1) - precursor - Oerskovia xanthineolytica  
 Oerskovia xanthineolytica  
 Date: 27-Nov-1991 #sequence\_revision 27-Nov-1991 #text\_change 22-Oct-1999  
 R:Shen S.H.; Chretien, P.; Bashkin, L.; Staliyev, S.N.  
 J. Biol. Chem. 265, 1059-1063, 1991  
 A:Title: Primary sequence of the glucanase gene from Oerskovia xanthineolytica. Express  
 A:Reference number: A39094; PMID:51093212; PMID:1985933  
 A:Accession: A39094  
 A:Accession: A39094  
 A:Molecule type: cDNA  
 A:Residues: 1-548 <SRE>  
 A:Cross-references: GB:M60826; GB:M8734; NID:q150444; PIDD:AA25520.1; PID:q150445  
 A:Keywords: glycosidase; hydrolytic

Query Match

Matches, 4

Qy 16

b6 422

QY 68

Db 488 SGRADTATWVLYICNQTAKRW----YDAKRLKRPQSGKCDAGGAFIRQKQVQL 513  
 QY 122 QTLDTYLGSG 132  
 Db 536 WTCNQTENRKH 546

Search completed: December 11, 2003, 13:55:45  
Job time : 9.20622 secs

Matches 116; Conservative 33; Mismatches 96; Indels 12; Gaps 6;

QY 5 CSASEPTVAVRNGKRVYRDDPHDQIQQLWPKSKNDPQQLMTIKDQTRNSG 64  
DB 316 CSVSEVTRIRISGMDGLCDVRGCHYIDHPVQLRF--CGNECKQLMTFRDTGTFMLKDC 373  
QY 65 LTTGTGTAGVYVIFPCNTAVREATVQVIMDNGTINFRSNVLAASSIGKGTITVQL 124  
DB 374 L-----TASSVHLIDQNTVPEPAIKVNSIDGTFNRSGLVLAQAQABTALSTLEN 428  
QY 125 DYTLGGQMLASNDTARREVITVSGPDCKMESNGS--VYFCTDSQKQGMALVNGS 182  
DB 429 IHAAQGMVIG-DVEPLVTFVGYKQKCLRENGENFWLEDCVLRVQ--ENALVGGT 486  
QY 183 IRPKQNDQLTSGRDSVTVINIVSGSAGSGRWFTNEGALINLKSGPMDVACNP 242  
DB 487 IRVNSNSLCVTSIDHPSDLVILKCEG-SGNQKRWENTNGTISNPKALMDVACRDV 545  
QY 243 KCRRTIIVATGKRNQML 261  
DB 546 SAKKILVPTQNNQML 564

## RESULT 11

Chitinase [EC 3.2.1.14] 35 - Streptomyces thermoviolaceus  
C:Species: Streptomyces thermoviolaceus  
C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
C/Accession: J07535  
E:Snijder, H.; Okamoto, T.; Hatanio, N.; Miyamoto, K.; Matsunabe, T.; Mitsunori, M.; Inano, E.; Kato, T.; Higuchi, F.; 2485-2453, 2000  
A:Title: Family 19 chitinases of Streptomyces thermoviolaceus CPC-520. Molecular cloning  
A:Reference number: J07535; PMID:21056507; PMID:11935414  
A:Accession: J07535  
A:Molecule type: DNA  
A:Residues: 1-377 <RES>  
A:Cross-references: DDBJ:A016842  
A:Experimental source: strain OPC-520  
C:Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation  
lysaccharide-binding domain that is important in the efficient hydrolysis of insoluble C  
c:genetics:  
A:Gene: chl35  
C:Keywords: glycosidase; hydrolase

Query Match 9.6%; Score 136; DB 2; Length 377;  
Best Local Similarity 20.8%; Pred. No. 0.00074;

Matches 60; Conservative 33; Mismatches 108; Indels 88; Gaps 9;

QY 7 ASEPTVAVRNGKRVYRDDPHDQIQQLWPKSKNDPQQLMTIKDQTRNSG 66  
DB 33 AQATGSLTGDKCLDPAAGSANGTPOVQIDQNTV--NQQVSGSGITIALKCLD 90  
QY 67 TGTGTA--GVYVIFPCNTAVREATVQVIMDNGTINFRSNVLAAS--SGIKGTITVQ 122  
DB 91 VYDRSTADAKVQMDCTGAGKAK--VYVTAADHYVNPADKCLDVTDNSANGTRVAV 148  
QY 123 TLDYTLGGQMLA-----GNQDAPREVLT-----VQPDCKMESNGS 162  
DB 149 TCTGSGNQKMAAPATGSGSPAPASQFVSEAPQNFNPNFTVYQGVQALAPQFA 208  
QY 163 ETCDSQKQV-----GKALYQDD 181  
DB 209 NNGDDTTRKQAAAFLANVNHETGQVYVELNTANVTFYTCMGSGSYGCPAGQALAYGR 268  
QY 182 STRPKQNDQLTSGRDSVTVINIVSGSAGSGRWFTNEGALINLKSGPMDVACNP 242  
DB 269 PIGLSNV-----VTKAKADALIGDLINRMVLENDAL 302

## RESULT 12

J050589  
endo-1,4-beta-xylanase [EC 3.2.1.8] A precursor - Streptomyces lividans  
N/Alternate names: xylanase A

C:Species: Streptomyces lividans  
C>Date: 10-Mar-1994 #sequence\_revision 22-Nov-1996 #text\_change 26-Feb-1999  
C/Accession: J050589; F50238  
R:Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kupefel, D.  
Gene 107, 75-82, 1991  
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.  
A:Reference number: J050589; PMID:92077439; PMID:1743521  
A:Accession: J050589  
A:Molecule type: DNA  
A:Residues: 1-477 <SHA>  
A:Cross-references: EMBL:A021529; FIDN:CA14648.1; GSPDB:GN00070; SCOPDB:SC10A5.36C  
A:Accession: P50238  
A:Molecule type: protein  
A:Residues: 42-92 <SHA>  
C:Genetics:  
A:Gene: xlnA  
A:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylanosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylanase  
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F:1-41/Domain: signal sequence #status predicted <SH>  
F:1-41/Domain: signal sequence #status predicted <SH>  
F:74-134/Domain: endo-1,4-beta-xylanase A #status experimental <SH>  
F:134-477/Domain: endo-1,4-beta-xylanase A #status experimental <SH>  
F:169/277/Active site: glu #status predicted

Query Match 8.8%; Score 125.5; DB 1; Length 477;  
Best Local Similarity 29.9%; Pred. No. 0.0076;

Matches 40; Conservative 20; Mismatches 61; Indels 13; Gaps 6;

QY 7 ASEPTVAVRNGKRVYRDDPHDQIQQLWPKSKNDPQQLMTIKDQTRNSG 61  
DB 346 SEEPADGGQIKVNG-SGRCIDVPASTSGTQQLMDCHSST--NQQVATPAGELRY 402  
QY 62 G-STVYCTAGVYVIFPCNTAVREATVQVIMDNGTINFRSNVLAAS--SGIKGT 118  
DB 403 GPKLLAAGTSGNSVYVITSCMGDMQK--NRINDSIVGVQSGCLDPAAGNAGNLT 460  
QY 119 LTVQGLDYLTCQGV 132  
DB 461 TQVTCGNSGNDRW 474

## RESULT 13

Xylanase A - Streptomyces coelicolor (fragment)  
C:Species: Streptomyces coelicolor  
C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 28-Jul-2000  
C/Accession: J134603  
R:Murphy, L.; Harris, D.; Parkhill, C.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1996  
A:Reference number: Z1548  
A:Accession: J134603  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-383 <SHA>  
A:Cross-references: EMBL:A021529; FIDN:CA14648.1; GSPDB:GN00070; SCOPDB:SC10A5.36C  
A:Experimental source: strain A312  
C:Genetics:  
A:Gene: xlnA; SCOPDB:SC10A5.36C  
C:Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylanase  
F:1-247/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SH>

Query Match 8.6%; Score 122.5; DB 2; Length 383;  
Best Local Similarity 29.9%; Pred. No. 0.01;

Matches 40; Conservative 19; Mismatches 62; Indels 13; Gaps 6;

QY 7 ASEPTVAVRNGKRVYRDDPHDQIQQLWPKSKNDPQQLMTIKDQTRNSG 61  
DB 252 SEEPADGGQIKVNG-SGRCIDVPASTSGTQQLMDCHSST--NQQVATPAGELRY 308  
QY 62 G-STVYCTAGVYVIFPCNTAVREATVQVIMDNGTINFRSNVLAAS--SGIKGT 118

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RESULT B  
S16022

N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Abrus precatorius (Indian Licorice)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C:Accession: S16022  
R:Wood, R.A.; Lord, J.M.; Wawrzyniak, B.J.; Patrak, M.  
E:Title: Biochem J, 198, 723-730, 1991  
A:Reference number: S16022; PMID:91266957; PMID:2050149  
A:Accession: S16022  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residue: 1-562 <MO>  
A:Cross-references: EMBL:X55667; NID:g16084; PID:CAA3202.1; PID:g16085  
C:Comment: Abtin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.  
C:Superfamily: ricin; rRNA N-glycosidase; homology  
F:1-287/Product: Abtin-A chain A status predicted <ACH>  
F:1-287/Product: Abtin-B chain B status predicted <ACH>  
F:1295-562/Product: Abtin-C chain C status predicted <ACH>  
F:515/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted  
F:108,147,229,230/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted  
F:196,201/Active site: Glu, Arg #status predicted  
F:333,287,335,435,453/Binding site: carbonylase (Asn) (covalent) #status predicted  
F:383-303,335,339,451-464,490-507/Distalile bonds: #status predicted  
F:122,356/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted  
F:194,356/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 53.6% Score 761; DB 2; Length 562;  
Best Local Similarity 54.8%; Pred. No. 3.e-56;  
Matches 143; Conservative 42; Mismatches 74; Indels 2; Gaps 2;

5 CSAS-EPTTVKIVSNGRVVDDEPDQDGIQLTWESKNNDPVQALTIKEIGITIRNOS 63  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::  
63 CSAREPTEVATIGSRDOKVDVDDGHNSNNILAMKRCERENQVLWLSKRTIRNKR 362  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::  
64 CTTCGTACCTVMFACTGAGTGGTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::  
363 CTTEGVARGNYMVIYDSNTANVAIWEIMDGHTINPKSAVLASBSSMSGTLTYGT 422  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

124 LYLTLGGGLAGNDPRPEVTLYTFEDLOHNSGGRVWETCSOXRQGNALYGSGSI 183  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::  
423 NEELMRGMRGNANTSPPVTSISGYDLDMAQSNNWALADCDNNKKXQ-QNALVTGSI 481  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

184 RFKONDOCLTSGSDSVSTIVIVSCGASGSGRGVFTVEGALINIKRGPDVDAQNR 243  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::  
482 RSYQNINCLSKDKHGKSGISTVALACSNNASOFRLFRDNDSITYNLHDWDVDAZSDS 541  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

Oy 244 IRRITIPATKGKRWMLPIF 264  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

542 LKEILLPHFGKRNQMLTF 562  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

RESULT 9  
832431  
Abtin-d.precursor - Indian licorice (fragment)  
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Abrus precatorius (Indian Licorice)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C:Accession: S16022  
R:Wood, R.A.; Lord, J.M.; Wawrzyniak, B.J.; Patrak, M.  
E:Title: Biochem J, 198, 723-730, 1991  
A:Reference number: S16022; PMID:91266957; PMID:2050149  
A:Accession: S16022  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residue: 1-562 <MO>  
A:Cross-references: EMBL:X55667; NID:g16084; PID:CAA3202.1; PID:g16085  
C:Comment: Abtin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.  
C:Superfamily: ricin; rRNA N-glycosidase; homology  
F:1-287/Product: Abtin-A chain A status predicted <ACH>  
F:1-287/Product: Abtin-B chain B status predicted <ACH>  
F:1295-562/Product: Abtin-C chain C status predicted <ACH>  
F:515/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted  
F:108,147,229,230/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted  
F:196,201/Active site: Glu, Arg #status predicted  
F:333,287,335,435,453/Binding site: carbonylase (Asn) (covalent) #status predicted  
F:383-303,335,339,451-464,490-507/Distalile bonds: #status predicted  
F:122,356/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted  
F:194,356/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

A: Cross  
R: Hund.

A:cross-references: GB:069246  
R:King, C. J.; Lee, M.; Lee, T. J.; Lin, T.  
A:Reference number: S34408  
A:Accession: S34408  
A:Molecule type: mRNA  
A:Residues: 1-169, 'C', 171-320, 'L', 322-528 <HU2>  
A:cross-references: GB:M89346  
A:Comment: Abtin kinase is part of a chain, which inhibits protein synthesis by inactivating eukaryotic initiation factor 2. The chain is composed of a 17 kDa subunit, which is essential for complex formation, and a 35 kDa subunit, which is essential for catalytic activity.  
C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin  
P:1-251/Product: abtin-d chain A #status predicted <ACH>  
P:7-246/Domain: RNA N-glycosidase homology <RNG>  
F:7-261/528/Product: abtin-d chain B #status predicted <BCH>  
F:863-335/356-366-407, 414-449, 453-452, 495-528/Region: 40-residue repeat  
F:1161/Modified site: pyroglutamate carboxylic acid (Glu) #status predicted  
F:1161/167/Active site: Glu. Arg #status predicted  
F:240-253, 361-401, 402/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:240-259, 361-401, 402/Binding site: carboxylate (Asp) #status predicted  
F:288, 312/Binding site: N-acetylglucosamine (Asp) #status predicted  
F:500, 531/Binding site: N-acetylglucosamine (Asp) #status predicted

Query Match  
Match Local 53.5% Score 760. DB 2. Length 528;  
Match Local 54.8% Field No. 3e-50  
Matches 143, Complement 43, Mismatch 73, Indels 2, Gaps 2,

OY 5 CANS-EPYVRVGNRNVVYEDDDPDNDONIOPLMPSRNSNPNOJLWTKRDKDTRNSG 63  
DB 269 CCSRREYVYIGSRDQCVDDYDGHNNNNILAWKCKRLTENQJMLTKEDTTRNSGK 123  
OY 64 CLTIVYTRAGVYVNFDCNTARENTNLTWIDNGTILNPESNLVLAASGIKETLYTCQ 328  
DB 323 CLTIVYTRAGVYVNFDCNTARENTNLTWIDNGTILNPESNLVLAASGIKETLYTCQ 368  
OY 124 LDVTLQGLVAGNDPAPEVLTYSERLQENSGSGVWETGDSQKQKMLVGGDSG 183  
DB 369 NELLWRGMRGTGNNSPFTVYSISYSLDQKQSGNWLADLNNKKQ -QMLVLTDSI 447  
OY 184 RPNQNDQCTSRGDSVSTVYVYVSGSGSSGRPTFTFGLILNKKGPHVYDANK 243  
DB 448 RSVQVNNGLTISRDKQSGSYLVASCSNMGSRVLPNDGISTYSLDPMVQGSDE 507

OY 244 LRLIIVPATKRNQNMVPEF 264  
DB 508 LKRIILPFTKRNQIMTLFE 528

RESULT 10  
S36287  
agglutinin I precursor - European elder  
C:Species: Sambucus nigra (European elder)  
C:Date: 24-Aug-1996 #sequence revision 13-Mar-1997 #text change 20-Aug-1999  
A:Accession: S62827; S62619  
R:Van Damme, E. J. M.; Barre, A.; Rouge, P.; van Leuven, F.; Peumans, W. J.  
S:R. V. N. Biochem. 235, 128-137, 1996  
A:Reference number: S62619, S62619, NID:96203262, PMID:8631319  
A:Accession: S62827  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-570 <VAN>  
A:cross-references: EMBL:U27122; NID:91411772; PID:AAQ94158.1; PID:91411773  
A:Accession: S62819  
A:cross-references: S62819  
A:Molecule type: protein  
A:Residues: 29-319/305-319 <VA2>  
C:Superfamily: ricin; rRNA N-glycosidase homology  
P:317-283/Domain: rRNA N-glycosidase homology <RNG>

Query Match  
Match Local 37.8% Score 537. DB 2. Length 570;  
Match Local 45.6% Field No. 3e-37  
Matches 143, Complement 43, Mismatch 73, Indels 2, Gaps 2,



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Matches 145; Conservative 42; Mismatches 72; Indels 2; Gaps 2;  
QY 5 CSAS-EPTVRIYVGNKRVYVDDPFDDNQIOLMPSKSNNDPQTLTKDGTISNSG 63  
DB 269 CSRRYETVRIYVGNKRVYVDDPFDDNQIOLMPSKSNNDPQTLTKDGTISNSG 328  
QY 64 CLTYGYTAGVYVNIEDCNTRVREKATVQWMDNQTINPESNTVLAASGIGKTLTYQT 123  
DB 329 CLTYGYTAGVYVNIEDCNTRVREKATVQWMDNQTINPESNTVLAASGIGKTLTYQT 388  
QY 124 LDYTLGGWLAGNDTPREVTIYGRDLCSBNSGVSWEVETCSSQKNGKALYDGS1 183  
DB 389 NEIWRQKATGNTSPFTVTSIGSDLCMQKQSVWMLADCKSNKEQ-QVALYDGS1 447  
QY 184 RPKNOQCLTSGRDSVSTVNIYVSCGASGSGQVFTNEGALINLKKGPADYDQAPK 243  
DB 448 RSVQTNKCLTISKHQSSTILLMCSGMSQWVFNKDGSIYSLVDPMVWYKSDPS 507  
QY 244 LRITTYPATGKPKQMLPVF 264  
DB 508 LKQILMPYKPKQMLPVF 528

RESULT 6

AbnB precursor - castor bean  
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Ricinus communis (castor bean)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
C:Accession: A24261, A24210  
R:Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.  
J. Biol. Chem. 260, 15682-15686, 1985  
A:Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
A:Reference number: A24261; MUID:86059449; PMID:2993130  
A:Accession: A24261  
A:Molecule type: mRNA  
A:Residues: 1-564 <RDB>  
A:Cross-references: GB:M12089; NID:9169700; PIDN:AAA3865.1; PID:9169701  
A:Superfamily: rRNA N-glycosidase homology  
A:Keywords: duplication; glycoprotein; glycosylase; hydrolase; lectin; RNA binding; seed  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:1-240/Product: agglutinin chain A #status predicted <ACH>  
F:1-240/Product: agglutinin chain B #status predicted <ACH>  
F:303-564/Product: agglutinin chain B #status experimental <RCH>  
F:319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats  
F:324,289/Binding site: carbohydrate (Asn) #status predicted  
F:104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:200,203/Active site: Glu, Arg #status predicted  
F:282-306,322-341,365-382,453-466,492-509/Distal/Region: 40-residue repeats  
F:324,337,348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted  
F:337,437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:536,557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 54.3%; Score 770.5; DB 1; Length 564;  
Best Local Similarity 55.4%; Pred. No. 56-57;  
Matches 144; Conservative 41; Mismatches 74; Indels 1; Gaps 1;  
QY 5 CSAS-EPTVRIYVGNKRVYVDDPFDDNQIOLMPSKSNNDPQTLTKDGTISNSG 64  
DB 306 CSRRYETVRIYVGNKRVYVDDPFDDNQIOLMPSKSNNDPQTLTKDGTISNSG 365  
QY 65 CLTYGYTAGVYVNIEDCNTRVREKATVQWMDNQTINPESNTVLAASGIGKTLTYQT 124  
DB 366 CLTYGYTAGVYVNIEDCNTRVREKATVQWMDNQTINPESNTVLAASGIGKTLTYQT 425

QY 125 DPTLGGWLAGNDTPREVTIYGRDLCSBNSGVSWEVETCSSQKNGKALYDGS1R 184  
DB 426 IVASGQWLPNTVQVPTVTVLXMKLQMSGKVLKED-TEBAEQWALYDGS1R 484  
QY 185 RPKNOQCLTSGRDSVSTVNIYVSCGASGSGQVFTNEGALINLKKGPADYDQAPK 244  
DB 485 RSVQTNKCLTISKHQSSTILLMCSGMSQWVFNKDGSIYSLVDPMVWYKSDPS 544  
QY 245 LRITTYPATGKPKQMLPVF 264  
DB 545 LKQILMPYKPKQMLPVF 528

RESULT 7

AbnB precursor - Indian licorice (fragment)  
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Abrus precatorius (Indian licorice)  
C:Date: 20-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 20-Aug-1999  
C:Accession: S32430, J01399  
R:Blum, C.H.; Lee, W.C.; Lee, T.C.; Lin, D.Y.  
J. Mol. Biol. 229, 263-267, 1999  
A:Title: Primary structure of three distinct isobritins determined by cDNA sequencing.  
A:Reference number: S32430, S32429; MUID:93132789; PMID:8421313  
A:Molecule type: mRNA  
A:Residues: 1-527 <RDB>  
A:Cross-references: GB:M8345; NID:9166296; PIDN:AAA3625.1; PID:9166297  
R:Kimura, M.; Sumizawa, T.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 57, 166-169, 1993  
A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, tox  
A:Reference number: J01399; MUID:93169023; PMID:7763422  
A:Accession: J01399  
A:Molecule type: Protein  
A:Residues: 260-281, 'D', 283-290, 'N', 292-349, 'EQ', 352-377, 'N', 379-425, 'W', 427, 'D', 429-4  
A:Experimental source: seed  
A:Superfamily: rRNA N-glycosidase homology  
F:1-250/Product: abrin-b chain A #status predicted <RCH>  
F:1-245/Domain: rRNA N-glycosidase homology <RNG>  
F:260-527/Product: abrin-b chain B #status experimental <RCH>  
F:282-324,325-368,406,413-448,452-491,494-527/Region: 40-residue repeats  
F:1/Modified site: pyrrolidone carboxylic acid (Glu) #status predicted  
F:74,113,199,199/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:163,166/Active site: Glu, Arg #status predicted  
F:246-288,289-304,326-343,416-429,435-450/Region: 40-residue repeats  
F:287,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted  
F:493,520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 53.9%; Score 765; DB 2; Length 527;  
Best Local Similarity 55.2%; Pred. No. 1-36-56;  
Matches 144; Conservative 41; Mismatches 74; Indels 2; Gaps 2;  
QY 5 CSAS-EPTVRIYVGNKRVYVDDPFDDNQIOLMPSKSNNDPQTLTKDGTISNSG 63  
DB 268 CSRRYETVRIYVGNKRVYVDDPFDDNQIOLMPSKSNNDPQTLTKDGTISNSG 327  
QY 64 CLTYGYTAGVYVNIEDCNTRVREKATVQWMDNQTINPESNTVLAASGIGKTLTYQT 123  
DB 328 CLTYGYTAGVYVNIEDCNTRVREKATVQWMDNQTINPESNTVLAASGIGKTLTYQT 387  
QY 124 LDYTLGGWLAGNDTPREVTIYGRDLCSBNSGVSWEVETCSSQKNGKALYDGS1 183  
DB 388 NEIWRQKATGNTSPFTVTSIGSDLCMQKQSVWMLADCKSNKEQ-QVALYDGS1 446  
QY 184 RPKNOQCLTSGRDSVSTVNIYVSCGASGSGQVFTNEGALINLKKGPADYDQAPK 243  
DB 447 RSVQTNKCLTISKHQSSTILLMCSGMSQWVFNKDGSIYSLVDPMVWYKSDPS 506  
QY 244 LRITTYPATGKPKQMLPVF 264  
DB 507 LKQILMPYKPKQMLPVF 528





Thu Dec 11 16:09:46 2003

US-09-601-667C-10.rpr

Page 1

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 8.2622 Seconds

Title: US-09-601-667C-10  
3095:817 million cell updates/sec

Perfect score: 1420

Sequence: 1 DVTCSASEPTVIVGRNGM.....SRITVPAKGNQMLVFP 264

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR 76:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARY

Result No.	Score	Match	Length	DB ID	Description
1	1405	98.9	264	2 PD0019	miscletoe lectin I
2	1394.5	98.2	265	2 JMO090	lectin-I B chain -
3	899.5	63.3	376	1 R1030	ricin D precursor
4	894.5	63.3	376	1 R1030	ricin D precursor
5	775	54.6	528	1 T215A	abrin-a precursor
6	770.5	54.3	564	1 R1030	abrin-a precursor
7	765	53.9	527	2 S12430	abrin-b precursor
8	761	53.6	522	2 S12430	abrin-b precursor
9	760	53.5	528	2 S12431	abrin-d precursor
10	537	37.8	570	2 S62627	agglutinin I precur
11	136	9.6	377	2 UC7555	chitinase (BC 3.2.
12	125.5	8.8	477	1 UC8569	endo-1,4-beta-xyla
13	122.5	8.6	382	2 T34603	xyylanase A - Strep
14	113.2	8.0	448	2 A35604	arabinosyltransfera
15	113.2	8.0	448	2 T35943	probable hydrolase
16	113	8.0	464	2 T35943	probable hydrolase
17	111	7.8	525	2 A45033	actinobivarin precur
18	106	7.5	160	2 UC7622	polypeptide N-acet
19	102	7.2	563	2 A88515	probable polypepti
20	102	7.2	612	2 T42243	hypothetical prote
21	101	7.1	386	2 A81936	hypothetical prote
22	98.5	7.0	1067	2 T28663	probable lipoprote
23	98.5	6.9	452	2 T34988	alpha-galactosidas
24	98.5	6.9	452	2 T34988	probable N-acetyl
25	98.5	6.9	452	2 T34988	probable N-acetyl
26	94.5	6.7	962	2 A80835	lactate repetitive p
27	93.5	6.6	875	2 A80835	lactate repetitive p
28	93	6.5	875	2 A80835	lactate repetitive p
29	93	6.5	1723	2 H85557	polymorphic membra

30	93	6.5	1723	2 E72067	polymorphic membra
31	93	6.5	1723	2 C81601	polymorphic membra
32	92	6.5	895	1 IUX1CP	SP-cadherin precur
33	90.5	6.4	908	2 A82254	hypothetical prote
34	90.5	6.4	1008	2 T32986	hypothetical prote
35	90.5	6.4	1711	2 A81283	peptidoglycan link
36	88.5	6.3	471	2 A41478	cytolysin vha pre
37	88.5	6.3	624	2 T42247	polypeptide N-acet
38	88.5	6.3	624	2 T42247	polypeptide N-acet
39	88.5	6.3	624	2 T42247	polypeptide N-acet
40	88	6.2	2232	2 T42245	hypothetical prote
41	88	6.2	1526	2 AC2239	probable polypepti
42	88	6.2	1704	2 A55426	MD-40 repeat prote
43	88	6.2	3083	2 A82493	glucopain R (BC 3.
44	86.5	6.1	1032	2 T42257	hypothetical prote
45	86.5	6.1	1231	1 A48450	beta-1,3 exoglucan

#### ALIGNMENTS

##### RESULT 1

PD0019 miscletoe lectin I B chain - Viscum album (fragment)

C/Date: 03-Jul-1998 #sequence revision 10-Jul-1998 #text change 07-May-1999

C/Accession: PD0019 #sequence revision 10-Jul-1998 #text change 07-May-1999

C/Accession: S. J. Szusterman, R. Mikhaylov, A. Scoeva, S. J. Betzel, C. J. Voelker, N. J. B. Jones, B. Jones, R. Jones, 267 367-372 1998

A/Title: Primary structure and molecular modelling of miscletoe lectin I from Viscum album

A/Reference number: PD0019, WUID:98108123, PMID:9642133

A/Accession: PD0019

A/Molecule type: protein

A/Residues: 1-264 <BSC>

C/Superfamily: ricin, RNA N-glycosidase homology

Query/Match 98.9% Score 1405, DB 2, Length 264, Identical 99.2%, Pident. No. 18-11, Indels 0, Gaps 0, Mismatches 262, Conservative 0, Mismatches 2, Indels 0, Gaps 0

QY	1	DVTCSASEPTVIVGRNGMVDVDDPDHGNQIQLMPSKSNDDNQLTIRKQGTIRS	60
DB	1	DVTCSASEPTVIVGRNGMVDVDDPDHGNQIQLMPSKSNDDNQLTIRKQGTIRS	60
QY	61	NSCLTYGYTAAQYVIMPCQVYVBEATWQINDNTINFRSNVYLAASGICGTYLT	120
DB	61	NSCLTYGYTAAQYVIMPCQVYVBEATWQINDNTINFRSNVYLAASGICGTYLT	120
QY	121	VQTDVLTAAQQAAGNPAAPREPTVGPDPQMSNGSGSWTEPCSSQKQKALYED	180
DB	121	VQTDVLTAAQQAAGNPAAPREPTVGPDPQMSNGSGSWTEPCSSQKQKALYED	180
QY	181	GSIRKXNODQCTSGSDSVSVINIVSCASGSCRWYPTVEGATILNKKGFANDVQA	240
DB	181	GSIRKXNODQCTSGSDSVSVINIVSCASGSCRWYPTVEGATILNKKGFANDVQA	240
QY	241	NPKLRIITVPAKGNQMLVFP 264	
DB	241	NPKLRIITVPAKGNQMLVFP 264	

RESULT 2

JMO090 lectin-I B chain - European miscletoe

N/Alternate names: MW-I

C/Species: Viscum album (European miscletoe)

C/Date: 18-Jun-1998 #sequence revision 10-Jul-1998 #text change 19-May-2000

F/Solter, M. J. Scoeva, S. J. Voelker, N. J. B. Jones, B. Jones, R. Jones, 267 367-372 1998

A/Title: Complete amino acid sequence of the B chain of miscletoe lectin I.

A/Reference number: JMO090, WUID:98289555, PMID:9618285

A/Accession: JMO090

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.ra1

Db 224 AKQAVYVWVDFKSGVPIDC-----VGFSGHNSGPNVNRRTLLQAPAL-GVDV 276  
Qy 120 TVQTLDTYTLGGMTLAGNDTAPRE-----VTTGPRD-----LC 152  
Db 277 EYTELDI-----ENADPQTVASVIRDLAVDECTGITWGVDRDSDWSRYQNPIL 326  
Qy 153 MESN-----GGSVWV-----BT 164  
Db 327 FNNNSKQKQAYATLALNBSDDGGGSRPVSPFGSSGQJNGVANSKCIQVWNT 386  
Qy 165 CDSSQ-----KNGKQKALYGDGSTRPKQNDQCLAGSDSVATVINYSCGASGS 215  
Db 387 ADGTVOVLVCHSGSNC-QWYTSSEPRIFPN-KTLNAGSSNGAVVOIYSCWGA-N 442  
Qy 216 QRWVFTNKGALNLTQGLAM-VAGANPKIRIIIPATGKPNQW 260  
Db 443 QKWEMLADGTIVGVQSLCLDAVGAGTGNGTRLQVSCWGNQK 488

RESULT 15  
US-08-468-812-5  
; Sequence 5, Application US/08468812  
; Patent No. 5935836  
; GENERAL INFORMATION:  
; APPLICANT: Vehmaaper, Jari  
; APPLICANT: M nyl, Atja  
; APPLICANT: Fagerstr m, Richard  
; APPLICANT: Laitto, Raija  
; APPLICANT: Paloheimo, Marja  
; APPLICANT: Suominen, Pekko  
; APPLICANT: Kuitinen, Raula  
; APPLICANT: Kuitinen, Raula  
; TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLSTEIN & FOX  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER: IBM PC compatible  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,812  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/332,412  
; FILING DATE: 01-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/282,001  
; FILING DATE: 29-JUL-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bugalsky, Larry B.  
; REGISTRATION NUMBER: 35,086  
; REFERENCE/DOCKET NUMBER: 1050.0340002  
; TELEPHONE: 202-371-2540  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 480 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear

MOLECULE TYPE: peptide  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: AM50  
US-08-468-812-5  
Query Match 8.6%; Score 122.5; Db 2; Length 480;  
Best Local Similarity 32.4%; Pred.No.0.00029;  
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;  
Qy 22 VPRGDDPRFGNQQLMBSKSNQNDPLTKNDSTIRSGS-CLTTGTCATVYMTD 80  
Db 379 IDVPKNTADGTQVLVCHSGS--NQWYTSSEPRIFPKKCLDAGSSNANAVVOIY 436  
Qy 81 CMTAVREATIWOIWDNGTIIINPSNIVLAASSGIKGTLTVQ 122  
Db 437 CWGANQK--NELRADGTIVGVQSLCLDAVGAGTGNGTQLQ 476

Search completed: December 11, 2003, 14:11:35  
Job time : 10.1403 secs

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.rat

Page 7

APPLICANT: Palohelmo, Marja  
APPLICANT: Suominen, Pirkko  
TITLE OF INVENTION: Production and Secretion of Proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,621  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/590,563  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050,0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2600  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-770-621-4

Query Match 8.8% Score 124.5; DB 4; Length 492;  
Best Local Similarity 20.8%; Pred. No. 0.00019;  
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

23 DYRDDDFHGNQGLMPS--KSNDPNQWTKKEDTIR--SNGLTYYG-----70  
168 DVAEAEEDNSGRCDNSNQTND---WIEVAFRTAGQDPSAKCYNDNIEMWNA 223  
71 --TAGYVWI-----PDGNTAVRATITQWIDNGITINPESNVLVAASGIXGTTL 119  
224 AKQAVYNNVNDKSRGVPLD-----VGFQSHNSGNPNPVPFTLQGRALGVVV 276  
120 TVQTLDTYLLQGLAGNDTPPE-----VTYGERD-----LC 152  
277 EYTELDT-----ENHPQYASVIRDCIADVRCGITWGVGRDSNRSYQWPL 326  
153 MESN-----GGSYVW-----ET 144  
327 FDNNGKCAVAVVLDALNNGSDGGSNPPIVSPGQSSQIRGVASRCLDVPRGNT 366  
165 CDSGQ-----KNGKMALYGDGSLRPKQNGCLTSGPDSVTVINISGASGS 215  
387 ADGTQVQVLDCHGSGNQ--CWYTSGRFRIRGN--KILDAQGSNAGAVVQITSWGA-N 442  
QY 216 GRWVFNIGAILNLKTLGLAMD-VQANFRERIRIITFRATKPKNQW 260

443 GWEVLEADGTTIVAGSCLCLADVAGGTGNGTNGTFLQVYSCWGNQW 488  
US-09-770-621-7  
Sequence 7, Application US/09770621  
Filing No. 650593  
Current Application:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,621  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/590,563  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050,0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2600  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50  
US-09-770-621-7

Query Match 8.8% Score 124.5; DB 4; Length 492;  
Best Local Similarity 20.8%; Pred. No. 0.00019;  
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

23 DYRDDDFHGNQGLMPS--KSNDPNQWTKKEDTIR--SNGLTYYG-----70  
168 DVAEAEEDNSGRCDNSNQTND---WIEVAFRTAGQDPSAKCYNDNIEMWNA 223  
71 --TAGYVWI-----PDGNTAVRATITQWIDNGITINPESNVLVAASGIXGTTL 119  
224 AKQAVYNNVNDKSRGVPLD-----VGFQSHNSGNPNPVPFTLQGRALGVVV 276  
120 TVQTLDTYLLQGLAGNDTPPE-----VTYGERD-----LC 152  
277 EYTELDT-----ENHPQYASVIRDCIADVRCGITWGVGRDSNRSYQWPL 326  
153 MESN-----GGSYVW-----ET 144  
327 FDNNGKCAVAVVLDALNNGSDGGSNPPIVSPGQSSQIRGVASRCLDVPRGNT 366  
165 CDSGQ-----KNGKMALYGDGSLRPKQNGCLTSGPDSVTVINISGASGS 215  
387 ADGTQVQVLDCHGSGNQ--CWYTSGRFRIRGN--KILDAQGSNAGAVVQITSWGA-N 442  
QY 71 --TAGYVWI-----PDGNTAVRATITQWIDNGITINPESNVLVAASGIXGTTL 119

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.ra1

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 1050  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
FAX: 202-371-2640  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-590-563-4

Query Match 8.8%; Score 124.5; DB 4; Length 492;  
Best Local Similarity 20.8%; Pred No 0.0019;  
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DVARDDEPDGNOQLMPG---KSNNDPQOLMTKEDGTIR---SNQSCLTYYGY-----70  
DB 168 DVNNAEFDGNSGRCDNLTQRTGND---WIEVAFRTAQDPSAKLCYNDVNIEMNNA 223  
QY 71 --TAGYTYNI-----FDCNTAVREATTWQINDGTTINPRSNLYLAASGIXKQTL 119  
DB 224 AKTQAVYNNVADPKRGVPIIDC-----VQSHFNSGNTNPNFRFTLQOPAL-GVDV 276  
QY 120 TVQCLDYLGGCWLANDTAPR-----VITYGPRD-----LC 152  
DB 277 EYVELDI-----ENAPQYASVIRDLAVDRCTGTTWGVYRDSMSRYGNPL 326  
QY 153 MSNN-----GGSVWV-----ET 164  
DB 327 FDNNGKKAQYAVVLDALNCSDDGGGSPVSPFGGSGQIRGVASRCIDVNGNT 386  
QY 165 CDSGQ-----INQGMALYGDGSIKPKQNOQCLTSGADSVYTNIVSCGASGS 215  
DB 387 ADGTVQVLDCHGSSNQ-QWTTTSSGFRIFRN-KCLDAGSSNGAVQVYSCMGQ-N 442  
QY 216 QRMVFTNBEALILNKTGLAMD-VQANPNKLRILIIYPRATGKPNQW 260  
DB 443 QKWEIRADQTVGVQSGCLDAVGGGTGNGTLLDYSCMGANNQW 488

RESULT 12  
US-08-590-563-7  
Sequence 7, Application US/08590563  
GENERAL INFORMATION:  
APPLICANT: M. RYU, Arita  
APPLICANT: Weinmayer, Jari  
APPLICANT: Fagerstr m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Paloheimo, Maria  
APPLICANT: Suominen, Pirkko  
TITLE OF INVENTION: Production and secretion of proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESS: J. K. KESLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,563  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 1050  
REFERENCE/DOCKET NUMBER: 1050.0340003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
FAX: 202-371-2640  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
STANDARDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50  
US-08-590-563-7

Query Match 8.8%; Score 124.5; DB 4; Length 492;  
Best Local Similarity 20.8%; Pred No 0.0019;  
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DVARDDEPDGNOQLMPG---KSNNDPQOLMTKEDGTIR---SNQSCLTYYGY-----70  
DB 168 DVNNAEFDGNSGRCDNLTQRTGND---WIEVAFRTAQDPSAKLCYNDVNIEMNNA 223  
QY 71 --TAGYTYNI-----FDCNTAVREATTWQINDGTTINPRSNLYLAASGIXKQTL 119  
DB 224 AKTQAVYNNVADPKRGVPIIDC-----VQSHFNSGNTNPNFRFTLQOPAL-GVDV 276  
QY 120 TVQCLDYLGGCWLANDTAPR-----VITYGPRD-----LC 152  
DB 277 EYVELDI-----ENAPQYASVIRDLAVDRCTGTTWGVYRDSMSRYGNPL 326  
QY 153 MSNN-----GGSVWV-----ET 164  
DB 327 FDNNGKKAQYAVVLDALNCSDDGGGSPVSPFGGSGQIRGVASRCIDVNGNT 386  
QY 165 CDSGQ-----INQGMALYGDGSIKPKQNOQCLTSGADSVYTNIVSCGASGS 215  
DB 387 ADGTVQVLDCHGSSNQ-QWTTTSSGFRIFRN-KCLDAGSSNGAVQVYSCMGQ-N 442  
QY 216 QRMVFTNBEALILNKTGLAMD-VQANPNKLRILIIYPRATGKPNQW 260  
DB 443 QKWEIRADQTVGVQSGCLDAVGGGTGNGTLLDYSCMGANNQW 488

RESULT 13  
US-09-770-621-4  
Sequence 4, Application US/09770621  
Patent No. 6506593  
GENERAL INFORMATION:  
APPLICANT: M. RYU, Arita  
APPLICANT: Weinmayer, Jari  
APPLICANT: Fagerstr m, Richard  
APPLICANT: Lantto, Raija

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.rai

Page 5

QY 71 --TAGYVWY-----FCNTAVREATIWMNGTINPRLNLAASGKGTLL 119  
DB 224 AKTQAVYVWYVDFKRGVPIDC-----VQSHNSGNPYNFRFTLQCFAL-GYDV 276  
QY 120 TVQTLDTLTLGGMWLAGNDTAPRE-----VTYGFPRD-----LC 152  
DB 277 EYVELDI-----ENAPQYVAVIADCLAVDRCCTGIVWGVGRDSDRSYONPPL 326  
QY 153 MESN-----GSGVWV-----ET 164  
DB 327 PNNGNKQAVYAVDALNBSDDGSPNPVSPPGSSGQIRGVASNRCTDVPNGNT 386  
QY 165 CDSQ-----KNGKMALVGDGSIRKQNOPOCLTSGRDSVSTYINIVSCGSGS 215  
DB 387 ADGTQVQLYDCHGSSNQ-QWYTSSEFRIFGN-KCLDAGSSNGAVQVYSCWGA-N 442  
QY 216 QRWFTNKGALNKTGLAND-VAQNPRLRIIYFANGKPNQW 260  
DB 443 QWELRADGTIVQSGELCLDVGSGTNGTIRLOYSCWGNQW 488

RESULT 10

US-08-468-812-7  
Sequence 7, Application US/08468812  
Patent No. 5935836  
GENERAL INFORMATION:  
APPLICANT: Vehmanner, Jari  
APPLICANT: M. Neily, Arja  
APPLICANT: Fagerstr m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Palohelmo, Marja  
APPLICANT: Shominen, Pirkko  
APPLICANT: Lantinen, Taina  
APPLICANT: Kestio, Paula  
TITLE OF INVENTION: Cl Use  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: STERN KESSLER, GOLDSTEIN & FOX  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,812  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bigsley, Larry B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050, 0340002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
FAX: 202-371-2600  
INFORMATION FOR SBO ID NO.: 7  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
STANDARDNESS: not relevant

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: AM50

US-08-468-812-7  
Query Match 8.88; Score 124.5; DB 2; Length 492;  
Local 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;  
Matches

QY 23 DVPRDDFHGNOIOLMPS---KSNWPNQMLTKREDGTR---SWSCLTYYGY---- 70  
DB 168 DVYKAFEDSNGRCDJMLRTGND---MIEVAFTRQDPSAKLCYNVINENMA 223  
QY 71 --TAGYVWY-----FCNTAVREATIWMNGTINPRLNLAASGKGTLL 119  
DB 224 AKTQAVYVWYVDFKRGVPIDC-----VQSHNSGNPYNFRFTLQCFAL-GYDV 276  
QY 120 TVQTLDTLTLGGMWLAGNDTAPRE-----VTYGFPRD-----LC 152  
DB 277 EYVELDI-----ENAPQYVAVIADCLAVDRCCTGIVWGVGRDSDRSYONPPL 326  
QY 153 MESN-----GSGVWV-----ET 164  
DB 327 PNNGNKQAVYAVDALNBSDDGSPNPVSPPGSSGQIRGVASNRCTDVPNGNT 386  
QY 165 CDSQ-----KNGKMALVGDGSIRKQNOPOCLTSGRDSVSTYINIVSCGSGS 215  
DB 387 ADGTQVQLYDCHGSSNQ-QWYTSSEFRIFGN-KCLDAGSSNGAVQVYSCWGA-N 442  
QY 216 QRWFTNKGALNKTGLAND-VAQNPRLRIIYFANGKPNQW 260  
DB 443 QWELRADGTIVQSGELCLDVGSGTNGTIRLOYSCWGNQW 488

RESULT 11

US-08-550-563-4  
Sequence 4, Application US/08590563  
Patent No. 6306114  
GENERAL INFORMATION:  
APPLICANT: Vehmanner, Jari  
APPLICANT: M. Neily, Arja  
APPLICANT: Fagerstr m, Richard  
APPLICANT: Lantto, Raija  
APPLICANT: Palohelmo, Marja  
APPLICANT: Shominen, Pirkko  
APPLICANT: Lantinen, Taina  
APPLICANT: Kestio, Paula  
TITLE OF INVENTION: production and secretion of proteins of  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P. L. L. C.  
STREET: 1100 New York Ave., N.W. Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/550,563  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 08/468,812  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536  
APPLICATION NUMBER: US 08/332,412  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 536



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Page 4

```
/ APPLICANT: Halkier, Torben
/ APPLICANT: Hedegaard, Lisbeth
/ TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
/ FILE REFERENCE: 4693.204-05
/ CURRENT APPLICATION NUMBER: US/09/159,106
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER FILING DATE: 1996-12-04
/ EARLIER APPLICATION NUMBER: 0885/96
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER APPLICATION NUMBER: PCT/DK97/00160
/ EARLIER FILING DATE: 1997-04-14
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ TYPE: SEQUENCE
/ ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15
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Query Match 9.6%; Score 136; DB 3; Length 132;
Best Local Similarity 36.3%; Pred. No. 1.7e-06;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;
```

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OY 18 NNNRVYVDDDFHNDGNOIQLPKSKNDPQWLTKIKDITRNSGCLTY--GYTAVGY 75
DB 14 NNNRVYVDDDFHNDGNOIQLPKSKNDPQWLTKIKDITRNSGCLTY--GYTAVGY 71
CY 76 VMTFDNTAVREATWQW--DNGT--IINRSNLYLAASGI--KQTLTVQTLDTYL 128
DB 72 VQWVTCN-----GTGAKWYADGSKALNPSGLDIDATGAPLRDQRLQWTCNGIT 126
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US-09-159-106-11
RESULT 8
/ Sequence 11; Application US/09159106
/ Patent No. 4693
/ GENERAL INFORMATION:
/ APPLICANT: Petter, Pan
/ APPLICANT: Dietz, Ivan
/ APPLICANT: Halkier, Torben
/ APPLICANT: Hedegaard, Lisbeth
/ TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
/ FILE REFERENCE: 4693.204-05
/ CURRENT APPLICATION NUMBER: US/09/159,106
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER FILING DATE: 1996-12-04
/ EARLIER APPLICATION NUMBER: 0885/96
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER APPLICATION NUMBER: PCT/DK97/00160
/ EARLIER FILING DATE: 1997-04-14
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 11
/ LENGTH: 135
/ TYPE: SEQUENCE
/ ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11
```

```
Query Match 9.6%; Score 136; DB 3; Length 132;
Best Local Similarity 36.3%; Pred. No. 9.9e-06;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;
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OY 76 VMTFDNTAVREATWQW--DNGT--IINRSNLYLAASGI--KQTLTVQTLDTYL 128
DB 375 VQWVTCN-----GTGAKWYADGSKALNPSGLDIDATGAPLRDQRLQWTCNGIT 429
CY 129 GQGW 132
DB 430 AQGW 433
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US-08-468-812-4
RESULT 9
/ Sequence 4; Application US/08468812
/ Patent No. 5935836
/ GENERAL INFORMATION:
/ APPLICANT: Vehmeyer, Jari
/ APPLICANT: Mätyl, Arja
/ APPLICANT: Fagerström, Richard
/ APPLICANT: Lantto, Ralf
/ APPLICANT: Raitoharju, Marja
/ APPLICANT: Sjöström, Jarmo
/ APPLICANT: Kahkonen, Tarmo
/ APPLICANT: Kristo, Paula
/ TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
/ STREET: 1100 New York Ave., N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ PRIORITY: 2003
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 06-JUN-1995
/ APPLICATION NUMBER: US/08/468,812
/ PRIORITY: 1995
/ PRIORITY NUMBER: 135
/ PRIORITY DATE: 08/332,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bysastry, Larry B.
/ REGISTRATION NUMBER: 35,086
/ REGISTRATION DATE: 05/050,0340002
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2640
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 492 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-468-812-4
```

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Query Match 8.6%; Score 124.5; DB 2; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00019;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;
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QY 5 CSASEPTVATVGRNKRVDVDDPHDQNOQLWPFSGSNNDPNQMTIKEDGTIRNSGSC 64  
DB 282 QNDPEPIVATVGRNKLCTVDVGTGEPPDQNPQLWPFCKSNNDPNQMTIKEDGTIRNSGSC 341  
QY 65 LTTGYTAGVYVIMFDCTAVRENTIWOINDGTIIPRSALVLAASSGKGTLLVOTL 124  
DB 342 LTTKSSEPPQOVIVYVNCSTAVGATVQVINDRTIIPRSGLVLAATSGSGTLLVOTN 401  
QY 125 DYLGGWLAGNDTAPREVITVYGRDLCKESNGSVWETCDSSQKQKALYGDGSR 184  
DB 402 IVAVSQWLPNNQPEVITVYGLQVQWGLQNSGKWLSDC-TSEKADQWALYADGSR 460  
QY 185 PRONDOCTSGRDSVSTVIVYVSGASGSGQWVFTNEGALINLTGLAMVQANPDL 244  
DB 461 PQONRNCITTDANIKQIVYVILSCGPPSGQWPFKNDGTIINLTGLVLDVRRSDPSL 520  
QY 245 RRIIYVATGKRNQWMLPVF 264  
DB 521 KQIIVHPHGNINQIWLPLF 540

## RESULT 5

US-08-485-286-77

Sequence 77, Application US/08485286

Patent No. 5646026 5646119

GENERAL INFORMATION:

APPLICANT: MALSH, TERENCE A

APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESS: ANDREA T. BORUCKI

STREET: 633 MIDWAYVILLE ROAD

CITY: INDIANAPOLIS

STATE: IN

COUNTRY: US

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,286

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/778761

FILING DATE: 26-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: BORUCKI, ANDREA T

REGISTRATION NUMBER: 33651

REFERENCE/DOCKET NUMBER: 382728

TELECOMMUNICATION INFORMATION:

TELEPHONE (317) 337-4846

INFORMATION: SEQ ID NO: 77:

SOURCE: CHROMATIDIS:

LENGTH: 540 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-286-77

Query Match 54.3%; Score 777.5; DB 1; Length 540;  
Best Local Similarity 55.8%; Pred. No. 46-72;  
Matches 145; Conservative 41; Mismatches 73; Indels 1; Gaps 1;

QY 5 CSASEPTVATVGRNKRVDVDDPHDQNOQLWPFSGSNNDPNQMTIKEDGTIRNSGSC 64  
DB 282 QNDPEPIVATVGRNKLCTVDVGTGEPPDQNPQLWPFCKSNNDPNQMTIKEDGTIRNSGSC 341  
QY 65 LTTGYTAGVYVIMFDCTAVRENTIWOINDGTIIPRSALVLAASSGKGTLLVOTL 124  
DB 342 LTTKSSEPPQOVIVYVNCSTAVGATVQVINDRTIIPRSGLVLAATSGSGTLLVOTN 401  
QY 125 DYLGGWLAGNDTAPREVITVYGRDLCKESNGSVWETCDSSQKQKALYGDGSR 184  
DB 402 IVAVSQWLPNNQPEVITVYGLQVQWGLQNSGKWLSDC-TSEKADQWALYADGSR 460  
QY 185 PRONDOCTSGRDSVSTVIVYVSGASGSGQWVFTNEGALINLTGLAMVQANPDL 244  
DB 461 PQONRNCITTDANIKQIVYVILSCGPPSGQWPFKNDGTIINLTGLVLDVRRSDPSL 520  
QY 245 RRIIYVATGKRNQWMLPVF 264  
DB 521 KQIIVHPHGNINQIWLPLF 540

## RESULT 6

US-09-512-342-14

Sequence 14, Application us/09512342

Patent No. 6388068

GENERAL INFORMATION:

APPLICANT: SATOH, SHINBU

APPLICANT: NAGATA, SUSUMU

APPLICANT: IYER, RAGHUNATHAN

TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT

FILE REFERENCE: 2003/0136742

CURRENT APPLICATION NUMBER: US/09/512,342

CURRENT FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 14

LENGTH: 293

TYPE: PRT

ORGANISM: Cucumis sativus

US-09-512-342-14

Query Match 13.1%; Score 185; DB 4; Length 293;

Best Local Similarity 27.5%; Pred. No. 4,6e-11;

Matches 67; Conservative 36; Mismatches 101; Indels 40; Gaps 11;

14 IVGNKGRVDDPHDQNOQLWPFSGSNNDPNQMTIKEDGTIRNSGSC 59

41 LVGDDGLKLENSP-----WYKPGINPRLSPDCKKQKQWLTIVDGHIFM 89

60 SNGSCLT---YGYTAGVYVIMFDCTAVRENTIWOINDGTIIPRSALVLAASSGK 116

90 NKRCLAAVEFYVIN---KAVVSRCKGVSDNKNVTOQKNDGTIIVDSKVLVGDLDY-- 145

117 TTLVYVTDITDQGMALAGNDTAPREVITVYGRDLCKESNGS--VWETCDSSQK 174

146 --VLDGSKITPQWNETESLNSMNTIEMVNLCLQSTDDSSRIGALGNDTNRKYR 202

175 NALYGDGSRPRONDOCTSGRDSVSTVIVYVSGASGSGQW-VFTNEGALINLTGL 233

203 WALVADGTIRHVNKNCLTSDQGFGRFY--VVSCKERKQGRMSLDADVITDHNH 260

234 ANDV 237

261 VLDV 264

US-09-512-342-14

Query Match 13.1%; Score 185; DB 4; Length 293;  
Best Local Similarity 27.5%; Pred. No. 4,6e-11;  
Matches 67; Conservative 36; Mismatches 101; Indels 40; Gaps 11;  
GENERAL INFORMATION:  
APPLICANT: SATOH, SHINBU  
APPLICANT: NAGATA, SUSUMU  
APPLICANT: IYER, RAGHUNATHAN  
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT  
FILE REFERENCE: 2003/0136742  
CURRENT APPLICATION NUMBER: US/09/512,342  
CURRENT FILING DATE: 2000-02-24  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 14  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Cucumis sativus  
US-09-512-342-14

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Page 2

```

RESULT 2
US-08-776-059-33
Sequence 33, Application US/087760593
Patent No. 6271368
APPLICANT: BAYER, Bayer AG
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776-059B
EARLIER FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: 674503-2003
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 264
TYPE: PRT
ORGANISM: Viscum album

Query Match          91.7%; Score 1127.5; Ds 3; Length 264;
Best local similarity 95.1%; Pctd No:126-129;
Matches 250; conservative 2; Mismatches 10; Indels 1; Gaps 1

Qy      1  DVTGSSASEPTVRIVRNRKRVVADDDPFDDGNOIGLAMPSSKNPNPQGLWTKKDDTSS 60
Db      2  DVTGSSASEPTVRIVRNRKRVVADDDPFDDGNOIGLAMPSSKNPNPQGLWTKKDDTSS 61
Qy      61 NSGCLTGVTHGAYVIMPDONTNREKTIWQINDGNTINPSNMLVLAASSGKSTLT 120
Db      62 NSGCLTGVTHGAYVIMPDONTNREKTIWQINDGNTINPSNMLVLAASSGKSTLT 121
Qy      121 VQVLTLYTSGGLKGLNDAPREFTTYGPRILCMSSNGSSWVETQSSQKNGALYSD 180
Db      122 VQVLTLYTSGGLKGLNDAPREFTTYGPRILCMSSNGSSWVETQSSQKNGALYSD 180
Qy      181 GSIRPKQDQQLGSRGSRVATVIVNSGSGSGSGSRWVFTNSGAILNLTATLAMPVQA 240
Db      181 GSIRPKQDQQLGSRGSRVATVIVNSGSGSGSGSRWVFTNSGAILNLTATLAMPVQA 240
Qy      241 NPTRETTTTVATKCKKPKMCTPT 263
Db      241 NPTRETTTTVATKCKKPKMCTPT 263

RESULT 3
US-08-776-059-35
Sequence 35, Application US/08776059B
Patent No. 6271368
APPLICANT: BAYER, Bayer AG
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776-059B
EARLIER FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: 674503-2003
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album

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US-08-378-059-35
Query Match 93.7% Score 137.5 DB 3 Length 564:
Best Local Similarity 95.1% Pred. No. 3,8e-19; Indels 1; Gaps 1;
Matches 250; Conservative 2; Mismatches 10;

OY 1 DDVCSASEPTVIVIGRRKGRVDFDDPDHGNQGLQGLSPKSNNDNDQMTIRGGTIS 60
DB 302 DDVCSASEPTVIVIGRRKGVDFDDPDHGNQGLQGLSPKSNNDNDQMTIRGGTIS 361
OY 61 NSCLTIVGTVAVYVIMPCQVAVTEATIMQIMNGTINRESNVIYLAASGIGTTL 120
DB 362 NSCLTIVGTVAVYVIMPCQVAVTEATIMQIMNGTINRESNVIYLAASGIGTTL 421
OY 121 VQGLDPTLGGGAGNDPAAREVTVIGFPLCMENSGSVWETCCSGKQCKALYGD 180
DB 422 VQGLDPTLGGGAGNDPAAREVTVIGFPLCMENSGSVWETCCSGKQCKALYGD 480
OY 181 GSIRKKNODQCLTGRSRSVTVINIVSGASGSGRWVTEGAILNLTGADVAAQ 240
DB 481 GSIRKKNODQCLTGRSRSVTVINIVSGASGSGRWVTEGAILNLTGADVAAQ 540
OY 241 NPLKRIITVYAPCKGNMLEY 263
DB 541 NPLKRIITVYAPCKGNMLEY 563

RESULT 4
US-08-378-761A-77
Sequence 77, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
INVENTOR: HEI, TIMOTHY D
TITLE OF INVENTION: BIOSensor- INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEROF, A PROCESS FOR MAKING A
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
PUBLICATION NO. 2002/014268
COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/378,761A
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
PRIORITY DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 382728
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STANDARD: single
TORUSLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-77
Query Match 54.9%; Score 777.5; DB 1; Length 540;
Best Local Similarity 55.8%; Pred. No. 4e-72; Indels 1; Gaps 1;
Matches 145; Conservative 4; Mismatches 73; Indels 1; Gaps 1;

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Thu Dec 11 16:10:07 2003

us-09-601-667c-9.rapb

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/770,621
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/590,563
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/332,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ EXPIRATION DATE: 09/30/2003
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2640
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 492 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: No
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ POSITION IN GENOME:
/ ORIGIN: cDNA
/ ORGANISM: HOMO SAPIENS
/ US-09-770-621-7

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Query Match 8.8%; Score 124.5; DB 9; Length 492;  
Best Local Similarity 20.8%; Pred. No. 0.0005;  
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

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QY 23 DVEDDPEHDSNQIQLMPS--KSNNDPNOIWTIKDGTIR---SNQSCLTYGY----- 70
DB 168 DVNNEAFEDNSGRCDNSLQRTAND---MIEVAFRTAQDPSAKLCINDYINENRNA 223
QY 71 --TQGVYNT-----PDCITAVRENTIQIWMQNTIINRSNLVLAASSGKGTLL 119
DB 224 AKQAVNNVWDFPKSGVPIDC-----VGFQSHFNSGNPNYNNPFTLLQOPAL-GVGV 276
QY 120 TVQTLDTLGGWLAGNDIAPRE-----VTYGFPRD-----LC 152
DB 277 EYVELDI-----ENAPQIYASVIRDCIADVRCCTGIYWGVDSDSRSYQNPFL 326
QY 153 MASN-----GSYVW-----ET 164
DB 327 FDNNGNKQAYAVLDALNBSDDGGSPSPVSPFGQSGQIRGVASNRCLIDVPRNT 386
QY 165 CDSGQ-----KNGKALYGGGSRPKQNDQCTSGSPSVYINIVSGSGASG 215
DB 387 ADGTQVQLYDCHSGSNQ--QWYYSSEGRFRFGN--KCLDAGGSSNVAVQYISCGWGA-N 442
QY 216 QRWVETNKGALINLKTGLAND--VAQANFKLRIRIITYPATGKPNQW 260
DB 443 QKWEIPLADCTIVGVQSLCLDAVAGGTGNGCTRLQLYSCWGNQW 488

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RESULT 15  
US-10-286-993-4  
SEQUENCE 4 Application US/10286693  
Publication No US20030148453A1  
GENERAL INFORMATION:  
APPLICANT: Mantyla, Arja  
APPLICANT: Palcheimo, Marja  
APPLICANT: Lantto, Ralja

```

/ APPLICANT: Fagerstrom, Richard
/ APPLICANT: Lantto, Marja
/ APPLICANT: Palcheimo, Marja
/ APPLICANT: Vahvanperä, Jari
/ TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
/ TITLE OF INVENTION: Fungi
/ FILE REFERENCE: 1716.034004
/ CURRENT APPLICATION NUMBER: US/10/286,993
/ PRIOR APPLICATION NUMBER: 08/110,804
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: PCT/FR97/00037
/ PRIOR FILING DATE: 1997-01-24
/ PRIOR APPLICATION NUMBER: US 08/590,563
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 4
/ LENGTH: 492
/ ORIGIN: Actinomyces flexuosa
/ US-10-286-993-4

```

Query Match 8.8%; Score 124.5; DB 12; Length 492;  
Best Local Similarity 20.8%; Pred. No. 0.0005;  
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

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QY 23 DVEDDPEHDSNQIQLMPS--KSNNDPNOIWTIKDGTIR---SNQSCLTYGY----- 70
DB 168 DVNNEAFEDNSGRCDNSLQRTAND---MIEVAFRTAQDPSAKLCINDYINENRNA 223
QY 71 --TQGVYNT-----PDCITAVRENTIQIWMQNTIINRSNLVLAASSGKGTLL 119
DB 224 AKQAVNNVWDFPKSGVPIDC-----VGFQSHFNSGNPNYNNPFTLLQOPAL-GVGV 276
QY 120 TVQTLDTLGGWLAGNDIAPRE-----VTYGFPRD-----LC 152
DB 277 EYVELDI-----ENAPQIYASVIRDCIADVRCCTGIYWGVDSDSRSYQNPFL 326
QY 153 MASN-----GSYVW-----ET 164
DB 327 FDNNGNKQAYAVLDALNBSDDGGSPSPVSPFGQSGQIRGVASNRCLIDVPRNT 386
QY 165 CDSGQ-----KNGKALYGGGSRPKQNDQCTSGSPSVYINIVSGSGASG 215
DB 387 ADGTQVQLYDCHSGSNQ--QWYYSSEGRFRFGN--KCLDAGGSSNVAVQYISCGWGA-N 442
QY 216 QRWVETNKGALINLKTGLAND--VAQANFKLRIRIITYPATGKPNQW 260
DB 443 QKWEIPLADCTIVGVQSLCLDAVAGGTGNGCTRLQLYSCWGNQW 488

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Search completed: December 11, 2003, 14:48:50  
Job time: 18.0129 secs

Thu Dec 11 16:10:07 2003

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Page 5

APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIMA, TADASHI  
APPLICANT: SHIMA, TADASHI  
APPLICANT: HATTORI, HISAKO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQUENCE ID NO: 12246  
LENGTH: 647  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-10246

Query Match 8.9%; Score 126; DB 15; Length 647;

Best Local Similarity 26.3%; Pred. No. 0.00051;  
Matches 45; Conservative 20; Mismatches 60; Indels 46; Gaps 8;

QY 9 BEFTVIRGNKGVYDDDPDNDNOIQMPKSKNDPNQMTIKDGIKNSGCL-T 66  
DB 520 DGTGSGFVGLAKCLDVSSSSANGTAVLYD--DNGSTPGRKTVKADSSVVALSGCLDVT 577  
QY 67 TGYTAGVYVYVDPDQVAVRFACTNCTDNDGTINPNSMVLAAAGCKITLTVQTDV 126  
DB 578 SASTADAKIQLYDCLN---CTAAGRNSYV-----ASTGVVNTAAKXLDV 620  
QY 127 TVGGWMLAGNDTAPREVTVYGRDLCSNSGSSVWVETCSSGQKQKAL 177  
DB 621 T-----GNSA-----NQAQAQWSC-TGANO-KWKL 646

RESULT 13

US-09-770-621-4

Sequence 4; Application US/09770621  
Patent No. US20010024815A1

GENERAL INFORMATION:  
APPLICANT: M nyl, Arja

APPLICANT: Vehmanner, Jari

APPLICANT: Lantto, Raija

APPLICANT: Palohelmo, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,001  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: B  
INVENTOR: Lantinen, Tarja  
REGISTERED/DOCKET NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 1050,0340003  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
MOLECULE TYPE: linear  
US-09-770-621-4

Query Match 8.8%; Score 124.5; DB 9; Length 492;

Best Local Similarity 20.8%; Pred. No. 0.0005;  
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DVADDPDNDNOIQMPKSKNDPNQMTIKDGIKNSGCL-T 70  
DB 168 DVNAPFEDNSGRCDNSLQRTGND--MVEAFRTARQSPAKLCYNDYMIENNA 223  
QY 71 --TAYGVYVYVDPDQVAVRFACTNCTDNDGTINPNSMVLAAAGCKITLTVQTDV 119  
DB 120 TVGGWMLAGNDTAPREVTVYGRDLCSNSGSSVWVETCSSGQKQKAL 177  
QY 224 AKQAVYVYVDPDQVAVRFACTNCTDNDGTINPNSMVLAAAGCKITLTVQTDV 126  
DB 120 TVGGWMLAGNDTAPREVTVYGRDLCSNSGSSVWVETCSSGQKQKAL 177  
QY 277 EYVTELDI-----ENAAQTVASVIRDLAVDRCGTITWGVSDSWRSYQPL 326  
DB 153 MESN-----GSSVWV-----ET 164  
QY 327 FDNNAKQAYVYVDPDQVAVRFACTNCTDNDGTINPNSMVLAAAGCKITLTVQTDV 126  
DB 165 CBSGQ-----KQCVYVYVDPDQVAVRFACTNCTDNDGTINPNSMVLAAAGCKITLTVQTDV 126  
QY 387 ADQVYVYVDPDQVAVRFACTNCTDNDGTINPNSMVLAAAGCKITLTVQTDV 126  
DB 216 QKVEAFRTARQSPAKLCYNDYMIENNA 223  
QY 443 QKVEAFRTARQSPAKLCYNDYMIENNA 223

RESULT 14

US-09-770-621-7

Sequence 7; Application US/09770621  
Patent No. US20010024815A1

GENERAL INFORMATION:  
APPLICANT: M nyl, Arja

APPLICANT: Vehmanner, Jari

APPLICANT: Lantto, Raija

APPLICANT: Palohelmo, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

APPLICANT: Lantinen, Tarja

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; LENGTH: 536
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match
  9.5%; Score 134; DB 15; Length 536;
Best Local Similarity 30.1%; Pred. No. 6e-05;
Matches 40; Conservative 18; Mismatches 59; Indels 16; Gaps 6;

QY 14 IVGNMNR-IVPDDPHDQIOLPKSKNNDPQMLWTI--KQDGTIRNGS-CLFTT 68
DB 409 IVASNRCTDAVDNQTAPGKTHIDC--GAGQAVITTAAGELFYGCTCLDAVDN 465

QY 69 GTTAGYVYVMPDQNTAVREATWQIMDNGTIIINRSNLV-----AASGIGKTTLTVO 122
DB 466 GTTSGTVOVLYTCNGANOK--MSLNPQVTVTQSGCLDVTGAGQASGNVGNALIELM 523

QY 123 TLDTYTAGGNTLAG 135
DB 524 TONGANQOMRLG 536
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RESULT 9
US-10-137-077-18
; Sequence 18, Application US/10137077
; Publication No. US20030092109A1
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Irwin J.
; APPLICANT: Wainer, Harry C.
; APPLICANT: Kruger, Robert P.
; TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
; FILE REFERENCE: US-07124
; CURRENT FILING DATE: 2002-05-02
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/288,596
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/354,322
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Rictinus communis
US-10-137-077-18

Query Match
  9.4%; Score 133; DB 15; Length 41;
Best Local Similarity 56.1%; Pred. No. 2.3e-06;
Matches 23; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
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QY 224 GAINLKTGLANDVQANPKRIIRIIPATGKPNQMLPVE 264
DB 1 GTINLVSGVLDVPRADPSLKIITLPLHDPNQMLPLF 41

RESULT 10
US-09-973-457-5
; Sequence 5, Application US/09973457
; Patent No. US2002016474EAL
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
; FILE REFERENCE: 10448-099001 US/09/973,457
; CURRENT APPLICATION NUMBER: US/09/973,457
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,849
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 135
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match
  9.0%; Score 127; DB 10; Length 135;
Best Local Similarity 25.0%; Pred. No. 4.8e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNMNRVDY--RDDPHDQIOLPKSKNNDPQMLWTI--KQDGTIRNGS-CLFTT 67
DB 7 ICGNMGCLDVNGNSSKSDNPVQIMDCHGGG--NOLMKLTNSDGLRINSIDCLTV 64

QY 68 VGTAGYVYVMPDQNTAVR--EATWQIMDNGTIIINRSNLVLAASGIGKTTLTVO 125
DB 65 NG-----TVTISCGTGDGKMDQKQMEVNDYITNPK--NSKQGVDS----- 106

QY 126 VTLGQMLAGNDPLAPREYVYIIGRDLCKE--SNGSIVETGDSQKNGK 175
DB 107 -----LCLDYDQKVKVQLTNGSDAPVQK 132
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RESULT 11
US-10-074-527-6
; Sequence 6, Application US/10074527
; Publication No. US2002014242EAL
; GENERAL INFORMATION:
; APPLICANT: Olander, Peter J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Olander, Kristine A.
; TITLE OF INVENTION: Mammalian pharmaceuticals Inc.
; TITLE OF INVENTION: 33945, A Human Glycosyltransferase and
; FILE REFERENCE: MF2001-01891RCP1M
; CURRENT APPLICATION NUMBER: US/10/074,527
; CURRENT FILING DATE: 2002-02-12
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/469202
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus
US-10-074-527-6

Query Match
  9.0%; Score 127; DB 14; Length 135;
Best Local Similarity 25.7%; Pred. No. 4.8e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;
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QY 14 IVGNMNRVDY--RDDPHDQIOLPKSKNNDPQMLWTI--KQDGTIRNGS-CLFTT 67
DB 7 ICGNMGCLDVNGNSSKSDNPVQIMDCHGGG--NOLMKLTNSDGLRINSIDCLTV 64

QY 68 VGTAGYVYVMPDQNTAVR--EATWQIMDNGTIIINRSNLVLAASGIGKTTLTVO 125
DB 65 NG-----TVTISCGTGDGKMDQKQMEVNDYITNPK--NSKQGVDS----- 106

QY 126 VTLGQMLAGNDPLAPREYVYIIGRDLCKE--SNGSIVETGDSQKNGK 175
DB 107 -----LCLDYDQKVKVQLTNGSDAPVQK 132

RESULT 12
US-10-156-761-10246
; Sequence 10246, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIGAWA, JUN
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Qy 121 VQTLDTYLGQGMAGNDTAPREVITYGFRDLCHESNGSSVWERTCSSQKQKQKALYGD 180  
 Db 121 VQTLDTYLGQGMAGNDTAPREVITYGFRDLCHESNGSSVWERTCSSQKQKQKALYGD 179  
 Qy 181 GSIRPKQNDQCLTSGDSVSTVINIVCSGASGSGRWFTNEGALINLKTGLANDVAQA 240  
 Db 180 GSIRPKQNDQCLTSGDSVSTVINIVCSGASGSGRWFTNEGALINLKTGLANDVAQA 239  
 Qy 241 NPKLRRIIYPATGKPNQMLPV 263  
 Db 240 NPKLRRIIYPATGKPNQMLPV 262

RESULT 2  
 US-09-347-064-4  
 / Sequence 4, Application US/09347064A  
 / Patent No. US20020045208A1  
 / ORIGINATOR: Vascum album  
 / APPLICANT: Schmitz, Bruno  
 / APPLICANT: Schmitz, Bruno  
 / TITLE OF INVENTION: Recombinant Fusion Proteins Based on  
 / TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Vascum  
 / TITLE OF INVENTION: album  
 / FILE REFERENCE: 09282-5  
 / CURRENT APPLICATION NUMBER: US/09/347,064A  
 / EARLIER FILING DATE: 1999-07-02 / PCT/EP98/00009  
 / EARLIER FILING DATE: 1998-04-02 / PCT/EP98/00009  
 / EARLIER FILING DATE: 1997-01-02 / PCT/EP97/00012  
 / EARLIER FILING DATE: 1997-01-02 / PCT/EP97/00012  
 / NUMBER OF SEQ ID NOS: 18  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 4  
 / LENGTH: 267  
 / TYPE: PRT  
 / ORGANISM: Vascum album  
 / US-09-347-064-4

Query Match 83.7%; Score 1327.5; DB 9; Length 267;  
 Best Local Similarity 95.1%; Pred. No. 36-127;  
 Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;  
 Qy 1 DDTVCASEPTVIVGNNMCVDRDDPRDQNOIQLPKSKNDPNQTLTKREDGTIS 60  
 Db 1 DDTVCASEPTVIVGNNMCVDRDDPRDQNOIQLPKSKNDPNQTLTKREDGTIS 60  
 Qy 61 NQSCLTYYGTAQVYVIMPCVAVBEATVIMQNGFTIINFRSNVLAASGIGTIT 120  
 Db 61 NQSCLTYYGTAQVYVIMPCVAVBEATVIMQNGFTIINFRSNVLAASGIGTIT 120  
 Qy 121 VQTLDTYLGQGMAGNDTAPREVITYGFRDLCHESNGSSVWERTCSSQKQKALYGD 180  
 Db 121 VQTLDTYLGQGMAGNDTAPREVITYGFRDLCHESNGSSVWERTCSSQKQKALYGD 179  
 Qy 181 GSIRPKQNDQCLTSGDSVSTVINIVCSGASGSGRWFTNEGALINLKTGLANDVAQA 240  
 Db 180 GSIRPKQNDQCLTSGDSVSTVINIVCSGASGSGRWFTNEGALINLKTGLANDVAQA 239  
 Qy 241 NPKLRRIIYPATGKPNQMLPV 263  
 Db 240 NPKLRRIIYPATGKPNQMLPV 262

RESULT 3  
 US-10-083-336A-1  
 / Sequence 1, Application US/1008336A  
 / Publication No. US2003018165A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Olson, Mark A  
 / APPLICANT: Willard, Charles B  
 / APPLICANT: Byrne, Michael P  
 / APPLICANT: Mannemacher, Robert W

Qy 5 CSASEPTVIVGNNMCVDRDDPRDQNOIQLPKSKNDPNQTLTKREDGTISNSC 64  
 Db 318 CSASEPTVIVGNNMCVDRDDPRDQNOIQLPKSKNDPNQTLTKREDGTISNSC 377  
 Qy 65 IITGQGMAGNDTAPREVITYGFRDLCHESNGSSVWERTCSSQKQKQKALYGD 124  
 Db 378 IITGQGMAGNDTAPREVITYGFRDLCHESNGSSVWERTCSSQKQKQKALYGD 123  
 Qy 125 DYTLCQGMAGNDTAPREVITYGFRDLCHESNGSSVWERTCSSQKQKQKALYGD 184  
 Db 438 IYAVSQCMPTNTPFTTIVGLGLQANSQGVETDC-SSEKAOQMALYADGSR 496  
 Qy 185 PKQNDQCLTSGDSVSTVINIVCSGASGSGRWFTNEGALINLKTGLANDVAQA 244  
 Db 497 PKQNDQCLTSGDSVSTVINIVCSGASGSGRWFTNEGALINLKTGLANDVAQA 244  
 Qy 245 PRRIIYPATGKPNQMLPV 264  
 Db 557 KQILYPLHDPNQMLPV 576

Query Match 64.0%; Score 907.5; DB 12; Length 576;  
 Best Local Similarity 63.8%; Pred. No. 6-76-84;  
 Matches 166; Conservative 33; Mismatches 60; Indels 1; Gaps 1;  
 US-10-083-336A-1  
 / Sequence 1, Application US/10074527  
 / Patent No. US20030092109A1  
 / ORIGINATOR: Ricinus communis  
 / APPLICANT: Mannemacher, Robert W  
 / APPLICANT: Mannemacher, Robert W  
 / TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin  
 / FILE REFERENCE: US-07124  
 / CURRENT APPLICATION NUMBER: US/10/137,077  
 / EARLIER FILING DATE: 2002-05-02  
 / EARLIER FILING DATE: 2001-05-03  
 / EARLIER FILING DATE: 2000-02-04  
 / EARLIER FILING DATE: 2000-02-04  
 / NUMBER OF SEQ ID NOS: 3  
 / SOFTWARE: PatentIn version 3.1  
 / SEQ ID NO 17  
 / LENGTH: 44  
 / TYPE: PRT  
 / ORGANISM: Ricinus communis  
 / US-10-137-077-17

Query Match 13.1%; Score 186; DB 15; Length 44;  
 Best Local Similarity 77.3%; Pred. No. 9-86-12;  
 Matches 34; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
 Qy 12 VYIVGNNMCVDRDDPRDQNOIQLPKSKNDPNQTLTKRED 55  
 Db 1 VYIVGNNMCVDRDDPRDQNOIQLPKSKNDPNQTLTKRED 44

RESULT 5  
 US-10-074-527-5  
 / Sequence 5, Application US/10074527

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Page 1

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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13: /cgn2\_6/p/cdata/1/pubpa/US10\_PUBCOMB.pep:\*

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	1307.5	93.7	267	9	US-09-347-064-10
5	1307.5	93.7	267	9	US-09-347-064-10
6	1307.5	93.7	267	9	US-09-347-064-10
7	1307.5	93.7	267	9	US-09-347-064-10
8	1307.5	93.7	267	9	US-09-347-064-10
9	1307.5	93.7	267	9	US-09-347-064-10
10	1307.5	93.7	267	9	US-09-347-064-10
11	1307.5	93.7	267	9	US-09-347-064-10
12	1307.5	93.7	267	9	US-09-347-064-10
13	1307.5	93.7	267	9	US-09-347-064-10
14	1307.5	93.7	267	9	US-09-347-064-10
15	1307.5	93.7	267	9	US-09-347-064-10

16	122.5	8.6	480	9	US-09-770-621-5	Sequence 5, Appl1
17	122.5	8.6	491	9	US-09-770-621-8	Sequence 8, Appl1
18	111	7.8	625	15	US-10-156-761-15008	Sequence 15008, A
19	109	7.7	41	15	US-10-137-077-20	Sequence 20, Appl1
20	107	7.6	612	14	US-10-001-851-25	Sequence 25, Appl1
21	104	7.3	45	15	US-10-137-077-19	Sequence 19, Appl1
22	104	7.3	45	15	US-10-137-077-19	Sequence 19, Appl1
23	95	6.7	295	9	US-09-841-132-395	Sequence 132, A
24	94	6.6	1723	9	US-09-841-132-395	Sequence 132, A
25	94	6.6	1723	9	US-09-841-132-395	Sequence 132, A
26	92	6.5	2771	10	US-09-808-602-82	Sequence 82, Appl1
27	92	6.5	2771	10	US-09-808-602-82	Sequence 82, Appl1
28	90.5	6.4	340	15	US-10-128-714-8037	Sequence 8037, Ap
29	89	6.3	770	9	US-09-815-654-31	Sequence 31, Appl1
30	88	6.2	1032	11	US-09-733-643-16	Sequence 16, Appl1
31	88	6.2	1032	11	US-09-733-643-16	Sequence 16, Appl1
32	87.5	6.2	826	10	US-09-858-528-10	Sequence 10, Appl1
33	87.5	6.2	826	10	US-09-858-528-10	Sequence 10, Appl1
34	87	6.1	1704	12	US-10-229-062-12	Sequence 12, Appl1
35	86.5	6.1	181	12	US-10-229-062-12	Sequence 12, Appl1
36	86.5	6.1	181	12	US-10-229-062-12	Sequence 12, Appl1
37	84.5	6.0	239	10	US-09-910-071-15	Sequence 15, Appl1
38	84	5.9	247	11	US-09-880-748-2127	Sequence 2127, Ap
39	83.5	5.9	788	11	US-09-733-643-14	Sequence 14, Appl1
40	83	5.9	247	11	US-09-880-748-1885	Sequence 1885, Ap
41	83	5.9	247	11	US-09-733-643-14	Sequence 14, Appl1
42	82.5	5.8	2353	10	US-09-797-862-33	Sequence 33, Appl1
43	82.5	5.8	955	15	US-10-156-761-15004	Sequence 15004, A
44	82.5	5.8	1732	12	US-10-229-066-11	Sequence 11, Appl1
45	82.5	5.8	3571	14	US-10-511-842-2	Sequence 2, Appl1

#### ALIGNMENTS

US-09-347-064-10	Sequence 10, Application US/09347064A
1	US-09-347-064-10
2	US-09-347-064-10
3	US-09-347-064-10
4	US-09-347-064-10
5	US-09-347-064-10
6	US-09-347-064-10
7	US-09-347-064-10
8	US-09-347-064-10
9	US-09-347-064-10
10	US-09-347-064-10
11	US-09-347-064-10
12	US-09-347-064-10
13	US-09-347-064-10
14	US-09-347-064-10
15	US-09-347-064-10
16	US-09-347-064-10
17	US-09-347-064-10
18	US-09-347-064-10
19	US-09-347-064-10
20	US-09-347-064-10
21	US-09-347-064-10
22	US-09-347-064-10
23	US-09-347-064-10
24	US-09-347-064-10
25	US-09-347-064-10
26	US-09-347-064-10
27	US-09-347-064-10
28	US-09-347-064-10
29	US-09-347-064-10
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31	US-09-347-064-10
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35	US-09-347-064-10
36	US-09-347-064-10
37	US-09-347-064-10
38	US-09-347-064-10
39	US-09-347-064-10
40	US-09-347-064-10
41	US-09-347-064-10
42	US-09-347-064-10
43	US-09-347-064-10
44	US-09-347-064-10
45	US-09-347-064-10

CC Fibroses. Non-cytotoxic forms of (1) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (1) and its  
 CC fragments are used to induce tumour growth (particularly of the  
 CC cancers) and if they lack cytotoxicity to tumours, fragments of the  
 CC immune response, particularly to a co-administered antigen  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains. In many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a mistletoe lectin I protein variant.

Seq Sequence 532 AA.

Query Match 94.1%; Score 133.5; DB 20; Length 532;  
 Best Local Similarity 95.4%; Pred. No. 1,9e-123;  
 Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DDTVCASAPPTVAIVGNKGVVDDPDDPHDGNQIQAMPKSNNDPNOIWTIKEDGTIS 60  
 DB 269 DDTVCASAPPTVAIVGNKGVVDDPDDPHDGNQIQAMPKSNNDPNOIWTIKEDGTIS 328  
 QY 61 NSCCTTGTGTAGTVMIFDONTAVKATINQINDGTTINPSNVLVAASGKGTIT 120  
 DB 329 NSCCTTGTGTAGTVMIFDONTAVKATINQINDGTTINPSNVLVAASGKGTIT 388  
 QY 121 VQTLDTLGGQWLAGNDTAPREVTYGFRLDQMSNGSVMWETCDSSQNOGKALYGD 180  
 DB 389 VQTLDTLGGQWLAGNDTAPREVTYGFRLDQMSNGSVMWETCDSSQNOGKALYGD 447  
 QY 181 GSIRKQNDQCLTGRDSVSTVINIVSCGASGSGQWVFTNKGALINLKTGLAMVDAQ 240  
 DB 448 GSIRKQNDQCLTGRDSVSTVINIVSCGASGSGQWVFTNKGALINLKTGLAMVDAQ 507  
 QY 241 NPKLRITITVPATKGNQWMLPV 263  
 DB 508 NPKLRITITVPATKGNQWMLPV 530

RESULT 15  
 AAM64662  
 ID AAM64662 standard; Protein; 263 AA.  
 AC AAM64662;  
 XX 23-OCT-1998 (first entry)  
 XX Mistletoe RMB variant protein.  
 DE Lectin B-chain; mistletoe; RMB; fusion protein; effector; cytotoxic;  
 KW intracellular; processing module; protease recombinant; targeting module;  
 KW internalisation; treatment; disorder; cell proliferation; activation;  
 KW autoimmune disease; allergy; tumour; rich; translocation.  
 OS Viscum album.  
 XX  
 XX  
 FT Key Location/Qualifiers  
 FT Protein 1..263  
 FT /note= "partial protein"  
 PV MO9829540-A2.  
 XX 09-JUL-1998.  
 XX 02-JAN-1998; 98MO-EP00009.  
 PF 02-JAN-1997; 97EP-0100012.  
 PR (BR1-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.  
 EA Eck J, Schmidt A, Zinke H;  
 XX WPI, 1998-386122/33.  
 DR N-PSDB; AAV51344.

XX Nucleic acid encoding fusion protein containing mistletoe lectin A  
 FT chain - useful for treatment of proliferative and autoimmune  
 PR diseases, allergies and tumours  
 XX  
 XX Disclosure; Fig 11b', 115pp; German.  
 CC This sequence represents a variant mistletoe lectin B-chain RMB. This  
 CC sequence can be used in the construction of a fusion protein which  
 CC comprises an effector module that is cytotoxic intracellularly, a  
 CC processing module covalently bonded to the effector module and  
 CC containing a protease recognition sequence, and a targeting module  
 CC covalently bonded to the processing module, able to bind specifically to  
 CC the surface of a cell so as to mediate internalisation of the fusion  
 CC protein. Such a fusion protein can be used for treating disorders  
 CC involving proliferation and/or elevated activation of cells, especially  
 CC e.g. by intracellular, allergy and tumours. The proteins can be administered  
 CC at 1 ng to 500 mg/kg/day of body weight, especially by intravenous injection,  
 CC Fusion proteins can develop toxic activity in a wide range of tissues and  
 CC cells. The processing module prevents extracellular dissociation and  
 CC fusion proteins based on mistletoe lectin A-chain are far more active  
 CC than those based on ricin and do have the associated problems of  
 CC non-specific toxicity. The protein may be expressed in a non-glycosylated  
 CC form that does not bind to sugar receptors in the liver, and which has a  
 CC long half-life in the blood. Where the mistletoe lectin B-chain is used,  
 CC it actively assists in translocation of the ML A-chain from the  
 CC endoplasmic reticulum to the cytoplasm.

Seq Sequence 263 AA;  
 Query Match 93.7%; Score 1327.5; DB 19; Length 263;  
 Best Local Similarity 95.1%; Pred. No. 2.8e-123;  
 Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 DDTVCASAPPTVAIVGNKGVVDDPDDPHDGNQIQAMPKSNNDPNOIWTIKEDGTIS 60  
 DB 1 DDTVCASAPPTVAIVGNKGVVDDPDDPHDGNQIQAMPKSNNDPNOIWTIKEDGTIS 60  
 QY 61 NSCCTTGTGTAGTVMIFDONTAVKATINQINDGTTINPSNVLVAASGKGTIT 120  
 DB 61 NSCCTTGTGTAGTVMIFDONTAVKATINQINDGTTINPSNVLVAASGKGTIT 120  
 QY 121 VQTLDTLGGQWLAGNDTAPREVTYGFRLDQMSNGSVMWETCDSSQNOGKALYGD 180  
 DB 121 VQTLDTLGGQWLAGNDTAPREVTYGFRLDQMSNGSVMWETCDSSQNOGKALYGD 179  
 QY 181 GSIRKQNDQCLTGRDSVSTVINIVSCGASGSGQWVFTNKGALINLKTGLAMVDAQ 240  
 DB 180 GSIRKQNDQCLTGRDSVSTVINIVSCGASGSGQWVFTNKGALINLKTGLAMVDAQ 239  
 QY 241 NPKLRITITVPATKGNQWMLPV 263  
 DB 240 NPKLRITITVPATKGNQWMLPV 262

Search completed: December 11, 2003, 14:07:45  
 Job time : 27.0864 secs

XX Sequence 264 AA;  
 SQ Query Match 94.1%; Score 1333.5; DB 20; Length 264;  
 Best Local Similarity 95.4%; Pred. No. 7.1e-124;  
 Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DPTGCSAEPPTVAVGKNGKAVVDDDDPHDQIQIAMPKSKNDPNQIWKIKDGTIRS 60  
 DB 1 DPTGCSAEPPTVAVGKNGKAVVDDDDPHDQIQIAMPKSKNDPNQIWKIKDGTIRS 60  
 QY 61 NGSCLTGYTGYAGYVWIPDCNTAVRENTIWOIDNGTINPRSNLYLAASGIGKTTLT 120  
 DB 61 NGSCLTGYTGYAGYVWIPDCNTAVRENTIWOIDNGTINPRSNLYLAASGIGKTTLT 120  
 QY 121 VQTLDTLGGKMLAGNDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKMAIYED 180  
 DB 121 VQTLDTLGGKMLAGNDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKMAIYED 180  
 QY 121 VQTLDTLGGKMLAGNDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKMAIYED 179  
 DB 121 VQTLDTLGGKMLAGNDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKMAIYED 179  
 QY 181 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGSGQWFTNKGALINLTGLANDVQA 240  
 DB 181 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGSGQWFTNKGALINLTGLANDVQA 239  
 QY 241 NPKLRRIIIVPATGKPNQMLPV 263  
 DB 240 NPKLRRIIIVPATGKPNQMLPV 262

RESULT 13  
 AA25979  
 ID AAY25979 standard; Protein: 531 AA.  
 XX AAY25979;  
 XX 18-OCT-1999 (first entry)  
 DT 18-OCT-1999 (first entry)  
 XX Mistletoe lectin I protein fragment.  
 DE Mistletoe lectin I protein fragment.  
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KW ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin I.  
 OS Viscum album.  
 XX Viscum album.  
 FN DE19804210-A1.  
 XX DE19804210-A1.  
 PD 12-AUG-1999.  
 XX 03-FEB-1998; 98DE-1004210.  
 PF 03-FEB-1998; 98DE-1004210.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 PI Morris P, Stiefel T, Voelter W, Welters P;  
 XX WPI; 1999-445335/38.  
 DR N-PSDB; AA209103.  
 XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX Claim 7; Fig 1b; 78pp; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancer) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a mistletoe lectin I protein fragment.  
 XX Sequence 531 AA;  
 SQ Query Match 94.1%; Score 1333.5; DB 20; Length 531;  
 Best Local Similarity 95.4%; Pred. No. 7.1e-123;  
 Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DPTGCSAEPPTVAVGKNGKAVVDDDDPHDQIQIAMPKSKNDPNQIWKIKDGTIRS 60  
 DB 1 DPTGCSAEPPTVAVGKNGKAVVDDDDPHDQIQIAMPKSKNDPNQIWKIKDGTIRS 328  
 QY 269 DPTGCSAEPPTVAVGKNGKAVVDDDDPHDQIQIAMPKSKNDPNQIWKIKDGTIRS 328  
 DB 269 DPTGCSAEPPTVAVGKNGKAVVDDDDPHDQIQIAMPKSKNDPNQIWKIKDGTIRS 328  
 QY 61 NGSCLTGYTGYAGYVWIPDCNTAVRENTIWOIDNGTINPRSNLYLAASGIGKTTLT 120  
 DB 61 NGSCLTGYTGYAGYVWIPDCNTAVRENTIWOIDNGTINPRSNLYLAASGIGKTTLT 120  
 QY 329 NGSCLTGYTGYAGYVWIPDCNTAVRENTIWOIDNGTINPRSNLYLAASGIGKTTLT 388  
 DB 329 NGSCLTGYTGYAGYVWIPDCNTAVRENTIWOIDNGTINPRSNLYLAASGIGKTTLT 388  
 QY 121 VQTLDTLGGKMLAGNDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKMAIYED 180  
 DB 121 VQTLDTLGGKMLAGNDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKMAIYED 180  
 QY 399 VQTLDTLGGKMLAGNDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKMAIYED 447  
 DB 399 VQTLDTLGGKMLAGNDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKMAIYED 447  
 QY 181 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGSGQWFTNKGALINLTGLANDVQA 240  
 DB 181 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGSGQWFTNKGALINLTGLANDVQA 507  
 QY 448 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGSGQWFTNKGALINLTGLANDVQA 507  
 DB 448 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGSGQWFTNKGALINLTGLANDVQA 507  
 QY 241 NPKLRRIIIVPATGKPNQMLPV 263  
 DB 508 NPKLRRIIIVPATGKPNQMLPV 530

RESULT 14  
 AA25982  
 ID AAY25982 standard; Protein: 532 AA.  
 XX AAY25982;  
 XX 18-OCT-1999 (first entry)  
 DT 18-OCT-1999 (first entry)  
 XX Mistletoe lectin I (variant) protein fragment.  
 DE Mistletoe lectin I (variant) protein fragment.  
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 KW ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;  
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KW cancer; cytotoxicity; antigen; isoform; lectin I.  
 OS Viscum album.  
 XX Viscum album.  
 FN DE19804210-A1.  
 XX DE19804210-A1.  
 PD 12-AUG-1999.  
 XX 03-FEB-1998; 98DE-1004210.  
 PF 03-FEB-1998; 98DE-1004210.  
 XX 03-FEB-1998; 98DE-1004210.  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX Morris P, Stiefel T, Voelter W, Welters P;  
 PI Morris P, Stiefel T, Voelter W, Welters P;  
 XX WPI; 1999-445335/38.  
 DR N-PSDB; AA209106.  
 XX Preparation of mistletoe lectins in heterologous systems,  
 PT particularly for use as anticancer agents and immunostimulants  
 XX Disclosure; Fig 4b; 78pp; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of

QY 61 NSGCLTGYGTAGYVWIFPCNFAVEATWQIMNGTIIINPRSNLYLAASGIGKTTLT 120  
 Db 61 NSGCLTGYGTAGYVWIFPCNFAVEATWQIMNGTIIINPRSNLYLAASGIGKTTLT 120  
 QY 121 VQTLDYTLGGGMLAGNDTAPREVTIYGPRLCWENSGSVWVETCSQNGKRALYGD 180  
 Db 121 VQTLDYTLGGGMLAGNDTAPREVTIYGPRLCWENSGSVWVETCSQNGKRALYGD 180  
 QY 181 GSIRKQNDQCLTSGSDSVSTVINIVSCSAGSQRWFTNEGALIMLKTGLADVAQA 240  
 Db 181 GSIRKQNDQCLTSGSDSVSTVINIVSCSAGSQRWFTNEGALIMLKTGLADVAQA 240  
 QY 241 NPKRRLIITYPATGKPNQMLTF 264  
 Db 241 NPKRRLIITYPATGKPNQMLTF 264

## RESULT 11

AAV25985 ID AAV25985 standard; Protein: 263 AA.

AAV25985; AC

18-OCT-1999 (first entry) DX

Mistletoe lectin B protein fragment. DE

Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 cancer; cytotoxicity; antigen; isoform; lectin B. KW

Viscum album. OS

DE19804210-A1. DX

12-AUG-1999. PD

03-FEB-1998; 98DB-1004210. PF

03-FEB-1998; 98DB-1004210. PR

(BIOS-) BIOSYN ARZNEIMITTEL GMBH. PA

Morris P, Stiefel T, Voelter W, Welters P; PI

WPI: 1999-44535/38. DX

N-PSDB; AAZ09109. DX

Preparation of mistletoe lectins in heterologous systems, PT

particularly for use as anticancer agents and immunostimulants PS

Claim 9; Fig 7B; 78pp; German. XX

This invention describes a novel mistletoe lectin (I) and its fragments  
 which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 fragments are used to treat uncontrolled cell growth (particularly  
 cancer) and if they also have cytotoxicity, to increase the strength of the  
 immune response, particularly to increase the antigen production of the  
 (tumour-associated, bacterial or viral). The method antigen production of  
 mistletoe lectin, and its individual chains, in many different systems  
 and on a large scale, at any time of the year. Recombinant products are  
 free from toxins present in natural mistletoe extracts. This sequence  
 represents a fragment of a mistletoe lectin B protein.

Sequence 263 AA; SX

Query Match 94.1%; Score 1331.5; DB 20; Length 263;  
 Best Local Similarity 95.4%; Pred. No. 7,10-124;

Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;  
 QY 1 DVTGSAEPTVRAIVGNQGVVDHDDPHDNGIQAFPSKSNPNQMLTKRDTGIS 60  
 Db 1 DVTGSAEPTVRAIVGNQGVVDHDDPHDNGIQAFPSKSNPNQMLTKRDTGIS 60  
 QY 61 NSGCLTGYGTAGYVWIFPCNFAVEATWQIMNGTIIINPRSNLYLAASGIGKTTLT 120  
 Db 61 NSGCLTGYGTAGYVWIFPCNFAVEATWQIMNGTIIINPRSNLYLAASGIGKTTLT 120  
 QY 121 VQTLDYTLGGGMLAGNDTAPREVTIYGPRLCWENSGSVWVETCSQNGKRALYGD 180  
 Db 121 VQTLDYTLGGGMLAGNDTAPREVTIYGPRLCWENSGSVWVETCSQNGKRALYGD 180  
 QY 181 GSIRKQNDQCLTSGSDSVSTVINIVSCSAGSQRWFTNEGALIMLKTGLADVAQA 240  
 Db 181 GSIRKQNDQCLTSGSDSVSTVINIVSCSAGSQRWFTNEGALIMLKTGLADVAQA 240  
 QY 241 NPKRRLIITYPATGKPNQMLTF 263  
 Db 241 NPKRRLIITYPATGKPNQMLTF 263

## RESULT 12

AAV25991 ID AAV25991 standard; Protein: 264 AA.

AAV25991; AC

18-OCT-1999 (first entry) DX

Mistletoe lectin B variant protein fragment. DE

Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;  
 ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 cancer; cytotoxicity; antigen; isoform; lectin B. KW

Viscum album. OS

DE19804210-A1. DX

12-AUG-1999. PD

03-FEB-1998; 98DB-1004210. PF

03-FEB-1998; 98DB-1004210. PR

(BIOS-) BIOSYN ARZNEIMITTEL GMBH. PA

Morris P, Stiefel T, Voelter W, Welters P; PI

WPI: 1999-44535/38. DX

N-PSDB; AAZ09115. DX

Preparation of mistletoe lectins in heterologous systems, PT

particularly for use as anticancer agents and immunostimulants PS

Disclosure; Fig 1B; 78pp; German. XX

This invention describes a novel mistletoe lectin (I) and its fragments  
 which have antitumour and immunostimulatory activity. The A-chain (MIA)  
 of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 fragments are used to treat uncontrolled cell growth (particularly  
 cancer) and if they also have cytotoxicity, to increase the strength of the  
 immune response, particularly to increase the antigen production of the  
 (tumour-associated, bacterial or viral). The method antigen production of  
 mistletoe lectin, and its individual chains, in many different systems  
 and on a large scale, at any time of the year. Recombinant products are  
 free from toxins present in natural mistletoe extracts. This sequence  
 represents a fragment of a variant mistletoe lectin B protein.



Thu Dec 11 16:10:07 2003

us-09-601-667c-9.rag

Page 5

1D	AAV25990 standard; Protein; 264 AA.
XX	
AC	AAV25990;
XX	
XX	18-OCT-1999 (first entry)
XX	
DE	Mistletoe lectin B5 protein fragment.
XX	
KW	Mistletoe; lectin; antitumor; immunostimulant; A-chain; MAb; immunity;
KW	ibodyze 268 subunit; non-cytotoxic; T-cell activation; immune response;
KW	lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW	cancer; cytotoxicity; antigen; isoform; lectin B5.
XX	
OS	Vascum album.
XX	
PN	DE19804210-A1.
PD	
PD	12-AUG-1999.
XX	
PF	03-FEB-1998; 98DE-1004210.
XX	
PI	03-FEB-1998; 98DE-1004210.
XX	
PA	(BIOG-) BIOSYM ARNEMITTEL GMBH.
XX	
PI	Morris P, Stiefel T, Voelter W, Welters P;
XX	
XX	WPI; 1999-44535/38.
DR	R-RSDH; AAZ09114.
XX	
PT	Preparation of mistletoe lectins in heterologous systems.
XX	
XX	Particular for use as anticancer agents and immunostimulants
XX	
XX	Claim 9; Fig 12b; 78pp; German.
XX	
XX	This invention describes a novel mistletoe lectin (I) and its fragments
CC	which have antitumor and immunostimulatory activity. The A-chain (MA)
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC	ribosomal protein synthesis (RPS) in tumor cells. The A-chain and (I) and its
CC	fragments are used to treat uncontrolled cell growth (particularly
CC	in cancer) and if they lack cytotoxicity, to increase the strength of the
CC	immune response, particularly to a co-administered antigen
CC	(tumor-associated, bacterial or viral). The method allows production of
CC	mistletoe lectin, and its individual chains, in many different isoforms
CC	and on a large scale, at any time of the year. Recombinant products are
CC	free from toxins present in natural mistletoe extracts. This sequence
CC	represents a fragment of a mistletoe lectin B5 protein.
XX	
XX	Sequence 264 AA:
XX	
XX	Query Match 98.6%; Score 1397; DB 20; Length 264;
XX	Best Local Similarity 98.5%; P-Val. No. 3.6e-130;
XX	Matches 260; Conservative 1; Mismatches 3; Indels 0; Gaps 0
QY	1 DPTVTSASBPTVTVRGNRGRVADDDPHDNGIQAFPSKSNNDPQIMTKIDDTIRTS 60
DB	1 DPTVTSASBPTVTVRGNRGRVADDDPHDNGIQAFPSKSNNDPQIMTKIDDTIRTS 60
QY	61 NSGCLTGYTGATGYVWVFDQNTAVRENTWIMDNGTIIPRSLVWVAASGAKITLT 120
DB	61 NSGCLTGYTGATGYVWVFDQNTAVRENTWIMDNGTIIPRSLVWVAASGAKITLT 120
QY	121 VQIDTVYDGGKAGNRRHREVTIYGRFLCNSSNGSSWVETCDSSQNGNCKALVYD 180
DB	121 VQIDTVYDGGKAGNRRHREVTIYGRFLCNSSNGSSWVETCDSSQNGNCKALVYD 180
QY	181 GSTRPKNDQGLCSGRDSVATVIVYVCSGASGSRWFNFGALIMLKTLGAMVDA 240
DB	181 GSTRPKNDQGLCSGRDSVATVIVYVCSGASGSRWFNFGALIMLKTLGAMVDA 240
QY	241 NPLARITLIVPAKTNQMLVPE 264
DB	241 NPLARITLIVPAKTNQMLVPE 264

Dbb		241 NPKRSLLIYVAGCGKQNMFLPVE 264
RESULT 8		
AAV25936	ID	AAV25996 standard; Protein; 265 AA.
AC	CD	AAV25996;
XX	EE	AAV25996;
DT	18-OCT-1999	(first entry)
DB		Mistletoe lectin B5 variant protein fragment.
XX		Mistletoe lectin, antitumor; immunostimulant; A-chain; MA; immunity; antibody; 265 amino acids; noncytotoxic; controlled cell growth; treatment; anticancer; cytotoxicity; antigen; isoform; lectin B5.
OS		Vileum album.
XX		
PX		DE19804210-A1.
PN		
ED		12-AUG-1999.
PD		
FE		03-FEB-1998; 98DE-1004210.
XX		
PR		03-FEB-1998; 98DE-1004210.
PA		BIO(-) BIOGVN ARZNEIMITTEL CMGH.
XX		
PI		Morris P, Stefefel T, Voelter W, Welters P,
DR		WF; 1999-445335/78.
N-PDBE:		RAA209120.
PT		Preparation of mistletoe lectins in heterologous systems particularly for use as anticancer agents and immunostimulants
P3		Disclosure; Fig 1B9; 78pp; German.
CC		This invention describes a novel mistletoe lectin (1) and its fragments CC which have antitumor and immunostimulatory activity. The A-chain (MA) CC of the mistletoe lectin binds to, and inactivates, the 2S8 subunit of CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and (1) and its CC lymphokine-producing macrophages, so stimulate immunity. Particularly CC cancer) and if they lack cytotoxicity to increase the strength of the CC immune response, particularly to a co-administered antigen CC (tumor-associated, bacterial or viral). The method allows production of CC mistletoe lectin, and its individual chains, in many different isoforms CC and on a large scale, at any time of the year. Recombinant products are CC free from toxins present in natural mistletoe extracts. This sequence CC represents a fragment of a variant mistletoe lectin B5 protein.
XQ	Sequence	265 AA;
Query Match		96.6%; Score 1397; DA 20; Length 265;
Best Local Similarity		98.5%; Pred. No. 3.6e-130;
Matches 260;	Consecutive	1; Mismatches 3; Indels 0; Gaps 0
Oy	1	DDVTSSASPFVTRIVRNKGAKVDVADDPHGANOIQLPKSKNDPVQLMTIKEDTIRLS 60
Db	1	DDVTSSASPFVTRIVRNKGARVDVADDPHGNOIQLPKSKNDPVQLMTIKEDTIRLS 60
Oy	61	NSGCITFTTGTCGTCTMIFPCFATAPRRTAQINGDGIINPSNVLAASSGKEETTLT 120
Db	61	NSGCITFTTGTCGTCTMIFPCFATAPRRTAQINGDGIINPSNVLAASSGKEETTLT 120
Oy	121	WDTLYTLQQGMANGSDVARREVIYGGPRDCMESNGSGVWVECTDSOGKQMGALYLD 180
Db	121	WDTLYTLQQGMANGSDVARREVIYGFEDLCESNGSGSVWEVECTDSOGKQMGALYLD 180
Oy	181	GSTRKKRNDQCILTSRGSRYSVTINIVYSCGASGSQGWFWENEGAILNTKTGLAMVQA 240

KW Lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KM cancer; cytotoxicity; antigen; isoform; lectin B4.  
 XX  
 OS Viscum album.  
 XX  
 KM DE19804210-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 03-FEB-1998; 98DE-1004210.  
 XX  
 PR 03-FEB-1998; 98DE-1004210.  
 XX  
 PA (BIOCS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 XI Morris P, Stiefel T, Voelter W, Welters P,  
 XX NPI, 1999-44535/38.  
 DR N-PSDB; AA029113.  
 XX  
 PT Preparation of mistletoe lectins in heterologous systems.  
 PT Particularly for use as anticancer agents and immunostimulants  
 XX  
 PS Claim 9; Fig 11B; 78pp; German.  
 XX  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen (particularly  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a mistletoe lectin B4 protein.  
 XX  
 SQ Sequence 264 AA.  
 XX  
 Query Match 99.1%; Score 1404; DB 20; Length 264;  
 Best Local Similarity 99.2%; Pred. No. 7.2e-131;  
 Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DDTVCASASPTVRIYGRNGKRVYDDDFPHQNOQLWPSKSNNDPQMLTKEDGTHS 60  
 DB 1 DDTVCASASPTVRIYGRNGKRVYDDDFPHQNOQLWPSKSNNDPQMLTKEDGTHS 60  
 QY 61 NSGCLTYGTYAGTYVMIPDCTAVERATINQIMDNGITINPSNULVLAASGIGKTLT 120  
 DB 61 NSGCLTYGTYAGTYVMIPDCTAVERATINQIMDNGITINPSNULVLAASGIGKTLT 120  
 QY 121 VQTLDTLGGMLAGNDTAPREVTYGFRLDQMSNGSVVWETCDSSQNGKMLAYD 180  
 DB 121 VQTLDTLGGMLAGNDTAPREVTYGFRLDQMSNGSVVWETCDSSQNGKMLAYD 180  
 QY 181 GSIRKQNDQCLTSGSDSVSTVINIVSGSAGSQRWFTNEGALINLKTGLAMDYAQA 240  
 DB 181 GSIRKQNDQCLTSGSDSVSTVINIVSGSAGSQRWFTNEGALINLKTGLAMDYAQA 240  
 QY 241 NPKLRRIIIPATGKRWMLPWF 264  
 DB 241 NPKLRRIIIPATGKRWMLPWF 264

XX Mistletoe lectin B4 variant protein fragment.  
 XX  
 KM Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
 KM ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 KM Lymphokine-producing macrophage; uncontrolled cell growth; treatment;  
 KM cancer; cytotoxicity; antigen; isoform; lectin B4.  
 XX  
 OS Viscum album.  
 XX  
 KM DE19804210-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 03-FEB-1998; 98DE-1004210.  
 XX  
 PR 03-FEB-1998; 98DE-1004210.  
 XX  
 PA (BIOCS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX  
 XI Morris P, Stiefel T, Voelter W, Welters P,  
 XX NPI, 1999-44535/38.  
 DR N-PSDB; AA029113.  
 XX  
 PT Preparation of mistletoe lectins in heterologous systems.  
 PT Particularly for use as anticancer agents and immunostimulants  
 XX  
 PS Disclosure; Fig 11B; 78pp; German.  
 XX  
 CC This invention describes a novel mistletoe lectin (I) and its fragments  
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 CC fragments are used to treat uncontrolled cell growth (particularly  
 CC cancers) and if they lack cytotoxicity, to increase the strength of the  
 CC immune response, particularly to a co-administered antigen (particularly  
 CC (tumour-associated, bacterial or viral). The method allows production of  
 CC mistletoe lectin, and its individual chains, in many different isoforms  
 CC and on a large scale, at any time of the year. Recombinant products are  
 CC free from toxins present in natural mistletoe extracts. This sequence  
 CC represents a fragment of a variant mistletoe lectin B4 protein.  
 XX  
 SQ Sequence 265 AA.  
 XX  
 Query Match 99.1%; Score 1404; DB 20; Length 265;  
 Best Local Similarity 99.2%; Pred. No. 7.2e-131;  
 Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DDTVCASASPTVRIYGRNGKRVYDDDFPHQNOQLWPSKSNNDPQMLTKEDGTHS 60  
 DB 1 DDTVCASASPTVRIYGRNGKRVYDDDFPHQNOQLWPSKSNNDPQMLTKEDGTHS 60  
 QY 61 NSGCLTYGTYAGTYVMIPDCTAVERATINQIMDNGITINPSNULVLAASGIGKTLT 120  
 DB 61 NSGCLTYGTYAGTYVMIPDCTAVERATINQIMDNGITINPSNULVLAASGIGKTLT 120  
 QY 121 VQTLDTLGGMLAGNDTAPREVTYGFRLDQMSNGSVVWETCDSSQNGKMLAYD 180  
 DB 121 VQTLDTLGGMLAGNDTAPREVTYGFRLDQMSNGSVVWETCDSSQNGKMLAYD 180  
 QY 181 GSIRKQNDQCLTSGSDSVSTVINIVSGSAGSQRWFTNEGALINLKTGLAMDYAQA 240  
 DB 181 GSIRKQNDQCLTSGSDSVSTVINIVSGSAGSQRWFTNEGALINLKTGLAMDYAQA 240  
 QY 241 NPKLRRIIIPATGKRWMLPWF 264  
 DB 241 NPKLRRIIIPATGKRWMLPWF 264

RESULT 6  
 AA025995  
 ID AA025995 standard; Protein; 265 AA.  
 AC  
 XX AA025995;  
 XX  
 DT 18-OCT-1999 (first entry)

RESULT 7  
 AA025990



XX 03-FEB-1998; 98DB-1004210.  
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.  
 XX PA Morris P, Stiefel T, Voelter W, Welters P;  
 XX PI WPI; 1999-44535/38.  
 XX DR N-PSDB; AA209110.  
 XX PT Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX Claim 9; Fig 8B; 78pp; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumour and immunostimulatory activity. The A-chain (MA)  
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX and on a large scale, at any time of the year. Recombinant products are  
 XX used as immunostimulants in natural mistletoe extracts. This sequence  
 XX represents a fragment of a mistletoe lectin B1 protein.  
 SQ Sequence 264 AA;  
 Query Match 99.6%; Score 1412; DB 20; Length 264;  
 Best Local Similarity 99.6%; Pred. No. 1, 2e-131;  
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DVTGCSAEPPTVAVRIGRQKRVDRDDPHDQNOQLMPKSNNDNDQWLTIKRDGTRIS 60  
 DB 1 DVTGCSAEPPTVAVRIGRQKRVDRDDPHDQNOQLMPKSNNDNDQWLTIKRDGTRIS 60  
 QY 61 NSCLTLYGTRAGVYVMIPECTAVREATVQIWMNGTIIINRSNTVLAASGIGKTLT 120  
 DB 61 NSCLTLYGTRAGVYVMIPECTAVREATVQIWMNGTIIINRSNTVLAASGIGKTLT 120  
 QY 121 VQTDVYTLGGQMLAGNDTAPREVTIVGPDLCMESNGSVMWETCSQKQCKXALYED 180  
 DB 121 VQTDVYTLGGQMLAGNDTAPREVTIVGPDLCMESNGSVMWETCSQKQCKXALYED 180  
 QY 181 GSIRPKNODCLTSGRDSVSVIVINIVSGASGQWFTNBGAILINKGLADVAQA 240  
 DB 181 GSIRPKNODCLTSGRDSVSVIVINIVSGASGQWFTNBGAILINKGLADVAQA 240  
 QY 241 NPGLARIIIVPATKRNQWMLVVF 264  
 DB 241 NPGLARIIIVPATKRNQWMLVVF 264  
 RESULT 4  
 AA25992  
 ID AA25992 standard; Protein; 265 AA.  
 AC AA25992;  
 DT 18-OCT-1999 (first entry)  
 DX Mistletoe lectin B1 variant protein fragment.  
 KY Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
 KW lymphokine-producing macrophages; non-cytotoxic; T-cell activation; immune response;  
 KV cancer; cytotoxicity; antigen; isoform; lectin B1.  
 XX Viscum album.

PN DB19804210-AL.  
 PD 12-AUG-1999.  
 XX 03-FEB-1998; 98DB-1004210.  
 XX PA Morris P, Stiefel T, Voelter W, Welters P;  
 XX PI WPI; 1999-44535/38.  
 XX DR N-PSDB; AA209110.  
 XX PT Preparation of mistletoe lectins in heterologous systems,  
 XX particularly for use as anticancer agents and immunostimulants  
 XX Disclosure; Fig 14B; 78pp; German.  
 XX This invention describes a novel mistletoe lectin (I) and its fragments  
 XX which have antitumour and immunostimulatory activity. The A-chain (MA)  
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of  
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and  
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its  
 XX fragments are used to treat uncontrolled cell growth (particularly  
 XX cancers) and if they lack cytotoxicity, to increase the strength of the  
 XX immune response, particularly to a co-administered antigen  
 XX (tumour-associated, bacterial or viral). The method allows production of  
 XX mistletoe lectin, and its individual chains, in many different isoforms  
 XX and on a large scale, at any time of the year. Recombinant products are  
 XX used as immunostimulants in natural mistletoe extracts. This sequence  
 XX represents a fragment of a variant mistletoe lectin B1 protein.  
 SQ Sequence 265 AA;  
 Query Match 99.6%; Score 1412; DB 20; Length 265;  
 Best Local Similarity 99.6%; Pred. No. 1, 2e-131;  
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DVTGCSAEPPTVAVRIGRQKRVDRDDPHDQNOQLMPKSNNDNDQWLTIKRDGTRIS 60  
 DB 1 DVTGCSAEPPTVAVRIGRQKRVDRDDPHDQNOQLMPKSNNDNDQWLTIKRDGTRIS 60  
 QY 61 NSCLTLYGTRAGVYVMIPECTAVREATVQIWMNGTIIINRSNTVLAASGIGKTLT 120  
 DB 61 NSCLTLYGTRAGVYVMIPECTAVREATVQIWMNGTIIINRSNTVLAASGIGKTLT 120  
 QY 121 VQTDVYTLGGQMLAGNDTAPREVTIVGPDLCMESNGSVMWETCSQKQCKXALYED 180  
 DB 121 VQTDVYTLGGQMLAGNDTAPREVTIVGPDLCMESNGSVMWETCSQKQCKXALYED 180  
 QY 181 GSIRPKNODCLTSGRDSVSVIVINIVSGASGQWFTNBGAILINKGLADVAQA 240  
 DB 181 GSIRPKNODCLTSGRDSVSVIVINIVSGASGQWFTNBGAILINKGLADVAQA 240  
 QY 241 NPGLARIIIVPATKRNQWMLVVF 264  
 DB 241 NPGLARIIIVPATKRNQWMLVVF 264  
 RESULT 5  
 AA25989  
 ID AA25989 standard; Protein; 264 AA.  
 AC AA25989;  
 DT 18-OCT-1999 (first entry)  
 DX Mistletoe lectin B4 protein fragment.  
 KY Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;  
 XX

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us-09-601-667c-9.rta

Page 2

PT Preparation of mistletoe lectins in heterologous systems.  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Claim 9; Fig 10B; 78pp; German.  
XX  
CC This invention describes a novel mistletoe lectin (I) and its fragments  
CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
CC of the mistletoe lectin binds to (i) activate T-cells, the 28S subunit of  
CC ribosomes. Non-cytotoxic forms of (i) activate T-cells and its  
CC lymphokine-producing macrophages, so stimulate immunity. (i) and its  
CC fragments are used to treat uncontrolled cell growth (particularly  
CC cancers) and if they lack cytotoxicity, to increase the strength of the  
CC immune response, particularly to a co-administered antigen  
CC (tumour-associated, bacterial or viral). The method allows production of  
CC mistletoe lectin, and its individual chains, in many different isoforms  
CC and on a large scale, at any time of the year. Recombinant products are  
CC also from coxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a mistletoe lectin B3 protein.

Sequence 264 AA;

Query Match 100.0%; Score 1417; DB 20; Length 264;  
Best Local Similarity 100.0%; Pred. No. 3.7e-132;  
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDTVCASAEPTVRIYVGNKGVVDVDDDFDQNOQLMPSKSNNDPQWLTIKRDGTRIS 60  
DB 1 DDTVCASAEPTVRIYVGNKGVVDVDDDFDQNOQLMPSKSNNDPQWLTIKRDGTRIS 60  
QY 61 NSGLTGYGTAGVYVMTFPCQNTANREATTQIWDNGTIIINRSNVLAASSGIKETTLT 120  
DB 61 NSGLTGYGTAGVYVMTFPCQNTANREATTQIWDNGTIIINRSNVLAASSGIKETTLT 120  
QY 121 VQTLDTLGGQMLAGNDFAPEVTVIGFPRDLCESSNGSVWVETCDSSQKQKALYGD 180  
DB 121 VQTLDTLGGQMLAGNDFAPEVTVIGFPRDLCESSNGSVWVETCDSSQKQKALYGD 180  
QY 121 VQTLDTLGGQMLAGNDFAPEVTVIGFPRDLCESSNGSVWVETCDSSQKQKALYGD 180  
DB 121 VQTLDTLGGQMLAGNDFAPEVTVIGFPRDLCESSNGSVWVETCDSSQKQKALYGD 180  
QY 181 GSIRPKONODQLTSGHDSVSTVINIVSCGASGSGQVWFTNEGAILNLKTGLANDVAQA 240  
DB 181 GSIRPKONODQLTSGHDSVSTVINIVSCGASGSGQVWFTNEGAILNLKTGLANDVAQA 240  
QY 241 NPKLRRIIIPATGRKQWMLPWF 264  
DB 241 NPKLRRIIIPATGRKQWMLPWF 264

RESULT 2

AAZ5994  
ID AAZ5994 standard; Protein; 265 AA.

AAZ5994;

18-OCT-1999 (first entry)

Mistletoe lectin B3 variant protein fragment.

XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin B3.

Viscum album.

DEL19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOG-) BIOSTN ARZNEIMITTEL GMBH.

PI Morris P, Stiefel T, Voelker W, Walters P,  
XX WPI; 1999-44535/38.  
DR N-PDB; AA209118.  
XX  
XX Preparation of mistletoe lectins in heterologous systems,  
XX particularly for use as anticancer agents and immunostimulants  
XX  
XX Disclosure; Fig 10B; 78pp; German.

CC This invention describes a novel mistletoe lectin (I) and its fragments  
CC which have antitumour and immunostimulatory activity. The A-chain (MA)  
CC of the mistletoe lectin binds to (i) activate T-cells, the 28S subunit of  
CC ribosomes. Non-cytotoxic forms of (i) activate T-cells and its  
CC lymphokine-producing macrophages, so stimulate immunity. (i) and its  
CC fragments are used to treat uncontrolled cell growth (particularly  
CC cancers) and if they lack cytotoxicity, to increase the strength of the  
CC immune response, particularly to a co-administered antigen  
CC (tumour-associated, bacterial or viral). The method allows production of  
CC mistletoe lectin, and its individual chains, in many different isoforms  
CC and on a large scale, at any time of the year. Recombinant products are  
CC also from coxins present in natural mistletoe extracts. This sequence  
XX represents a fragment of a variant mistletoe lectin B3 protein.

Sequence 265 AA;

Query Match 100.0%; Score 1417; DB 20; Length 265;  
Best Local Similarity 100.0%; Pred. No. 3.7e-132;  
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDTVCASAEPTVRIYVGNKGVVDVDDDFDQNOQLMPSKSNNDPQWLTIKRDGTRIS 60  
DB 1 DDTVCASAEPTVRIYVGNKGVVDVDDDFDQNOQLMPSKSNNDPQWLTIKRDGTRIS 60  
QY 61 NSGLTGYGTAGVYVMTFPCQNTANREATTQIWDNGTIIINRSNVLAASSGIKETTLT 120  
DB 61 NSGLTGYGTAGVYVMTFPCQNTANREATTQIWDNGTIIINRSNVLAASSGIKETTLT 120  
QY 121 VQTLDTLGGQMLAGNDFAPEVTVIGFPRDLCESSNGSVWVETCDSSQKQKALYGD 180  
DB 121 VQTLDTLGGQMLAGNDFAPEVTVIGFPRDLCESSNGSVWVETCDSSQKQKALYGD 180  
QY 121 VQTLDTLGGQMLAGNDFAPEVTVIGFPRDLCESSNGSVWVETCDSSQKQKALYGD 180  
DB 121 VQTLDTLGGQMLAGNDFAPEVTVIGFPRDLCESSNGSVWVETCDSSQKQKALYGD 180  
QY 181 GSIRPKONODQLTSGHDSVSTVINIVSCGASGSGQVWFTNEGAILNLKTGLANDVAQA 240  
DB 181 GSIRPKONODQLTSGHDSVSTVINIVSCGASGSGQVWFTNEGAILNLKTGLANDVAQA 240  
QY 241 NPKLRRIIIPATGRKQWMLPWF 264  
DB 241 NPKLRRIIIPATGRKQWMLPWF 264

RESULT 3

AAZ5996  
ID AAZ5996 standard; Protein; 264 AA.

AAZ5996;

18-OCT-1999 (first entry)

Mistletoe lectin B1 protein fragment.

XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;  
KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;  
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;  
KW cancer; cytotoxicity; antigen; isoform; lectin B1.

Viscum album.

DEL19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 16.5679 Seconds

(without alignments)  
3093.817 Million cell updates/sec

Title: US-09-601-667C-1

Sequence: 1 YERLRNLFVHTQYTKXKXKXFP.....RILIIYPAKGMQWMLPV 533

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 segs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR  
2: PIR  
3: PIR  
4: PIR

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1290	49.3	264	2	PM0019
2	1279.5	48.9	265	2	PM0030
3	1231	47.1	576	1	RLCD
4	1183.5	45.2	528	1	TLGA
5	1165.5	44.6	254	2	PM0018
6	1158.5	43.5	562	2	S16022
7	1137.5	43.2	528	2	S23431
8	1137.5	43.2	528	2	S23431
9	1137.5	43.2	528	2	S23431
10	1137.5	43.2	528	2	S23431
11	889.5	32.5	570	2	S62627
12	882	31.4	263	2	S63300
13	443.5	17.0	251	2	C39761
14	309.5	11.8	247	2	JO5032
15	308.5	11.8	289	1	RLT7
16	307.5	11.8	247	2	JO5032
17	307.5	11.8	247	2	JO5032
18	307.5	11.8	247	2	JO5032
19	284	10.3	316	2	JO5032
20	270	10.3	316	2	JO5032
21	261	10.0	286	1	RLPUG
22	256.5	9.8	278	2	S23519
23	247	9.4	277	2	S24494
24	241	9.2	250	2	JO5032
25	229	8.8	278	2	JO5032
26	196	7.5	261	2	JO5032
27	189.5	7.2	313	2	S17757
28	180.5	6.9	394	2	S24421
29	172.5	6.6	106	2	S39761

# ALIGNMENTS

30 161.5 6.2 272 2 UC4811  
31 159.5 6.1 253 2 S28539  
32 157.5 6.0 253 2 S28542  
33 157.5 6.0 253 2 S28542  
34 153.5 5.9 283 2 S65202  
35 150.5 5.8 253 2 S28541  
36 148.5 5.7 292 1 RLOH2  
37 138.5 5.3 253 2 A58923  
38 136 5.2 310 2 S46239  
39 128.5 4.9 293 2 S17519  
40 125.5 4.7 377 2 UC7935  
41 123.5 4.6 377 2 UC7935  
42 123.5 4.6 377 2 UC7935  
43 118.5 4.5 477 1 J80589  
44 116.5 4.5 281 2 S38664  
45 115.5 4.4 383 2 T34603

## RESULT 1

PM0019  
Mistlecote lectin I B chain - Viscum album (fragment)  
C:Species: Viscum album  
C:Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #ext\_change 07-May-1999  
C:Accession: PM0019  
R:Biochemdb, S.; Krauspehn, R.; Mikhalov, A.; Stoeva, S.; Betzel, C.; Voelter, B.; Blochem, Biophys. Res. Commun. 247, 367-372, 1998  
A:Title: Primary structure and molecular modeling of mistlecote lectin I from Viscum album  
A:Reference number: PM0019, WUID:96308123, PMID:9642133  
A:Accession: PM0019  
A:Protein type: protein  
A:Protein family: lectin, rRNA N-glycosidase homology  
C:Superfamily: lectin, rRNA N-glycosidase homology  
Query Match 49.3%; Score 1290; DB 2; Length 264;  
Best Local Similarity 92.4%; Pred. No. 1.3e-116;  
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
DB 270 DDVTGASEPTVAVIKKXKXVVDVDDPDGNOIOLMPSNNDDNOLTKKXITRS 329  
1 DDVTGASEPTVAVIKKXKXVVDVDDPDGNOIOLMPSNNDDNOLTKKXITRS 60  
QY 330 NSGCTVYGTAGVYVWIPDQNTRENTIWKNTINPSNKLVAASGCKKXIT 389  
DB 61 NSGCTVYGTAGVYVWIPDQNTRENTIWKNTINPSNKLVAASGCKKXIT 120  
QY 390 VGLTDTYGTAGVYVWIPDQNTRENTIWKNTINPSNKLVAASGCKKXIT 449  
DB 121 VGLTDTYGTAGVYVWIPDQNTRENTIWKNTINPSNKLVAASGCKKXIT 180  
QY 450 GSHVPOKQCCITGSDSVTVINVCSSXKXKXKXKXKXKXKXKXKXKXKX 509  
DB 181 GSHVPOKQCCITGSDSVTVINVCSSXKXKXKXKXKXKXKXKXKXKXKX 240  
QY 510 NPKRRIITVPAKGMQWMLPV 532  
DB 241 NPKRRIITVPAKGMQWMLPV 263  
RHSHT 2  
lectin-I B chain - European mistlecote  
N:Alternate names: MLI-I  
C:Species: Viscum album (European mistlecote)  
C:Date: 18-Jun-1998 #sequence\_revision 10-Jul-1998 #ext\_change 19-May-2000  
C:Accession: JN0090  
R:Solier, M.H.; Stoeva, S.; Voelter, W.  
Biochem. Biophys. Res. Commun. 246, 596-601, 1998  
A:Title: Complete amino acid sequence of the B chain of mistlecote lectin I.  
A:Reference number: JN0090, WUID:98289575, PMID:9618256  
A:Accession: JN0090



Db 341 RHNGNATQLPKSNNDPQNLMTKRTNSKCLTGYGSPGYVMYICNTAATD 400  
QY 357 ATTQWIKWNGTIIIPRSALVLAASSGKRTLLVYQTLDTLQAGMLAGNDAPREVIYV 416  
Db 401 ATRQWMDNGTIIIPRSALVLAASSGKRTLLVYQTLDTLQAGMLAGNDAPREVIYV 460  
QY 417 FDLQMSKXGYSWVETCSXSNQXVVAQNPFLRRITITYPATGKQNMWLPV 476  
Db 461 LYGCLQMSQGVWIDCSSEKXKQ-QWALVDSISIFRQGNRDNCLNSNRIETVALD 519  
QY 477 SCSSXXSXQRFVETNEKALINLKXXXXXVVAQNPFLRRITITYPATGKQNMWLPV 512  
Db 520 SCGPASSGQRWRFNDQSIISLYDDWVMYKVGSDPSLKMQLIIPYTGDNQIWLPL 575

## RESULT 4

abrin-a

abrin-a precursor - Indian licorice (fragment)

N/contains: rRNA N-glycosylase (EC 3.2.2.22)

C/species: Abrus precatorius (Indian licorice)

C/date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text change 16-Jul-1999

C/accession: S32429; J02022; A39761; U01398; S14472; S24133; S74110; S74111

R/hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.

J. Mol. Biol. 229, 263-267, 1993

A/Title: Primary structure of three distinct isobabins determined by cDNA sequencing. C

A/reference number: S32429; PMID:93132798; PMID:8421313

A/status: nucleic acid sequence not shown

A/molecule type: rRNA

A/residues: 757, 2-528 &lt;HN&gt;

A/cross-references: GB:M98344; NID:G166294; PIRN:PAA32624.1; PID:G166295

A/Note: the coding region for the sequence shown is preceded by an AUG codon

A/Note: residues 1-8 were derived from the synthesized primer

R/funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.

Agric. Biol. Chem. 52, 1095-1097, 1988

A/Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein fro

A/reference number: J02022

A/molecule type: protein

A/residues: 17201, 203-251 &lt;FN&gt;

A/Note: the amino terminal residue forms pyrrolidone carboxylic acid; therefore, we have

R/bjornsen, G.; Mathiesen, A.; Sundan, A.

J. Biol. Chem. 266, 6848-6852, 1991

A/Title: Direct molecular cloning and expression of two distinct abrin A-chains.

A/reference number: A39761; PMID:91201328; PMID:2016300

A/status: nucleic acid sequence not shown

A/molecule type: DNA

A/residues: 57, 2-251 &lt;EVE&gt;

A/cross-references: GB:X54872

A/Note: residues 1-8 were derived from the synthesized primer

R/kamata, M.; Sumitawa, T.; Funatsu, G.

Biochem. Biophys. Res. Commun. 57, 166-169, 1993

A/Title: The complete amino acid sequence of the B-chains of abrin-a and abrin-b, toxic

A/reference number: U01398; PMID:9169025; PMID:1765422

A/Contents: seeds

A/accession: U01398

A/molecule type: protein

A/residues: 261-347, 'T', 349-351, 'N', 353-357, 'L', 359-528 &lt;KIM&gt;

A/Experimental source: seed

R/bjornsen, G.; Mathiesen, A.; Sundan, A.

submitted to the EMBL Data Library, October 1990

A/Reference: Direct molecular cloning of two distinct abrin A-chains.

A/accession: S14472

A/status: preliminary

A/molecule type: DNA

A/residues: 'NE', 2-251 &lt;FV2&gt;

A/cross-references: EMBL:X54873; NID:G16090; PIRN:CAA39655.1; PID:G16091

R/chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y.

PSBS Lett. 309, 115-118, 1992

A/Title: The complete primary structure of abrin-a B chain.

A/reference number: S24133; PMID:92371656; PMID:1505674

A/accession: S24133

A/molecule type: protein

A/residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 &lt;CHE&gt;

R/lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.

Eur. J. Biochem. 240, 564-569, 1996

A/Title: Probing the domain structure of abrin-a by tryptic digestion.

A/reference number: S74110; PMID:97008945; PMID:8856055

A/accession: S74110

A/molecule type: protein

A/residues: 312-412 &lt;LIN&gt;

A/Experimental source: seed

A/accession: S74111

A/molecule type: protein

A/residues: 262-276, 'X', 278-280, 329-348, 369-388, 399-418 &lt;LIN&gt;

A/Experimental source: seed

C/comment: Abirin-a is more toxic than ricin. The toxin consists of an A chain, which

binds receptors on the cell surface. The A and B chains are linked by a single dis-

ulfide bond. The B chain is rich in N-glycosylated residues. The A chain is rich in

hydrophobic residues. The toxin is a dimer of two subunits. The A chain is a

single chain. The B chain is a single chain. The toxin is a dimer of two sub-

units. The A chain is a single chain. The B chain is a single chain. The toxin

is a dimer of two subunits. The A chain is a single chain. The B chain is a

single chain. The toxin is a dimer of two subunits. The A chain is a single

chain. The B chain is a single chain. The toxin is a dimer of two subunits.

The A chain is a single chain. The B chain is a single chain. The toxin is a

dimer of two subunits. The A chain is a single chain. The B chain is a single

chain. The toxin is a dimer of two subunits. The A chain is a single chain.

The B chain is a single chain. The toxin is a dimer of two subunits. The A

chain is a single chain. The B chain is a single chain. The toxin is a dimer

of two subunits. The A chain is a single chain. The B chain is a single chain.

The toxin is a dimer of two subunits. The A chain is a single chain. The B

chain is a single chain. The toxin is a dimer of two subunits. The A chain

is a single chain. The B chain is a single chain. The toxin is a dimer of

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The toxin is a dimer of two subunits. The A chain is a single chain. The B

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is a single chain. The B chain is a single chain. The toxin is a dimer of

two subunits. The A chain is a single chain. The B chain is a single chain.

The toxin is a dimer of two subunits. The A chain is a single chain. The B

chain is a single chain. The toxin is a dimer of two subunits. The A chain

is a single chain. The B chain is a single chain. The toxin is a dimer of

two subunits. The A chain is a single chain. The B chain is a single chain.

P00018  
 Mistletoe Lectin I A chain - Viscum album (Fragrant)  
 C|Species: Viscum album  
 C|Date: 03-01-1998 #sequence revision 10-01-1998 #ext. change 26-Aug-1999  
 A|Accession: P00018  
 B|Chen, H.-B., S.; Krauspehaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelker, W.  
 A|Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum alb  
 A|Reference number: P00018; MUID:9808123; PMID:962233  
 A|Accession: P00018  
 A|A: molecule type: protein  
 A|Residues: 1-254 <ES>  
 C|Superfamily: tctm; RNA N-glycosidase homology  
 F|7-246/Domain: RNA N-glycosidase Homology <RG>  
 Query Match 44.6% Score 1165.5 DB 2 Length 254  
 Best Local Similarity 92.2% Pval. No. 1.3e-104  
 Matches 235; Conservative 0; Mismatches 19; Indels 1; Gaps 1

QY 1 YRRARLVHQTGAEPFRRTILLRDVYSGGSEFNEIPILRSTIIVSDAQRFVLVELIN 60  
Db 1 YRRARLVHQTGAEPFRRTILLRDVYSSGSSSENIPIILRSTIIVSDAQRFVLVELIN 60  
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
61 QGGSTALINDVTNYYVAQQAGQGQGYFLNDAPRAEATLIFGTGRKSPKASGYIDE 120  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
61 QGGSTALINDVTNYYVAQQAGQGQGYFLNDAPRAEATLIFGTGRKSSPKNISYDE 119  
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
121 RVAGCHDQIPEIGIXOLIQSYALXEPGSGSTXQAQSILLIQMISGARPNPLMEKRX 180  
Db 120 RVAGCHDQIPEIGIDLIQSYTLPGSGSTPAQSILLIQMISGARPNPLMEKRY 179  
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
181 INSKGSFLPDYVMELSTNSGGSTVGHSTGCVNNPKRALIXGNFTLVANRPXYIAS 240  
Db 180 INSKGSFLPDYVMELSTNSGGSTVGHSTGCVNNPKRALIFGVNLINAKVDIYS 239  
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
241 LAIMEFLPCGEPPSSS 255  
Db 240 LAIMEFLPCGEPPSSS 254

RESULT 6  
S16022  
abrin-C precursor - Indian licorice  
N:contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Abrus precatorius (Indian licorice)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #extl\_change 20-Aug-1999  
R:Accession: S16022  
R:Author: R. J. M.; Kew-Ryzczak, E. J.; Ptacek, M.  
R:Pub J. Biochem 199, 723-732  
A:Title: Preproabrin: genomic cloning, characterization and the expression of the A-chain  
A:Accession: S16022  
A:Status: preliminary  
A:Molecule type: DNA  
A:Cross-references: EMBL:X55677; NID:g15084; PTD:CA93202.1; PTD:g16085  
A:Comments: The A-chain, which inhibits protein synthesis by inactivating  
the A and B chains are linked by a disulfide bond, which is essential for toxicity.  
C:Superfamily: ricin, rRNA N-glycosidase, glycosylase  
C:Keywords: duplication; glycoprotein; homology; hydroxylase; lectin; pyroglyutamic acid  
F:125-285/Product: abrin-C chain A #status predicted <RG>  
F:41-280/Domain: rRNA N-glycosidase homology <RG>  
F:255-562/Product: abrin-C chain B #status predicted <RG>  
F:11-359,380-400,403-441,448-481,525-562/Region: 40-residue repeats  
F:306/Motif/Match site: PYRROLIDINE CARBOXYLIC ACID (Glu) (in mature form) #status predicted  
F:199-201/Active site/Match site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:281-287,320-335,435-445/Binding site: N-acetylglucosamine (Asn) (covariant) #status predicted  
F:281-287,320-335,363-380,451-464,490-507/Dissulfide bonds: #status predicted  
F:322,346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted  
F:334,555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

```

Best Local Similarity 46 14, Prod.No. 14e-101,
Matches 242, Conservative 82, Mismatches 190, Indels 11, Gaps 9,

Oy      9  THQTYGKRFYRIILADRYVSSSSNEIPILQSTIPVSNRQPLWELITQKXDSXHA 68
Db      43  TEGATSGSYKQPIALRQRLTGQIHIDIPVLDPPIWESNRRIYITELSNSMESIEV 100

Oy      69  AIDVNNXYVVAQKQSGSPFLRQAPAEHFLFGTETXSSLSFPKSGXSLREYAGH-ED 127
Db      101  GIDVNNXYVVAARSGSPFLRQAPASASYFLFGTQYRSLSEFDSQXGLEMAHQTRE 159

Oy      128  QIFIGIQIQLQSLQXALEPQGSTGRQKARSLILQIMLSBAARENPILWEXQXINSGXSF 187
Db      160  EISLQDALHTHISFEGSSANBEKARKTILYIQLQMSLARRISNRQVSLRTQATF 219

Oy      188  LEPXMTLEHYSNQQSGYQVQSHQYQFNPNKALIXXQNTFLYANRYVSLIANMF 246
Db      220  QPQPMASLENNMNISGQYQGVDFPNNVILSSINQYGVVQSLSHPTAYALAMLF 279

Oy      247  VCGEPSSSDVNPVPIRPIADVTCAS-SEPTVINGXGKAVYEDPDQDFHQMGQO 305
Db      280  VCPN-PPNQS---PILIRSVESKICSSRSEYETRIQGDGMCVYDDGYNHGRIT 335

Oy      306  LMPSSKNPNQMLTEKDXITISNGSCLTAYGTATGYVMIPECKTVEATIQOITAN 365
Db      336  AMKCKDLERQMLTEKSKTISNGKCLITBGVARENVMIYDQSVLEVATYELMEN 395

Oy      366  GITIPNSNULVAASSGKIGTLLTYQVLLDTLYGGGMADNQTAPREVIYGFQDLQESN 425
Db      396  GITIPNSXALVNASSESSMGGLTYQVNLIELMQARMTNAPSFTVTSIGSVDLQCMQO 455

Oy      426  XGSIWATTCSSQSQXKMLYEDQSTIRPQKQOCLYIGEDQSVTINIVSCSXKXQ 485
Db      456  GSNVLDLQNNKREQ-QMLYIDSLSTIRPQKQOCLYIGEDQSVTINIVSCSXKXQ 514

Oy      486  RWTFNEXALNLEKXXXXDYLQAPALPRLRIIYVPAKSPQMWL 530
Db      515  RWLFQNGSIVNLEDMQVWVSSPSPLKSLITLTPFHKGKQVTL 559

```

SEQUIN 7  
S32431  
Abiridin precursor - Indian licofice (fragment)  
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Abrus precatorius (Indian licofice)  
C:Date: 30-Sep-1997 #sequence\_revision 01-Aug-1997 #text\_change 01-Aug-1997  
A:Accession: S32431; S34408  
R:Ring: C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
J. Mol. Biol. 229, 263-267, 1993  
U. Note: Primary structure of three distinct isoforms determined by cDNA sequencing  
A:Accession: S32431; S34425; X01D:9512756; F01D:842313  
A:Molecule type: mRNA  
A:Residues: 1-528 <HUN>  
A:Cross-references: GB:M96346  
R:Ring: C.; Lee, M.; Lee, T.; Lin, J.  
submitted to the EMBL Data Library, March 1993  
A:Reference number: S34408  
A:Accession: S34408  
A:Molecule type: mRNA  
A:Residues: 1-169  
C: 171-330, 'U', 322-528 <HUN>  
A:Cross-references: GB:M96346  
C:Comment: Abirin consists of an A chain, which inhibits protein synthesis by inacti  
The A and B chains are linked by a single disulfide bond, which is essential for  
C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolyase; leu  
A:1-251/Product: abirin-d chain A tetanus predicted <KCH>  
A:1-246/Domian: abrin-N-glycosidase homology <RNO>  
A:1-246/Product: abirin-d chain B tetanus predicted <BCH>  
P:182-223/326/336/367/401/414-449/453-492/495-528/Region: 40-residue repeats  
P:182-223/326/336/367/401/414-449/453-492/495-528/Region: 40-residue repeats  
P:174, 113, 195, 196/Binding site: substrate  
P:164, 187/Active site: Gly, Arg, Ser/Asn predicted  
P:164, 187/Active site: Gly, Arg, Ser/Asn predicted







A:Residues: 1-69, '86, '72-209, 'A, '211-241, 243-250, 'V, '252-263 <RBA>  
 A:Residues: 1-69, '86, '72-209, 'A, '211-241, 243-250, 'V, '252-263 <RBA>  
 C:Superfamily: rRNA N-glycosylase homology  
 C:Keywords: duplication, glycoprotein, glycosylase, hydrolase  
 F:1-263/Product: rRNA B chain B #status experimental <RBA>  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats  
 F:20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 31.48; Score 822; DB 2; Length 263;  
 Best Local Similarity 35.28; Pred. No. 1.8e-71;

Matches 154; Conservative 32; Mismatches 72; Indels 2; Gaps 2;

QY 274 CSASEPTVIRVGRGKXNDVDDPFGKQIQIMPESKNDPQMLTKEKXIRNSGSC 333  
 DB 4 QNDPEFVIRVGRGKXNDVDDPFGKQIQIMPESKNDPQMLTKEKXIRNSGSC 63

QY 334 LTTVGTAGVYVMTFCMTAATATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 393  
 DB 64 LTTVGTAGVYVMTFCMTAATATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 123

QY 394 DYLQGGTLAGMTAPRETTTIGFDDCHESKXSTVETTCSSQXKXALKQGGT 453  
 DB 124 LTVAGGMLFTMTQPTTIVGLKGCCLANSKXVLEDCSEKADQ-QMLKADSGIR 182

QY 454 PRONOGCTKGRDVSIVIVGSCXKXQKRVFTKXKILNKXXXXXDVQAKNP-R 512  
 DB 183 PQNRDNCILTDANKIKGVKILVSCGVSGQKRWKNDGTILNGLVLDVRRSDPS 242

QY 513 LRRIIVPATGKQWMLPV 532  
 DB 243 LKQILVHFRHGNLQMLPL 262

RESULT 12  
 C39761  
 abrin (clone 7.2) precursor - Indian licorice (fragment)  
 N:Contains: rRNA N-glycosylase (EC 3.2.2.22)  
 C:Species: Abrus precatorius (Indian licorice)  
 C:Date: 21-Feb-1992 #sequence revision 31-Dec-1993 #text\_change 20-Aug-1999  
 C:Accession: C39761; S14471  
 R:Accession: G3; Mathiesen, A.; Sundan, A.  
 F:1-263/Product: 263-residue protein  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats  
 F:20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

A:Reference number: A39761; MIMD:9120329; PMID:2016500  
 A:Accession: C39761  
 A:Molecule type: DNA  
 A:Residues: 1-251 <EVE>  
 R:Accession: G3; Mathiesen, A.; Sundan, A.  
 F:1-251/Product: 251-residue protein  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats  
 F:20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

A:Reference number: A39761; MIMD:9120329; PMID:2016500  
 A:Accession: C39761  
 A:Molecule type: DNA  
 A:Residues: 1-251 <EVE>  
 R:Accession: G3; Mathiesen, A.; Sundan, A.  
 F:1-251/Product: 251-residue protein  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats  
 F:20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

A:Reference number: A39761; MIMD:9120329; PMID:2016500  
 A:Accession: C39761  
 A:Molecule type: DNA  
 A:Residues: 1-251 <EVE>  
 R:Accession: G3; Mathiesen, A.; Sundan, A.  
 F:1-251/Product: 251-residue protein  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats  
 F:20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 17.08; Score 443.5; DB 2; Length 251;  
 Best Local Similarity 43.84; Pred. No. 5.6e-35;  
 Matches 106; Conservative 34; Mismatches 97; Indels 5; Gaps 5;

QY 9 THTQXKXFFETLADVYSSGSEFPLRQSTPVSDAQVAVVETNCKXSTVA 68  
 DB 9 THTQXKXFFETLADVYSSGSEFPLRQSTPVSDAQVAVVETNCKXSTVA 66  
 QY 69 AITVTKXVYVAGQDSYFLRNPAGKTHLFTGTKXSLPPGKSYKILERRAH RD 127

DB 67 GIVTNAVYVAGQDSYFLRNPAGKTHLFTGTKXSLPPGKSYKILERRAH RD 125  
 QY 128 QIDELNOLGQVYVMTFCMTAATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 393  
 DB 128 QIDELNOLGQVYVMTFCMTAATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 123  
 QY 128 QIDELNOLGQVYVMTFCMTAATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 393  
 DB 128 QIDELNOLGQVYVMTFCMTAATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 123  
 QY 188 LPTXVMELETSKQSDVQVHSTGVFNNPRLATKXGNFVTLKXV-KVYASLAIMLF 246  
 DB 188 LPTXVMELETSKQSDVQVHSTGVFNNPRLATKXGNFVTLKXV-KVYASLAIMLF 245  
 QY 247 VC 248  
 DB 247 VC 247

RESULT 13  
 J05032  
 Karasurin-B - Trichosanthes kirilowii var. japonica  
 C:Species: Trichosanthes kirilowii var. japonica  
 C:Date: 27-Feb-1997 #sequence revision 27-Feb-1997 #text\_change 23-May-1997  
 C:Accession: J05032  
 R:Accession: J05032; H. Takada, T. Ogihara, Y.  
 F:1-243/Product: 243-residue protein  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats  
 F:20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

A:Reference number: J05032; MIMD:9108848; PMID:8951159  
 A:Accession: J05032  
 A:Molecule type: protein  
 A:Residues: 1-247 <KON>  
 C:Superfamily: rRNA N-glycosylase homology  
 C:Keywords: This protein belongs to type I ribosomal-inactivating proteins which can  
 F:1-243/Product: 243-residue protein  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats  
 F:20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 11.84; Score 109.5; DB 2; Length 247;  
 Best Local Similarity 35.64; Pred. No. 4.6e-22;  
 Matches 85; Conservative 45; Mismatches 96; Indels 13; Gaps 8;

QY 11 TQXKXFFETLADVYSSGSEFPLRQSTPVSDAQVAVVETNCKXSTVA 68  
 DB 11 TQXKXFFETLADVYSSGSEFPLRQSTPVSDAQVAVVETNCKXSTVA 66  
 QY 128 QIDELNOLGQVYVMTFCMTAATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 393  
 DB 128 QIDELNOLGQVYVMTFCMTAATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 123  
 QY 128 QIDELNOLGQVYVMTFCMTAATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 393  
 DB 128 QIDELNOLGQVYVMTFCMTAATATQIMKXGIIINFSNVLTAASGIGKTLTIVQL 123  
 QY 188 LPTXVMELETSKQSDVQVHSTGVFNNPRLATKXGNFVTLKXV-KVYASLAIMLF 246  
 DB 188 LPTXVMELETSKQSDVQVHSTGVFNNPRLATKXGNFVTLKXV-KVYASLAIMLF 245  
 QY 247 VC 248  
 DB 247 VC 247

RESULT 14  
 R1272  
 rRNA N-glycosylase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - (Mongol)  
 N:Accession: rRNA N-glycosylase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - (Mongol)  
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
 C:Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text\_change 23-Mar-2001  
 C:Accession: J05056; A36274; J01059; A36273; J01003  
 R:Accession: J05056; A36274; J01059; A36273; J01003  
 F:1-243/Product: 243-residue protein  
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats  
 F:20-39, 63-80, 151-164, 190-207/Disulfide bonds: #status predicted  
 F:95, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

A:Reference number: J05056; MIMD:9113357; PMID:1992921  
 A:Accession: J05056  
 A:Molecule type: rRNA  
 A:Residues: 1-289 <SHA>  
 A:Cross-references: GB:M34858; NID:G170536; PID:AAA4207.1; PID:G170537  
 A:Experimental source: tuber  
 U:Chow, T.P.; Feldman, R.A.; Lovett, M.; Pitarik, M.  
 U:Biochem. Chem. 265, 8670-8674, 1990  
 A:Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type

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Page 8

A:Reference number: A36274; MUID:90256790; PMID:2341400  
 A:Accession: A36274  
 A:Residues: 232  
 A:Cross-references: GB|J05434; NID:54170834; PID:A044206.1; PID:9170535  
 R.Zhang, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.  
 Acta Genet. Sin. 21, 42-51, 1994  
 A>Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.  
 A:Reference number: JQ1093; MUID:94271613; PMID:8003348  
 A:Accession: JQ1093  
 A:Residues: 197  
 A:Cross-references: GB|S70176; NID:5417148; PIN:ABR1048.1; PID:9547749  
 R.Collins, E.J.; Roberts, J.D.; Lopesteil, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Heath  
 J. Biol. Chem. 265, 8665-8669, 1990  
 A>Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for antibody  
 A:Reference number: A36273; MUID:90256799; PMID:2341399  
 A:Accession: A36273  
 A:Residues: 234-270  
 R.Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z.  
 Pure Appl. Chem. 58, 789-798, 1986  
 A>Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application  
 A:Accession: JUT0003  
 A:Reference number: JUT0003  
 A:Residue type: protein  
 A:Experimental source: tuber  
 R.Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 Submitted to the Brookhaven Protein Data Bank, July 1994  
 A:Reference number: A67091; PDB:IMR1  
 A:Contents: annotation, X-ray crystallography, 1.6 angstroms, with adenine, residues 24-  
 R.Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 Submitted to the Brookhaven Protein Data Bank, July 1994  
 A:Reference number: A67092; PDB:IMR2  
 A:Contents: annotation, X-ray crystallography, 1.6 angstroms, with fermycin, residues 24-  
 R.Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 Submitted to the Brookhaven Protein Data Bank, December 1994  
 A:Reference number: A66711; PDB:1HCS  
 A:Contents: annotation, X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27  
 Naef, Struck, Biol. J., 695-700, 1994  
 R:Xiong, U.P.; Xia, Z.X.; Wang, Y.  
 A>Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re-  
 A:Reference number: A66711; PDB:1HCS  
 A:Contents: annotation, X-ray crystallography, 1.7 angstroms  
 C:Comment: Alpha-trichosanthin has been used to induce abortions.  
 A:Genetics:  
 C:Gene: tes  
 A:Function:  
 A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA thereby  
 A:Substrates: RNA N-glycosylase; RNA N-glycosidase; homology  
 A:Secondary structure: alpha-helix; beta-strand; beta-turn; coiled coil  
 F:1-33/Domain: signal sequence #status predicted <lit>  
 F:34-270/Product: trichosanthin alpha #status experimental <NMT>  
 F:37-266/Domain: rRNA N-glycosidase homology <PNO>  
 F:171-289/Domain: carboxyl-terminal propeptide #status predicted <CP>  
 F:93-186/Active site: Tyr, Glu, Asp #status predicted

Query Match	Similarity	Score	DB 1	Length	DB 2	
B	100%	23	Fasta	22		
Matches	83;	Conservative	49;	Mismatches	54;	
			Indels	13;	Gaps	8;

13 TGEYEFPTITLADYVSSGSFNEPLTGGSTLPVSODGPFVLVELTNOKSDXIAIVP 72  
 33 TSSESQVFISMLRKLPENKRYDIPLR-SGLPSG--GGVALHLTVADVETISAVLV 89  
 07 TNKYVAOAGDDSPFLERD-FRGATSLHTFGTKXSLSPEKSGYZOLERYACH-RDPQP 130  
 90 TNHYVMOHGDDGYIRFESASTSEIKAPYIOWTEAEARNILIMWGXKINSXSTEDP 149  
 111 LGVHQLGVSVAALEKPGSKPKAKRSKLTPIKNTKEARNDILMWGXKINSXSTEDP 190  
 150 LGHPIDDSAITLLFPYNNAN--ASASALVLIQSTBAARKIKIIOGIDKRVKD--FTLPS 205

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OY 131 XYMELEETSGGQGVQV--HSTDGVFENFKLAIKXGNPVTLLNVR--YIASLAIIM 245
DB 206 LAIISLNSMNAISKQIOLASTNNQGFSPVLLIMQONQRTITNDRAGVYSNIAL 264

RESULT 15
J00393
Karasurin - Mongolian snake-gourd
C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C:Name: 30-Sep-1991 sequence revision 30-Sep-1991 @text_change 12-Apr-1995
C:Accession: J00393; E60166 Xaa, Y; Yakubovskiy, K.; Ogihara, Y.
C:Accession: S111363e, 1244-1249, 1091
C:Title: The complete amino acid sequence of an abortifacient protein, Karasurin
A:Reference number: J00393; PMID:92005921, PMID:1914000
A:Accession: J00393
A:Molecule type: Protein
A:Residues: 1-247 <NO>
C:Note: A sequence which lacks Ala-247 is also shown in this publication
C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology
C:Keywords: abortifacient
F:4-243/Domain: RNA N-glycosidase homology <RNG>

Query Match 11.8%; Score 307.5; DB 2; Length 247;
Best Local Similarity 35.6%; Pred. No. 7,2e-22;
Matches 85; Conservative 45; Mismatches 96; Indels 13; Gaps 8;

OY 13 TXKEYPFFITLLPDVYSSGSFSENEITLLROGTFPVSDAGFVYVELTNGQXDSYTAIIDV 72
DB 10 TSSGIVFISLHKKALPYERKLIIDFLNR-STFGSS--QRTALHNLTKADETSLVALDV 66
OY 73 TTXVYVAYAGADGDSYFLADL--PRGAEITLLPTGTGKSLPTFGSDYXDERVYAGH--RQDF 130
DB 67 TTVVYVAGACDSDSYFNEKSKYFAKAYVFQDKKXVTLTPSGNYENRLOIAAGKIRENP 126
OY 131 LGAIKOLGVYALRKRFGSGTRKQKRSIIILIONISEARFNPIIMWRKQXINSKXSTLPD 190
DB 127 LGAPLDSATITLLPTVYNNNS--ASALVALGSTSEMAKRYFISQIQKAKVR--TFLS 162
OY 131 XHMELEETSGGQGVQV--HSTDGVFENFKLAIKXGNPVTLLNVR--YIASLAIIM 245
DB 133 LAIISLNSMNAISKQIOLASTNNQGFETPVLLIMQONQRTITNDRAGVYSNIAL 241

Search completed: December 11, 2003, 13:55:38
Job time : 17.5679 secs

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Search completed: December 11, 2003, 13:55:38  
Job time : 17.5679 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 9.15946 Seconds  
without a removed!

Title: US-09-601-667C-1

Sequence: 1 YERLRVRVTHQTGXEYFRF.....RRITYPATGKPNQMWLPVX 533

Scoring table: BLOSUM62

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of

and is derived by analysis

## SUMMARIES

## SUMMARIES

No.	Score	Query Match	length	DS	ID	Description
1	1390	49.3	264	1	MLB_VITAL	P81830 vitcum alb
2	1331	47.1	578	1	RICI_RICCO	P02879 ricinus sco
3	1183.5	45.2	526	1	ABRA_ABRM	P11140 abrus pree
4	1165.5	44.6	254	1	MLA_VITAL	P81846 vitcum alb
5	1139.5	43.5	562	1	ABRC_ABRM	P28590 abrus pree
6	1113.3	42.5	527	1	ABRB_ABRM	P00617 abrus pree
7	1102.2	41.4	534	1	MGSL_RICCO	P00650 ricinus sco
8	1087.8	40.8	525	1	ABRB_ABRM	P00617 abrus pree
9	322.5	12.3	283	1	RIP2_BERDI	P09188 bromelia
10	368.5	11.8	289	1	RIP1_TREKI	P09989 trichosan
11	307.5	11.1	289	1	RIP5_TREKI	P24478 trichosan
12	291	11.1	286	1	RIP2_MOMBA	P29339 momordica
13	282	10.8	294	1	RIP1_TREND	P56628 trichosan
14	280	10.7	290	1	RIP1_BERDI	P31858 bryonia cl
15	272	10.4	286	1	RIP1_GUDFI	Q97584 cucumis m
16	270	10.3	316	1	RIP3_GELMU	P33186 gelonium f
17	261	10.0	286	1	RIP1_MOMCH	P16094 momordica
18	247	9.4	277	1	RIP4_LUDCY	Q00465 luffa cylin
19	241	9.2	250	1	RIP1_LUDCY	P21257 luffa cylin
20	229	8.8	278	1	RIP1_MIRMA	P21258 mirabilis
21	193.6	7.5	261	1	RIP3_MIRMA	P21353 physalocsa
22	189.2	6.9	218	1	RIP1_MIRMA	Q10397 physalocsa
23	185.2	6.9	253	1	RIP1_SAPOF	Q41139 saponaria
24	157.5	6.0	253	1	RIP5_SAPOF	Q41139 saponaria
25	155.5	5.9	259	1	RIP1_SAPOF	P20656 saponaria
26	155	5.7	292	1	RIP2_SAPOF	P27559 saponaria
27	148.5	5.7	292	1	RIP2_SAPOF	P27559 saponaria
28	136	5.2	310	1	RIP2_PHYM4	Q40772 phyto-laccase
29	128.5	4.9	293	1	RIP1_DYDM	P24476 dianthus c
30	122.5	4.7	236	1	RIP3_SAPOF	P27560 saponaria
31	118.5	4.5	477	1	XYNA_STRLI	P26514 streptocomya
32	116.5	4.5	280	1	RIP1_HORUV	P22244 nordium vuv
33	114	4.4	525	1	SP1_ABRM	Q05305 ratibacora

[illegible]

